SEQUENCE LISTING

<110> CODEXIS, INC.

<120> TRANSGLUTAMINASE VARIANTS

<130> CX2-164USP1

<160> 756

<210> 1
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Streptomyces mobaraensis Transglutaminase with Pro Sequence and C-Terminus His Tag

<400> 1
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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<210> 2
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptomyces mobaraensis Transglutaminase with Pro Sequence and C-Terminus His Tag

<400> 2
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 3
<211> 1011
<212> DNA

<213> Artificial Sequence

<220>
<223> Streptomyces mobaraensis Mature Transglutaminase

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cgtaaatggc aacaggttta ctctcataga gatggtcgta aacaacaaat gacagaagag 180
cagagagagt ggctttctta tggatgcgtt ggagttacgt gggttaattc aggacaatat 240
ccaacgaacc gtcttgcatt tgcttctttt gacgaagacc gttttaaaaa cgagcttaag 300
aatggacgtc ctcgttctgg tgaaactcgt gctgagttcg aaggtagagt tgctaaggaa 360
tctttcgatg aagaaaaagg atttcaaaga gcacgtgaag tagcatctgt aatgaaccgt 420
gcattagaga acgctcatga cgagtcagca tatcttgata accttaagaa ggagcttgca 480
aacggtaatg atgcacttcg taacgaagac gcacgttctc ctttttattc tgcacttaga 540
aatacgcctt ctttcaaaga aagaaatggt ggtaaccatg atccatctag aatgaaagca 600
gttatctatt ctaagcattt ttggtctggt caggatcgtt cttcttcagc tgataaacgt 660
aagtacggtg accctgatgc atttagacca gcacctggaa caggtcttgt tgatatgtca 720
agagaccgta acatcccaag atcacctacg tctccaggtg aaggttttgt aaactttgat 780
tacggatggt ttggagctca gacagaagct gatgcagata agacagtatg gactcatgga 840
aatcattatc acgctcctaa cggttcttta ggtgcaatgc acgtatacga atcaaaattt 900
cgtaactggt ctgaaggata ttctgatttt gatcgtggtg cttacgttat cacttttatt 960
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<210> 4
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptomyces mobaraensis Mature Transglutaminase

<400> 4
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Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala
20 25 30
Glu Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser
35 40 45
His Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp
50 55 60
Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr
65 70 75 80
Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys
85 90 95
Asn Glu Leu Lys Asn Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu
100 105 110
Phe Glu Gly Arg Val Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe
115 120 125
Gln Arg Ala Arg Glu Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn
130 135 140
Ala His Asp Glu Ser Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala
145 150 155 160

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Asn Gly Asn Asp Ala Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr
                165                 170                 175
Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn
            180                 185                 190
His Asp Pro Ser Arg Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp
        195                 200                 205
Ser Gly Gln Asp Arg Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp
    210                 215                 220
Pro Asp Ala Phe Arg Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser
225                 230                 235                 240
Arg Asp Arg Asn Ile Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe
                245                 250                 255
Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala
            260                 265                 270
Asp Lys Thr Val Trp Thr His Gly Asn His Tyr His Ala Pro Asn Gly
        275                 280                 285
Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser
    290                 295                 300
Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile
305                 310                 315                 320
Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro
                325                 330                 335
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<210> 5
<211> 1230
<212> DNA
<213> Artificial Sequence

<220>
<223> Streptomyces mobaraensis Transglutaminase Pro Sequence and Bacillus Megaterium Signal Peptide

<400> 5
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agtgcagttt cttctgttca tgcttctact agtatggaca atggagctgg tgaagaaaca 120
aaatcttatg ctgaaacata tagacttact gcagatgatg tagctaacat caatgcttta 180
aatgaatcag ctcctgctgc atcttctgca ggaccttctt ttagagctcc agattctgat 240
gatagagtaa ctcctcctgc agagcctctt gatagaatgc cagatcctta cagaccatct 300
tatggacgtg ctgaaacagt agttaataac tatattcgta aatggcaaca ggtttactct 360
catagagatg gtcgtaaaca acaaatgaca gaagagcaga gagagtggct ttcttatgga 420
tgcgttggag ttacgtgggt taattcagga caatatccaa cgaaccgtct tgcatttgct 480
tcttttgacg aagaccgttt taaaaacgag cttaagaatg gacgtcctcg ttctggtgaa 540
actcgtgctg agttcgaagg tagagttgct aaggaatctt tcgatgaaga aaaaggattt 600
caaagagcac gtgaagtagc atctgtaatg aaccgtgcat tagagaacgc tcatgacgag 660
tcagcatatc ttgataacct taagaaggag cttgcaaacg gtaatgatgc acttcgtaac 720
gaagacgcac gttctccttt ttattctgca cttagaaata cgccttcttt caaagaaaga 780
aatggtggta accatgatcc atctagaatg aaagcagtta tctattctaa gcatttttgg 840
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agaccagcac ctggaacagg tcttgttgat atgtcaagag accgtaacat cccaagatca 960
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gaagctgatg cagataagac agtatggact catggaaatc attatcacgc tcctaacggt 1080
tctttaggtg caatgcacgt atacgaatca aaatttcgta actggtctga aggatattct 1140
gattttgatc gtggtgctta cgttatcact tttattccaa aatcttggaa tactgcacca 1200
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gataaagtaa agcagggatg gccataatga 1230

<210> 6
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Streptomyces mobaraensis Transglutaminase with Pro Sequence and Bacillus Megaterium Signal Peptide

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

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                325                 330                 335
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly
            340                 345                 350
Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr
        355                 360                 365
Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg
    370                 375                 380
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro
385                 390                 395                 400
Asp Lys Val Lys Gln Gly Trp Pro
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<210> 7
<211> 1230
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 7
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aaatcttatg ctgaaacata tagacttact gcagatgatg tagctaacat caatgcttta 180
aatgaatcag ctcctgctgc atcttctgca ggaccttctt ttagagctcc agattctgat 240
gatagagtaa ctcctcctgc agagcctctt gatagaatgc cagatcctta cagaccatct 300
tatggacgtg ctgaaacagt agttaataac tatattcgta aatggcaaca ggtttactct 360
catagagatg gtcgtaaaca acaaatgaca gaagagcaga gagagtggct ttcttatgga 420
tgcgttggag ttacgtgggt taattcagga caatatccaa cgaaccgtct tgcatttgct 480
tcttttgacg aagaccgttt taaaaacgag cttaagaatg gacgtcctcg ttctggtgaa 540
actcgtgctg agttcgaagg tagagttgct aaggaatctt tcgatgaaga aaaaggattt 600
caaagagcac gtgaagtagc atctgtaatg aaccgtgcat tagagaacgc tcatgacgag 660
tcagcatatc ttgataacct taagaaggag cttgcaaacg gtaatgatgc acttcgtaac 720
gaagacgcac gttctccttt ttattctgca cttagaaata cgccttcttt caaagaaaga 780
aatggtggta accatgatcc atctagaatg aaagcagtta tctattctaa gcatttttgg 840
tctggtcagg atcgttcttc ttcagctgat aaacgtaagt acggtgaccc tgatgcattt 900
agaccagcac ctggaacagg tcttgttgat atgtcaagag accgtaacat cccaagatca 960
cctacgtctc caggtgaacg ttttgtaaac tttgattacg gatggtttgg agctcagaca 1020
gaagctgatg cagataagac agtatggact catggaaatc attatcacgc tcctaacggt 1080
tctttaggtg caatgcacgt atacgaatca aaatttcgta actggtctga aggatattct 1140
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<210> 8
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 8

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Met Asn Ile Lys Arg Trp Leu Leu Thr Ala Thr Thr Val Ile Leu Ala
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Thr Phe Gly Val Ser Ala Val Ser Ser Val His Ala Ser Thr Ser Met
            20                  25                  30
Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr Arg
        35                  40                  45
Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser Ala
    50                  55                  60
Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp
65                  70                  75                  80
Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro
                85                  90                  95
Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile
            100                 105                 110
Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln
        115                 120                 125
Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val
    130                 135                 140
Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala
145                 150                 155                 160
Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro
                165                 170                 175
Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu
            180                 185                 190
Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser
        195                 200                 205
Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu
    210                 215                 220
Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn
225                 230                 235                 240
Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser
                245                 250                 255
Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala
            260                 265                 270
Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser
        275                 280                 285
Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro
    290                 295                 300
Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser
305                 310                 315                 320
Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp Phe
                325                 330                 335
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly
            340                 345                 350
Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr
        355                 360                 365
Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg
    370                 375                 380
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro
385                 390                 395                 400
Asp Lys Val Lys Gln Gly Trp Pro
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<210> 9
<211> 1230
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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aaatcttatg ctgaaacata tagacttact gcagatgatg tagctaacat caatgcttta 180
aatgaatcag ctcctgctgc atcttctgca ggaccttctt ttagagctcc agattctgat 240
gatagagtaa ctcctcctgc agagcctctt gatagaatgc cagatccgta cagaccatct 300
ggaggacgtg ctgaaacagt agttaataac tatattcgta aatggcaaca ggtttactct 360
catagagatg gtcgtaaaca acaaatgaca gaagagcaga gagagtggct ttcttatgga 420
tgcgttggag ttacgtgggt taattcagga caatatccaa cgaaccgtct tgcatttgct 480
tcttttgacg aagaccgttt taaaaacgag cttaagaatg gacgtcctcg ttctggtgaa 540
actcgtgctg agttcgaagg tagagttgct aaggaatctt tcgatgaaga aaaaggattt 600
aaaagagcac gtgaagtagc atctgtaatg aacaaagcat tagagaacgc tcatgacgag 660
tcagcatatc ttgataacct taagaaggag cttgcaaacg gtaatgatgc acttcgtaac 720
gaagacgcgc gttctccttt ttattctgca cttagaaata cgccttcttt caaagaaaga 780
aatggtggta accatgatcc atctagaatg aaagcagtta tctattctaa gcatttttgg 840
tctggtcagg atcggtctgg ctcagctgat aaacgtaagt acggtgaccc tgatgcattt 900
agaccagcac ctggaacagg tcttgttgat atgtcaagag accgtaacat cccaagatca 960
cctacgtctc caggtgaagg ttttgtaaac tttgattacg gatggtttgg agctcagaca 1020
gaagctgatg cagataagac agtatggact catggaaatc attatcacgc tcctaacggt 1080
tctttaggtg caatgcacgt atacgaatca aaatttcgta actggtctga aggatattcg 1140
gattttgatc gtggtgctta cgttatcact tttattccaa aatcttggaa tactgcacca 1200
gataaagtaa agcagggatg gccataatga   1230

<210> 10
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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            100                 105                 110
Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln
        115                 120                 125
Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val
    130                 135                 140
Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala
145                 150                 155                 160
Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro
                165                 170                 175
Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu
            180                 185                 190
Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala Ser
        195                 200                 205
Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu
    210                 215                 220
Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn
225                 230                 235                 240
Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser
                245                 250                 255
Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala
            260                 265                 270
Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly Ser
        275                 280                 285
Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro
    290                 295                 300
Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser
305                 310                 315                 320
Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe
                325                 330                 335
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly
            340                 345                 350
Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr
        355                 360                 365
Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg
    370                 375                 380
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro
385                 390                 395                 400
Asp Lys Val Lys Gln Gly Trp Pro
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<210> 11
<211> 1230
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 11
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aaatcttatg ctgaaacata tagacttact gcagatgatg tagctaacat caatgcttta 180
aatgaatcag ctcctgctgc atcttctgca ggaccttctt ttagagctcc agattctgat 240

gatagagtaa ctcctcctgc agagcctctt gatagaatgc cagatccgta cagaccatct 300
ggaggacgtg ctgaaacagt agttaataac tatattcgta aatggcaaca ggtttactct 360
catagagatg gtcgtaaaca acaaatgaca gaagagcaga gagagtggct ttcttatgga 420
tgcgttggag ttacgtgggt taattcagga caatatccaa cgaaccgtct tgcatttgct 480
tcttttgacg aagaccgttt taaaaacgag cttaagaatg gacgtcctcg ttctggtgaa 540
actcgtgctg agttcgaagg tagagttgct aaggaatctt tcgatgaaga aaaaggattt 600
caaagagcac gtgaagtagc atctgtaatg aaccgtgcat tagagaacgc tcatgacgag 660
tcagcatatc ttgataacct taagaaggag cttgcaaacg gtaatgatgc acttcgtaac 720
gaagacgcac gttctccttt ttattctgca cttagaaata cgccttcttt caaagaaaga 780
aatggtggta accatgatcc atctagaatg aaagcagtta tctattctaa gcatttttgg 840
tctggtcagg atcggtctgg ctcagctgat aaacgtaagt acggtgaccc tgatgcattt 900
agaccagcac ctggaacagg tcttgttgat atgtcaagag accgtaacat cccaagatca 960
cctacgtctc caggtgaagg ttttgtaaac tttgattacg gatggtttgg agctcagaca 1020
gaagctgatg cagataagac agtatggact catggaaatc attatcacgc tcctaacggt 1080
tctttaggtg cgatgcacgt atacgaatca aaatttcgta actggtctga aggatattct 1140
gattttgatc gtggtgctta cgttatcact tttattccaa aatcttggaa tactgcacca 1200
gataaagtaa agcagggatg gccataatga 1230

<210> 12
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu
    210                 215                 220
Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn
225                 230                 235                 240
Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser
                245                 250                 255
Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala
            260                 265                 270
Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly Ser
        275                 280                 285
Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro
    290                 295                 300
Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser
305                 310                 315                 320
Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe
                325                 330                 335
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly
            340                 345                 350
Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr
        355                 360                 365
Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg
    370                 375                 380
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro
385                 390                 395                 400
Asp Lys Val Lys Gln Gly Trp Pro
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<210> 13
<211> 1230
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 13
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aaatcttatg ctgaaacata tagacttact gcagatgatg tagctaacat caatgcttta 180
aatgaatcag ctcctgctgc atcttctgca ggaccttctt ttagagctcc agataaagat 240
gatagagtaa ctcctcctgc agagcctctt gatagaatgc cagatcctta cagaccatct 300
tatggacgtg ctgaaacagt agttaataac tatattcgta aatggcaaca ggtttactct 360
catagagatg gtcgtaaaca acaaatgaca gaagagcaga gagagtggct ttcttatgga 420
tgcgttggag ttacgtgggt taattcagga caatatccaa cgaaccgtct tgcatttgct 480
tcttttgacg aagaccgttt taaaaacgag cttaagaatg gacgtcctcg ttctggtgaa 540
actcgtgctg agttcgaagg tagagttgct aaggaatctt tcgatgaaga aaaaggattt 600
caaagagcac gtgaagtagc atctgtaatg aaccgtgcat tagagaacgc tcatgacgag 660
tcagcatatc ttgataacct taagaaggag cttgcaaacg gtaatgatgc acttcgtaac 720
gaagacgcac gttctccttt ttattctgca cttagaaata cgccttcttt caaagaaaga 780
aatggtggta accatgatcc atctagaatg aaagcagtta tctattctaa gcatttttgg 840
tctggtcagg atcgttcttc ttcagctgat aaacgtaagt acggtgaccc tgatgcattt 900
agaccagcac ctggaacagg tcttgttgat atgtcaagag accgtaacat cccaagatca 960
cctacgtctc caggtgaagg ttttgtaaac tttgattacg gatggtttgg agctcagaca 1020
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gaagctgatg cagataagac agtatggact catggaaatc attatcacgc tcctaacggt 1080
tctttaggtg caatgcacgt atacgaatca aaatttcgta actggtctga aggatattct 1140
gattttgatc gtggtgctta cgttatcact tttattccaa aatcttggaa tactgcacca 1200
gataaagtaa agcagggatg gccataatga 1230

<210> 14
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 14
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Thr Phe Gly Val Ser Ala Val Ser Ser Val His Ala Ser Thr Ser Met
20 25 30
Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr Arg
35 40 45
Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser Ala
50 55 60
Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys Asp
65 70 75 80
Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro
85 90 95
Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile
100 105 110
Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln
115 120 125
Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val
130 135 140
Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala
145 150 155 160
Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro
165 170 175
Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu
180 185 190
Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser
195 200 205
Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu
210 215 220
Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn
225 230 235 240
Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser
245 250 255
Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala
260 265 270
Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser
275 280 285
Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro
290 295 300
Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser

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305                 310                 315                 320
Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe
                325                 330                 335
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly
            340                 345                 350
Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr
        355                 360                 365
Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg
    370                 375                 380
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro
385                 390                 395                 400
Asp Lys Val Lys Gln Gly Trp Pro
                405
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<210> 15
<211> 1230
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 15
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aaatcttatg ctgaaacata tagacttact gcagatgatg tagctaacat caatgcttta 180
aatgaatcag ctcctgctgc atcttctgca ggaccttctt ttagagctcc agattctgat 240
gatagagtaa ctcctcctgc agagcctctt gatagaatgc cagatccgta cagaccatct 300
ggaggacgtg ctgaaacagt agttaataac tatattcgta aatggcaaca ggtttactct 360
catagagatg gtcgtaaaca acaaatgaca gaagagcaga gagagtggct ttcttatgga 420
tgcgttggag ttacgtgggt taattcagga caatatccaa cgaaccgtct tgcatttgct 480
tcttttgacg aagacagatt taaaaacgaa cttaagaatg gacgtcctcg ttctggtgaa 540
actcgtgctg agttcgaagg tagagttgct aaggaatctt tcgatgaaga aaaaggattt 600
aaaagagcac gtgaagtagc atctgtaatg aaccgtgcat tagagaacgc tcatgacgag 660
tcagcatatc ttgataacct taagaaggag cttgcaaacg gtaatgatgc acttcgtaac 720
gaagacgcgc gttctccttt ttattctgca cttagaaata cgccttcttt caaagaaaga 780
aatggtggta accatgatcc atctagaatg aaagcagtta tctattctaa gcatttttgg 840
tctggtcagg atcagtctag ctcagctgat aaacgtaagt acggtgaccc tgatgcattt 900
agaccagcac ctggaacagg tcttgttgat atgtcaagag accgtaacat cccaagatca 960
cctacgtctc caggtgaagg ttttgtaaac tttgattacg gatggtttgg agctcagaca 1020
gaagctgatg cagataagac agtatggact catggaaatc attatcacgc tcctaacggt 1080
tctttaggtg cgatgcacgt atacgaatca aaatttcgta actggtctga aggatattcg 1140
gattttgatc gtggtgctta cgttatcact tttattccaa aatcttggaa tactgcacca 1200
gataaagtaa agcagggatg gccataatga                                  1230
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<210> 16
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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1   5   10   15
Thr Phe Gly Val Ser Ala Val Ser Ser Val His Ala Ser Thr Ser Met
            20   25   30
Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr Arg
        35   40   45
Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser Ala
    50   55   60
Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp
65   70   75   80
Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro
                85   90   95
Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile
            100   105   110
Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln
        115   120   125
Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val
    130   135   140
Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala
145   150   155   160
Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro
                165   170   175
Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu
            180   185   190
Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala Ser
        195   200   205
Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu
    210   215   220
Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn
225   230   235   240
Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser
                245   250   255
Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala
            260   265   270
Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser Ser
        275   280   285
Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro
    290   295   300
Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser
305   310   315   320
Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe
                325   330   335
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly
            340   345   350
Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr
        355   360   365
Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg
    370   375   380
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro
385   390   395   400
Asp Lys Val Lys Gln Gly Trp Pro
                405

<210> 17
<211> 1230
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 17
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agtgcagttt cttctgttca tgcttctact agtatggaca atggagctgg tgaagaaaca 120
aaatcttatg ctgaaacata tagacttact gcagatgatg tagctaacat caatgcttta 180
aatgaatcag ctcctgctgc atcttctgca ggaccttctt ttagagctcc agattctgat 240
gatagagtaa ctcctcctgc agagcctctt gatagaatgc cagatcctta cagaccatct 300
ggtggacgtg ctgaaacagt agttaataac tatattcgta aatggcaaca ggtttactct 360
catagagatg gtcgtaaaca acaaatgaca gaagagcaga gagagtggct ttcttatgga 420
tgcgttggag ttacgtgggt taattcagga caatatccaa cgaaccgtct tgcatttgct 480
tcttttgacg aagaccgttt taaaaacgag cttaagaatg gacgtcctcg ttctggtgaa 540
actcgtgctg agttcgaagg tagagttgct aaggaatctt tcgatgaaga aaaaggattt 600
caaagagcac gtgaagtagc atctgtaatg aaccgtgcat tagagaacgc tcatgacgag 660
tcagcatatc ttgataacct taagaaggag cttgcaaacg gtaatgatgc acttcgtaac 720
gaagacgcac gttctccttt ttattctgca cttagaaata cgccttcttt caaagaaaga 780
aatggtggta accatgatcc atctagaatg aaagcagtta tctattctaa gcatttttgg 840
tctggtcagg atcgttcttc ttcagctgat aaacgtaagt acggtgaccc tgatgcattt 900
agaccagcac ctggaacagg tcttgttgat atgtcaagag accgtaacat cccaagatca 960
cctacgtctc caggtgaagg ttttgtaaac tttgattacg gatggtttgg agctcagaca 1020
gaagctgatg cagataagac agtatggact catggaaatc attatcacgc tcctaacggt 1080
tctttaggtg caatgcacgt atacgaatca aaatttcgta actggtctga aggatattct 1140
gattttgatc gtggtgctta cgttatcact tttattccaa aatcttggaa tactgcacca 1200
gataaagtaa agcagggatg gccataatga   1230

<210> 18
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 18
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1   5   10   15
Thr Phe Gly Val Ser Ala Val Ser Ser Val His Ala Ser Thr Ser Met
            20   25   30
Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr Arg
        35   40   45
Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser Ala
    50   55   60
Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp
65   70   75   80
Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro

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                85                  90                  95
Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile
            100                 105                 110
Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln
        115                 120                 125
Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val
    130                 135                 140
Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala
145                 150                 155                 160
Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro
                165                 170                 175
Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu
            180                 185                 190
Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser
        195                 200                 205
Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu
    210                 215                 220
Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn
225                 230                 235                 240
Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser
                245                 250                 255
Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala
            260                 265                 270
Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser
        275                 280                 285
Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro
    290                 295                 300
Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser
305                 310                 315                 320
Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe
                325                 330                 335
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly
            340                 345                 350
Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr
        355                 360                 365
Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg
    370                 375                 380
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro
385                 390                 395                 400
Asp Lys Val Lys Gln Gly Trp Pro
                405
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<210> 19
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 19
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 20
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 21
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 21
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agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca ttag 1164

<210> 22
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 22
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp

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            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 23
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 23
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 24
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 24
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 25
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 25
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 26
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 27
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 27
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960

ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 28
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 29
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 29
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 30
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 30
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 31
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 31
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga acctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 32
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 32
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160

Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 33
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 33
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780

cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca ttag 1164

<210> 34
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 34
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285

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Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 35
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 35
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca ttag                                       1164
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<210> 36
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 36
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 37

<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 37
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 38
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 39
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 40
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 41
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 41
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
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aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 42
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 42
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 43
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 43
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 44
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 44
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly

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            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 45
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 45
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360

tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 46
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 46
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240

Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 47
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 47
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 48
<211> 387

<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 48
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His

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    370                 375                 380
His His His
385


<210> 49
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 49
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164

<210> 50
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 50
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 51
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 51
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 52
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 52
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro

```
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 53
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 53
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 54
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 54
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350

Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 55
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 55
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 56
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 56
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp

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    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 57
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 57

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 58
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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

<210> 59
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 59
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020

tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 60
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 61
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 61
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 62
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 62
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 63
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 63
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 64
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 64
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala

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                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 65
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 65

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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 66
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 66
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

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Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 67
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 67
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagttc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 68
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 68
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 69
<211> 1164
<212> DNA

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 69
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 70
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 71
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 71
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 72
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 72
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg

```
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 73
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 73
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 74
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 74
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 75
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 75
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 76
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 76
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe

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        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 77
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 77
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480

gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagttc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 78
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 79
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 79
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 80
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 80
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His

385

<210> 81
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 81
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 82
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 82
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 83
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 83
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300

gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 84
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 84
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys

225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 85
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 85
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 86

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 86
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Ala Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 87
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 87
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 88
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 88
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr

65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 89
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 89
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagggc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 90
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 91
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 91

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca ttag 1164

<210> 92
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 92
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp

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            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 93
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 93

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 94
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 94

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 95
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 95
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 96
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 96
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr

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            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 97
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 97
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 98
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 99
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 99

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagggc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 100
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 100

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Gly Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 101
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 101
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 102
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 102
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160

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Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 103
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 103
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 104
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 104
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp

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    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 105
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 105
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagttc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 106
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 106

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 107
<211> 1164

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 107
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 108
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 108
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Ala Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg

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    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 109
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 109
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag aattgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg atgtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatctcg ataaccttaa gaaggagctt 600

gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 110
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 111
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 111
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg atgtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 112
<211> 387
<212> PRT
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 112
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Asp Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 113
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 113
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg atgtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 114
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 114
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

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Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Asp Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 115
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 115
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420

aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 116
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 117
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 117

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg atgtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 118
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 118
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Asp Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 119
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 119
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagttc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 120
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 121
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 121
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240

attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctcactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 122
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 123
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 123

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 124
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 124
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala

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        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 125
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 125
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 126
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 126
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
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Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 127
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 127
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 128
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 128
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg

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        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 129
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 129
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 130
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 131
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 131

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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ggccaccatc accatcacca ttag                                       1164
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<210> 132
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 132

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
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        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 133
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 133
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagggc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 134
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 134
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Gly Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 135
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 135
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 136
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 137
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 137
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg atgtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagggc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
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tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 138
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 138
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Asp Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Gly Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 139
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 139
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 140
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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

<210> 141
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 141
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgcta cgacagtagt taataactat 240
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg atgtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720

gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
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tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
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<210> 142
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 142
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Asp Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
275 280 285

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Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 143
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 143
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
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ggccaccatc accatcacca ttag                                       1164
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<210> 144
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 145

<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg atgtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca ttag 1164

<210> 146
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Asp Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 147
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag aattgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
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ggccaccatc accatcacca ttag 1164

<210> 148
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 149
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 149
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
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aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
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gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 150
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 151
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 152
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 152
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Ala Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly

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            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Ile Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 153
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 153
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360

tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag aattgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 154
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

```
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 155
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 155
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 156
<211> 387

<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 156
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His

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    370                 375                 380
His His His
385


<210> 157
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 157
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164

<210> 158
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 158
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 159
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 159
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 160
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

```
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 161
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 161

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag aattgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagggc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 162
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 162
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Ile Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Gly Ala Tyr
            180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340 345 350

Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 163
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 163
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 164
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 164
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp

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    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 165
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 165

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 166
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 167
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 167

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 168
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 169
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 169

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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctctc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 170
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 170

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Leu Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 171
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 171
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 172
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 172
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala

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                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 173
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 173
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
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tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
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ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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ggccaccatc accatcacca ttag 1164

<210> 174
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 174
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20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Gly Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 175
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 175
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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ggccaccatc accatcacca ttag 1164

<210> 176
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 176
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr

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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 177
<211> 1164
<212> DNA

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 177
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 178
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 179
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 179
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agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag aattgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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tttcgtaact ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca ttag 1164

<210> 180
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 181
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 181

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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
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<210> 182
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 182
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            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 183
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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agaatgccag atccttaccg tccatctaac ggacgtgctg aaacagtagt taataactat 240
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagttc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 184
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 184
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Asn Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe

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        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 185
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg tccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480

gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 186
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 186
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 187
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 187
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca ttag                                       1164
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<210> 188
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 188
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His

385

<210> 189
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 189
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 190
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 190
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 191
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300

gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
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cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
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gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 192
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 192
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Asp Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys

225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 193
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg tccatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca ttag 1164

<210> 194

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 194
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 195
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 195
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 196
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 197
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 197
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120

ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 198
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 198
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195 200 205

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Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 199
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 199
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctaac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca ttag 1164

<210> 200
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 201
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 201

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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 202
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 202

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 203
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 203
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 204
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 204
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr

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            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 205
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960

ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 206
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 207
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 207
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 208
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 208
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 209
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 209
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 210
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 211
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 211
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg tccatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 212
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

```
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 213
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 213
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctaac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtc atgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtacttc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 214
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 214

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Asn Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg His Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Leu Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 215
<211> 1164

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 215
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 216
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

```
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 217
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 217

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
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gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 218
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 219
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 219
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 220
<211> 387
<212> PRT
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 220
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 221
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 221
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 222
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 222
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

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Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 223
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 223
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420

aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 224
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 224
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly

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                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 225
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 225

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 226
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 226
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 227
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 227
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag aattgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtcgctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 228
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 228
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln

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                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Ile Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Arg Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 229
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 229
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240

attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 230
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 231
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 231
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 232
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 232
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala

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        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 233
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 233
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 234
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 234
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
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Pro Tyr Arg Ala Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 235
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 235
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 236
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 236
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg

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        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 237
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 237
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 238
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 238
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335

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Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 239
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 239
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctgac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttaaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 240
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 240
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
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        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Asp Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Lys Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 241
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 241
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 242
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 242
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 243
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 243
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc ggtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaattatt tgtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 244
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 244
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Leu Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His

305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 245
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 245
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag agcgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gtagctcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 246
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 246
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Ala Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 247
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 247
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
agagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtacttc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 248
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 248
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys

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

<210> 249
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 249
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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctaac ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720

gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca ttag 1164

<210> 250
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 251
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 251

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accgtcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagagc gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 252
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 252
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 253

<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga tgttgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact gggaggaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 254
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Glu Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 255
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 255
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 256
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 256
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala

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            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 257
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 257
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ccttctttta gagctccaga taaggatgca agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 258
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 258
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 259
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 259
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct catggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 260
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 260
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly

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            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser His Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 261
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 261

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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
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tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ccaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 262
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 262
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240

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Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Pro Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 263
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 263
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcaa agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a          1131
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<210> 264
<211> 387

<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 264
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Gln Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His

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    370                 375                 380
His His His
385


<210> 265
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 265
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcttgggat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a          1131


<210> 266
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 266
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Trp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 267
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 267
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct gttggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 268
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 268
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro

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    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 269
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 269

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ccttctttta gagctccaga taaggatttt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a          1131
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<210> 270
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 271
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 271
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgaggccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a   1131

<210> 272
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 272
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp

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    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 273
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 273

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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct tgttctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 274
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 274
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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

<210> 275
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 275
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttat ttaggtgcaa tgcacgtata cgaatcaaaa 1020

tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 276
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 276
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Tyr Leu Gly Ala Met His Val

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                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 277
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 277
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct aggggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a          1131
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<210> 278
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 278
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Arg Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 279
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 279
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ccttctttta gagctccaga taaggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggtcat ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 280
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 280
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala

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                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly His Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 281
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 281
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ccttctttta gagctccaga taagtatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 282
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 282
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Tyr Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

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Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 283
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 283

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcttgggct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 284
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 284

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Trp Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
```

<210> 285
<211> 1164

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 285
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcttacgct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct tgccgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatagcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 286
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 286
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Tyr Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125

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Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Cys Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 287
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 287
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 288
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 288
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala

```
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 289
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 289
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcttgggct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 290
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 290
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Trp Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His

385

<210> 291
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 291
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 292
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 292
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 293
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 293
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 294
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 294
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys

225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 295
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 295
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcttggcga agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgagcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttat gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatagcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 296
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 296
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Trp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Tyr Val Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala

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        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 297
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 297
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctcattttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtactgc agggatggcc a   1131

<210> 298
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 298
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
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Pro Tyr Glu Pro Ser Gly Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Leu Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 299
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 299
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60

gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcttgggct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgagcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg cttggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatcgcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 300
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 300
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Trp Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Arg Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 301
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 301

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 302
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 302
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val

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                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
```

<210> 303
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 303

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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a          1131
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<210> 304
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 304

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 305
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 305
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 306
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 306
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala

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                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 307
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 307
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840

tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 308
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 308
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
290 295 300

Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 309
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 309
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 310
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 310
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr

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1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 311
<211> 1164
<212> DNA

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 311
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttat cctggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatagcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 312
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 312
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg

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    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Tyr Pro Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 313
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 313
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
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gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctcattttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 314
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 314
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270

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Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 315
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 315
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcgggtgct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg cctggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 316
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 316
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Gly Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Pro Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 317
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 317
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 318
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 318
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly

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            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 319
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 319
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360

tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtactgc agggatggcc a 1131

<210> 320
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

```
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Leu Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 321
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 321
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a          1131
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<210> 322
<211> 387

<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 322
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His

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    370                 375                 380
His His His
385


<210> 323
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 323
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtactgc agggatggcc a          1131


<210> 324
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 324
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Leu Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 325
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 325
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 326
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 326
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro

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    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 327
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 327

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ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a          1131
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<210> 328
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 328
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350

Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 329
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 329
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gatgatgtag ctaacatcag cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtactgc agggatggcc a   1131

<210> 330
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 330
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Ser Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp

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    50                  55                  60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Leu Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 331
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 331

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ccttctttta gagctccaga taaatgggct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatagcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcaccc ttag 1164

<210> 332
<211> 393
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 332
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Trp Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr

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            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His Pro His His His His His His
385                 390
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<210> 333
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 333
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcattttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 334
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 334
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 335
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 335
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ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a          1131
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<210> 336
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 336
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Ser Ala Leu Asn Glu Ser
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 337
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 337
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 338
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 338
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160

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Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 339
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 339
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg gccatctgga ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 340
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 341
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 341

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a          1131
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<210> 342
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 342

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 343
<211> 1131

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 343
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcattttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 344
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 344
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg

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    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 345
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 345

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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
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gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 346
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 346
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270

Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 347
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 347
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ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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<210> 348
<211> 387
<212> PRT
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 348

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Ser Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 349
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 349
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agaatgccag atccttacga gccatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 350
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 350
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

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Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 351
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 351
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420

aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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<210> 352
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 352
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Ser Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser

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                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 353
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 353

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ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
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tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 354
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 354
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 355
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 355
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg gccatcttat ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
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aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 356
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 356
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln

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                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 357
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 357
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgctg agacagtagt taataactat 240

attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 358
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 358
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220

Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 359
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 359
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 360
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 360
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala

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        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 361
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 361
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a          1131
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<210> 362
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 362
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
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Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 363
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 363
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg gccatctgga ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 364
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 364
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg

```
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 365
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 365
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 366
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 366
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335

Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 367
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 367
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gatgatgtag ctaacatcag cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtactgc agggatggcc a   1131

<210> 368
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 368
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Ser Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val

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        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Leu Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 369
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 369
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 370
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 370
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 371
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 371
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 372
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 372
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His

305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 373
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 373
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 374
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 374
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 375
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 375
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 376
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 376
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys

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

<210> 377
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 377
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720

gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 378
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 378
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285

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Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 379
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 379

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ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 380
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 380
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 381

<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 381
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 382
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 382
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125

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Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 383
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 383

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
```

cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtactgc agggatggcc a 1131

<210> 384
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 384
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala

```
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Leu Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 385
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 385
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a          1131
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<210> 386
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 386
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 387
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 387
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg gccatcttat ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctcatttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 388
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 388
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly

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            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser His Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 389
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 389
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga gccatctgga ggacgtgctg agacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
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tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 390
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 390
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240

```
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 391
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 391
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttcttaccaa agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 392

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 392
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Tyr Gln Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 393
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 393
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttat gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 394
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 394
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60

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Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Tyr Val Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 395
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 395
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ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc gagatcacct acgagtccag gtcgtggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taatggtagc ttaggtccga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 396
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 396
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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

<210> 397
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 397
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaatgggct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020

tttcgtaggt ggtctcacgg atatcgcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 398
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 398
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Trp Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Arg Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 399
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 399

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ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a          1131
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<210> 400
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 400

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 401
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 401
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ccttctttta gagctccaga taaaggggct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatagcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 402
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 402
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Gly Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys

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

<210> 403
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 403
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720

gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 404
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 404
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285

Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 405
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 405
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatcgcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 406
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 406
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Arg Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 407
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 407
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 408
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 408
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe

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        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 409
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 409
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480

gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 410
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 410
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 411
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 411

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagggcaa agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatcgcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 412
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 412
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Gly Gln Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Arg Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 413
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 413
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatcgcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 414
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 414
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80

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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Arg Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 415
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 415
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 416
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 416
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205

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Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 417
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 417
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a          1131
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<210> 418
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 418
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp

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            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 419
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 419

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttat cctggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 420
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 420

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
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        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Tyr Pro Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 421
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 421
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 422
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 422
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 423
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 423
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga tgccgatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgaaaccag gtgagggtta tgtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 424
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 424
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ala
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Ser Arg
275 280 285
Ser Pro Thr Lys Pro Gly Glu Gly Tyr Val Asn Phe Asp Tyr Gly Trp
290 295 300

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Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 425
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 425
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
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ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttaccg accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a          1131
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<210> 426
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 426
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
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1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 427
<211> 1131
<212> DNA

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 427
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtagatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 428
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 428
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140

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

<210> 429
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 429
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgcta cgacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660

agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a 1131

<210> 430
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 430
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg

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        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 431
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 431
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a          1131
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<210> 432
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 432
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 433
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 433
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 434
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 434
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe

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        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 435
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 435
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ccttctttta gagctccaga taaagatgct agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480

gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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<210> 436
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 436
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Ala Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser

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                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 437
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 437

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ccttctttta gatcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc tgaaggtagc ttaggtgcga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 438
<211> 387

<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 438
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ser Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Lys Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Glu Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His

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    370                 375                 380
His His His
385


<210> 439
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 439
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgcgcccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164


<210> 440
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 440
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
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65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Arg Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 441
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 441
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ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgagggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 442
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 442
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg

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        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Glu Gly Ser Leu Gly Pro Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 443
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 443
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aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
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gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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tttcgtaggt ggtctcacgg atatcgcgat tttgatcgtg gtgcttacgt tatcactttt 1080
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 444
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 444
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Val Gly Ala Met His Val

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                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Arg Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 445
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 445
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agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
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tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
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ggaaatcatt atcacgctcc taatggtagc ttaggtccga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 446
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 446
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Pro Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 447
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 447
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttcg gtcggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 448
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 448
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys

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

<210> 449
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 449
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga tgccgatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720

gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgtctccag gtgagggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc tgaaggtagc ttaggtccga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 450
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 450
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ala
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Ser Arg

```
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Tyr Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Glu Gly Ser Leu Gly Pro Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 451
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 451
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a          1131
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<210> 452
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 452
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 453
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 453
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc a 1131

<210> 454
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 454
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe

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        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 455
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 455
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga tgccgatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480

gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 456
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 456
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ala
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser

```
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 457
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 457

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga tgccgatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc gagatcacct acgaaaccag gtgagggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 458
<211> 387

<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 458
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ala
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Lys Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His

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    370                 375                 380
His His His
385


<210> 459
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 459
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164


<210> 460
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 460
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
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65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Ser Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 461
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 461
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120

ccttctttta gagcgccaga tgccgatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacg gtaacatccc gagatcacct acgaaaccag gtgagggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtccga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 462
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 462
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ala
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg

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        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Gly Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Lys Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Pro Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 463
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 463
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gatcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgagtccag gtgagggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc tgaaggtagc ttaggtccga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 464
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 464
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ser Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Ser Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Glu Gly Ser Leu Gly Pro Met His Val

```
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 465
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 465
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgagtccag gtcgtggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 466
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 466
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
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            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Ser Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Arg Gly Tyr Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 467
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 467
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgaaaccag gtgagggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 468
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 468
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys

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

<210> 469
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 469
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720

gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc gagatcacct acgaaaccag gtgagggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 470
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 470
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg

```
        275                 280                 285
Ser Pro Thr Lys Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 471
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 471
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc a          1131
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<210> 472
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 472
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 473
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 473
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc gagatcacct acgagtccag gtcgtggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 474
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 474
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

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Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Arg Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 475
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 475
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga tgccgatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
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aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgaaaccag gtgagggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 476
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 476
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ala
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240

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Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Lys Pro Gly Glu Gly Tyr Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 477
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 477
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc gagatcacct acgaaaccag gtgagggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 478

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 478
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Lys Pro Gly Glu Gly Tyr Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 479
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 479
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc gagatcacct acgagtccag gtgagggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc tgaaggtagc ttaggtgcga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag   1164

<210> 480
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 480
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60

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Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Tyr Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Glu Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 481
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 481
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60

gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgaaaccag gtcgtggtta tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcga tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 482
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 482
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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

<210> 483
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 483
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgagtccag gtgagggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taatggtggc ttaggtccga tgcacgtata cgaatcaaaa 1020

tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 484
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 484
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Ser Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Gly Leu Gly Pro Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 485
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 485

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagcgccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatctc gagatcacct acgaaaccag gtgagggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag                                       1164
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<210> 486
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 486

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Ser Arg
        275                 280                 285
Ser Pro Thr Lys Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 487
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 487
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc a 1131

<210> 488
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 488
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys

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

<210> 489
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 489
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gatgatgtag ctaacatcaa cgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720

gcagttatct attctaagca tttttggtct ggtcaggatc gttctagctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 490
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 490
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
275 280 285

Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 491
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 491
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ccttctttta gagctccaga taaggatcgt agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacttaa atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttat cttggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaggt ggtctcacgg atatagcgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca ttag 1164

<210> 492
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 492
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Arg Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Tyr Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 493
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 493
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ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 494
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 494
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

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Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 495
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 495
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420

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aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc agaccaaact 1140
ggccaccatc accatcacca t                                          1161


<210> 496
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 496
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
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Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Asp Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 497
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 497
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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ggccaccatc accatcacca t                                          1161
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<210> 498

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 498
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 499
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 499
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 500
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 500
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60

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Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 501
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 501
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60

gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 502
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 502
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 503
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 503
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 504
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 504
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 505
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 505
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t   1161

<210> 506
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 506
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 507
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 507
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc tgggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 508
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 508
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140

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

<210> 509
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 509
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660

agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 510
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 510
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270

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Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 511
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 511
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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<210> 512
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 512
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 513
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 513
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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ggccaccatc accatcacca t 1161

<210> 514
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 514
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 515
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 515
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300

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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca t                                          1161
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<210> 516
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 516

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
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Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 517
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
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tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 518
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 518
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350

Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 519
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 519
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
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<210> 520
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 520
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45

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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
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<210> 521
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 522
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 522
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 523
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 523
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ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 524
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 524
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Glu Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

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Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 525
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 525

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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 526
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 526

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 527
<211> 1161

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 527
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 528
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 528
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125

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Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 529
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 529
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 530
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 530
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 531
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 531
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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<210> 532
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 532
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 533
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 533
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 534
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 534
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80

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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 535
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 535
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 536
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 536
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205

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Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 537
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 537
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca t 1161

<210> 538
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 538
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335

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Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 539
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 539
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t   1161

<210> 540
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 540
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 541
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 541
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 542
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 542
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160

Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 543
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 543
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
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<210> 544
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
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<210> 545
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
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gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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<210> 546
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 547
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
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aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
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gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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<210> 548
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
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    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
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<210> 549
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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agaatgccag atccttacga accatctggc ggacgtgctg aaacagtagt taataactat 240
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gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
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ggccaccatc accatcacca t 1161

<210> 550
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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

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Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
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<210> 551
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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<210> 552

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
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<210> 553
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ggccaccatc accatcacca t 1161

<210> 554
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60

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Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 555
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 555
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60

gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 556
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 556
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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

<210> 557
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 557
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020

tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 558
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 558
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 559
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 559
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t   1161

<210> 560
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 560
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 561
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 561
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 562
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 562
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140

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Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 563
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 563
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 564
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 564
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270

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Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
```

<210> 565
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 565
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 566
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 566
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 567
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 567
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 568
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 568
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 569
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 569
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300

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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161


<210> 570
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 570
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
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Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 571
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 571
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 572
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 572
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340 345 350

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Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 573
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 573

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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 574
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 574

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 575
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 575
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 576
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 576
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Asp Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175

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Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 577
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 577

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
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gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 578
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 578
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 579
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 579
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 580
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 580

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 581
<211> 1161

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 581
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 582
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 582
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125

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Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 583
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 583
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 584
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 584
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 585
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 585
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accattacca t                                          1161
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<210> 586
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 586
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His Tyr His
385

<210> 587
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 587
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 588
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 588
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80

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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 589
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 589
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 590
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 590
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205

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Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 591
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 591
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca t 1161

<210> 592
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 592
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335

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Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 593
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 593
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t   1161

<210> 594
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 594
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 595
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 595
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 596
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 596
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160

Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 597
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 597
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780

cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 598
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 598
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
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20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285

Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 599
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 599
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 600
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 600
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 601
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 601
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 602
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 602
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 603
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 603
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420

aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacga cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 604
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 604
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Thr
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240

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Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 605
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 605
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca t                                          1161
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<210> 606

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 606
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 607
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 607
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
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tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 608
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 608
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60

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Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 609
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 609
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60

gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 610
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 610
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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

<210> 611
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 611
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020

tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 612
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 612
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 613
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 613

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 614
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 614

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 615
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 615
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 616
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 616
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Glu Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140

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Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 617
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 617
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 618
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 618
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270

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Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 619
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 619
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 620
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 620
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 621
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 621
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 622
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 622
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 623
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 623
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300

gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 624
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 624
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220

Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 625
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 625
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 626
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 626
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325 330 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340 345 350

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Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 627
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 627
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 628
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 628
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 629
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 629
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgttacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 630
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 630
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Tyr Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 631
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 631
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 632
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 632
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 633
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 633
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 634
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 634

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 635
<211> 1161

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 635
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 636
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 636
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125

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Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 637
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 637
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 638
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 638
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 639
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 639
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 640
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 640
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 641
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 641
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 642
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 642
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80

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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 643
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 643
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 644
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 644
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205

```
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 645
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 645
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca t 1161

<210> 646
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 646
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335

```
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 647
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 647
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacga accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 648
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 648
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
```

```
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Glu Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 649
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 649
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 650
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 650
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160

```
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 651
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 651
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatctggc ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 652
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 652
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Gly Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285

Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 653
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 653
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctgaagg atattctgat tttgatcgtg gtacttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 654
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 654
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Thr Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 655
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 655
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 656
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 656
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

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Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 657
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 657
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420

aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggacttat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 658
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 658
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240

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Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr Tyr
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 659
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 659
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 660

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 660
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 661
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 661
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ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 662
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 662
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60

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Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 663
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 663
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60

gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 664
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 664
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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

<210> 665
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 665
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020

tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 666
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 666
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 667
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 667
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 668
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 668
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 669
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 669
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 670
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 670
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140

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Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 671
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 671
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 672
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 672
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270

```
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 673
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 673
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
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ggccaccatc accatcacca t                                          1161
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<210> 674
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 674
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 675
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 676
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 676
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 677
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 677

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ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca t                                          1161
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<210> 678
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 678

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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
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Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 679
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 679

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 680
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 680
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1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340 345 350

Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 681
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 681
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
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ggccaccatc accatcacca t   1161

<210> 682
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 682
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45

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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 683
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 683
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ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 684
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 684
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 685
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 685
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 686
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 686
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

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Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 687
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 687

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 688
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 688

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 689
<211> 1161

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 689
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 690
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 690
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125

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Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 691
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 691
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 692
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 692
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 693
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 693

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 694
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 694
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 695
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 695
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 696
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 696
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80

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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 697
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 697
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 698
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 698
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205

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Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 699
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 699
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca t 1161

<210> 700
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 700
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335

Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 701
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 701
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 702
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 702
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30

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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 703
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>

<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 703
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 704
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 704
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160

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Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 705
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 705
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
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cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 706
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 706
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
275 280 285

Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
340 345 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
355 360 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 707
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 707
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgttact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 708
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 708
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Tyr Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 709
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 709
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtcgtt ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 710
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 710
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110

Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Arg Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 711
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 711
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420

aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 712
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 712
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240

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Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 713
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 713
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ccttctttta gagctccaga tgtggatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacgtga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttctggctc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca t                                          1161
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<210> 714

<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 714
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Val
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Val Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Gly
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365

Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
370 375 380
His His His
385

<210> 715
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 715
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 716
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 716
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60

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Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 717
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 717
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60

gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 718
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 718
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190

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

<210> 719
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 719
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020

tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 720
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 720
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320

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Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 721
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 721
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
```

<210> 722
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 722
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 723
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 723
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 724
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 724
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140

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Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 725
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 725
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
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agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 726
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 726
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270

```
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 727
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 727
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
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ggccaccatc accatcacca t                                          1161
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<210> 728
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 728
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1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 729
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 729
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 730
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 730
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95

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Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 731
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300

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gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161


<210> 732
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 732
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
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Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 733
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 733

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 734
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 734
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Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325 330 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340 345 350

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Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 735
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 735

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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 736
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 736

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
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Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 737
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 737
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ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 738
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 738
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175

Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380
His His His
385

<210> 739
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 739
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900

gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgcggg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 740
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 740
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300

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Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Ala Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 741
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 741

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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 742
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 742

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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                  10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 743
<211> 1161

<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 743
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtagtgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 744
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 744
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125

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Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Val Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 745
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 745
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gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
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aaagcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaacgttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 746
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 746
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255

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Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Arg Phe Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 747
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 747
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ccttctttta gagctccaga taaagatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtaacatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacctga atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc agtcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctcatgg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaatgc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 748
<211> 387
<212> PRT

<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 748
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1   5   10   15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20   25   30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Lys
        35   40   45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50   55   60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65   70   75   80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85   90   95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100   105   110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115   120   125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
    130   135   140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145   150   155   160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Thr
                165   170   175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180   185   190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Leu Asn Asp Ala Leu Arg
        195   200   205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210   215   220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225   230   235   240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Ser Ser
                245   250   255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260   265   270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275   280   285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
    290   295   300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305   310   315   320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325   330   335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser His Gly Tyr Ser Asp Phe Asp
            340   345   350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355   360   365
Pro Asp Lys Val Met Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370   375   380

His His His
385

<210> 749
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 749
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 750
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 750
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80

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Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 751
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 751
atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180

agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaact atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t 1161

<210> 752
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 752
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205

```
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn Tyr Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 753
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 753
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgcta ccacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttttaa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctaactttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaagagacc gtaacatccc aagatcacct acgtctccag gtgaaggttt tgtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
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ggccaccatc accatcacca t 1161

<210> 754
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 754
Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1 5 10 15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
20 25 30
Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
35 40 45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
50 55 60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Thr Thr Val Val Asn Asn Tyr
65 70 75 80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
85 90 95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
100 105 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
115 120 125
Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg
130 135 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145 150 155 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
165 170 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
180 185 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
195 200 205
Asn Glu Asp Ala Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro
210 215 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225 230 235 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
245 250 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
260 265 270
Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg
275 280 285
Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp
290 295 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305 310 315 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
325 330 335

```
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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<210> 755
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 755
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atggacaatg gagctggtga agaaacaaaa tcttatgctg aaacatatag acttactgca 60
gatgatgtag ctaacatcaa tgctttaaat gaatcagctc ctgctgcatc ttctgcagga 120
ccttctttta gagctccaga ttctgatgat agagtaactc ctcctgcaga gcctcttgat 180
agaatgccag atccttacag accatcttat ggacgtgctg aaacagtagt taataactat 240
attcgtaaat ggcaacaggt ttactctcat agagatggtc gtaaacaaca aatgacagaa 300
gagcagagag agtggctttc ttatggatgc gttggagtta cgtgggttaa ttcaggacaa 360
tatccaacga accgtcttgc atttgcttct tttgacgaag accgttataa aaacgagctt 420
aagaatggac gtcctcgttc tggtgaaact cgtgctgagt tcgaaggtag agttgctaag 480
gaatctttcg atgaagaaaa aggatttcaa agagcacgtg aagtagcatc tgtaatgaac 540
cgtgcattag agaacgctca tgacgagtca gcatatcttg ataaccttaa gaaggagctt 600
gcaaacggta atgatgcact tcgtaacgaa gacgcacgtt ctccttttta ttctgcactt 660
agaaatacgc cttctttcaa agaaagaaat ggtggtaacc atgatccatc tagaatgaaa 720
gcagttatct attctaagca tttttggtct ggtcaggatc gttcttcttc agctgataaa 780
cgtaagtacg gtgaccctga tgcatttaga ccagcacctg gaacaggtct tgttgatatg 840
tcaaaagacc gtaacatccc aagatcacct acgtctccag gtgaaggttg ggtaaacttt 900
gattacggat ggtttggagc tcagacagaa gctgatgcag ataagacagt atggactcat 960
ggaaatcatt atcacgctcc taacggttct ttaggtgcaa tgcacgtata cgaatcaaaa 1020
tttcgtaact ggtctgaagg atattctgat tttgatcgtg gtgcttacgt tatcactttt 1080
attccaaaat cttggaatac tgcaccagat aaagtaaagc agggatggcc aggccaaact 1140
ggccaccatc accatcacca t                                          1161
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<210> 756
<211> 387
<212> PRT
<213> Artificial Sequence

<220>
<223> Varaint of Streptomyces mobaraensis Transglutaminase

<400> 756
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Met Asp Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr
1               5                   10                  15
Arg Leu Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser
            20                  25                  30
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Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser
        35                  40                  45
Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp
    50                  55                  60
Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr
65                  70                  75                  80
Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln
                85                  90                  95
Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly
            100                 105                 110
Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe
        115                 120                 125
Ala Ser Phe Asp Glu Asp Arg Tyr Lys Asn Glu Leu Lys Asn Gly Arg
    130                 135                 140
Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys
145                 150                 155                 160
Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala
                165                 170                 175
Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr
            180                 185                 190
Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg
        195                 200                 205
Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro
    210                 215                 220
Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys
225                 230                 235                 240
Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser
                245                 250                 255
Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala
            260                 265                 270
Pro Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Asn Ile Pro Arg
        275                 280                 285
Ser Pro Thr Ser Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp
    290                 295                 300
Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His
305                 310                 315                 320
Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val
                325                 330                 335
Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp
            340                 345                 350
Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala
        355                 360                 365
Pro Asp Lys Val Lys Gln Gly Trp Pro Gly Gln Thr Gly His His His
    370                 375                 380
His His His
385
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