

SEQUENCE LISTING

<110> JAPAN TOBACCO INC
 <120> Modified biotin-binding protein
 <130> FA0392-09090PCT
 <150> JP 2008-208766
 <151> 2008-08-13

<160> 34

<210> 1

<211> 840

<212> DNA

<213> *Pleurotus cornucopiae*

<220>

<221> CDS

<222> (226)... (651)

<400> 1

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gctcagactc ttgtgctgac gggatatagat tcacaagccg tgcaggttgt gggagtactc      120
agagggtgag tgatigaatg gaagcacatc ggcgctggtt tcaagccgag aatigaggaa      180
gtaatactcc aagccgatga gaggitacag agatcctcta ccacc atg tca gac gtt      237
                               Met Ser Asp Val
                               1
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caa tct tca ctc acc gga acc tgg tac aat gaa ctc aac tcc aag atg      285
Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu Asn Ser Lys Met
   5              10              15              20
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gaa ttg act gca aac aaa gac ggt act ctc act gga aag tac ctc tcc      333
Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly Lys Tyr Leu Ser
              25              30              35
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aaa gtt ggg gat gtc tac gtg ccc tac cca ctc tct ggt cgc tat aac      381
Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser Gly Arg Tyr Asn
              40              45              50
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ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg tgg gcg gta tcc      429
Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly Trp Ala Val Ser
              55              60              65
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tgg gag aac agt aaa att cat tcc gct acg aca tgg agc gga cag ttc      477
Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp Ser Gly Gln Phe
              70              75              80
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ttc tct gag tgg tct cca gtg att ctt act cag tgg ttg ttg tca tgg      525
Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp Leu Leu Ser Ser
   85              90              95              100
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agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt gtg ggg aat gat      573
Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu Val Gly Asn Asp
              105              110              115
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tgg ttt aca aag acg gcg ccg act gag cag cag atc gct cat gct caa      621
Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile Ala His Ala Gln
              120              125              130
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ctc cat tgt cgc gca ccg agg ttg aag taa cgagggtcat cgcaaacaaa ccc      674
Leu His Cys Arg Ala Pro Arg Leu Lys
              135              140 141
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catcggtctt gaccggtgat ccaaccccaa ggictaatca atgccggatg actccatttg      734
aggatgtgaa ttagtggcca ttgtatgac ttgatttgic tgttgigttag tatcggattia      794
agaatcacat ctggttaacc ttcaaaaaaa aaaaaaaaaa aaaaaa      840
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<210> 2

<211> 141

<212> PRT

<213> *Pleurotus cornucopiae*

<400> 2

Met Ser Asp Val

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Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu Asn Ser Lys Met
   5              10              15              20
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2

Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly Lys Tyr Leu Ser
 25 30 35
 Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser Gly Arg Tyr Asn
 40 45 50
 Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly Trp Ala Val Ser
 55 60 65
 Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp Ser Gly Gln Phe
 70 75 80
 Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp Leu Leu Ser Ser
 85 90 95 100
 Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu Val Gly Asn Asp
 105 110 115
 Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile Ala His Ala Gln
 120 125 130
 Leu His Cys Arg Ala Pro Arg Leu Lys
 135 140 141

<210> 3
 <211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TM2 K26A

<400> 3
 atg tca gac gtt caa tct tca ctc acc gga acc tgg tac aat gaa ctc 48
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 aac tcc aag atg gaa ttg act gca aac gca gac ggt act ctc act gga 96
 Asn Ser Lys Met Glu Leu Thr Ala Asn Ala Asp Gly Thr Leu Thr Gly
 20 25 30
 aag tac ctc tcc aaa gtt ggg gat gtc tac gtg ccc tac cca ctc tct 144
 Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
 35 40 45
 ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
 Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
 50 55 60
 tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg 240
 Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
 65 70 75 80
 agc gga cag ttc ttc tct gag tgc tct cca gtg att ctt act cag tgg 288
 Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
 85 90 95
 ttg ttg tca tgc agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt 336
 Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
 100 105 110
 gtg ggg aat gat tgc ttt aca aag acg gcg ccg act gag cag cag atc 384
 Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
 115 120 125
 gct cat gct caa ctc cat tgt cgc gca ccg agg ttg aag taa 426
 Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
 130 135 140

<210> 4
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TM2 K26A

<400> 4
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 1 5 10 15
 Asn Ser Lys Met Glu Leu Thr Ala Asn Ala Asp Gly Thr Leu Thr Gly
 20 25 30
 Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
 35 40 45

3

Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
130 135 140 141

<210> 5
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> TM2 K73Q

<400> 5
atg tca gac gtt caa tct tca ctc acc gga acc tgg tac aat gaa ctc 48
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1 5 10 15
aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga 96
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30
aag tac ctc tcc aaa gtt ggg gat gtc tac gtg ccc tac cca ctc tct 144
Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45
ggc cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60
tgg gcg gta tcc tgg gag aac agt caa att cat tcc gct acg aca tgg 240
Trp Ala Val Ser Trp Glu Asn Ser Gln Ile His Ser Ala Thr Thr Trp
65 70 75 80
agc gga cag ttc ttc tct gag tcg tct cca gtg att ctt act cag tgg 288
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95
ttg ttg tca tcg agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt 336
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110
gtg ggg aat gat tcg ttt aca aag acg gcg ccg act gag cag cag atc 384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125
gct cat gct caa ctc cat tgt cgc gca ccg agg ttg aag taa 426
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
130 135 140

<210> 6
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> TM2 K73Q

<400> 6
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1 5 10 15
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30
Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60
Trp Ala Val Ser Trp Glu Asn Ser Gln Ile His Ser Ala Thr Thr Trp

Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu
 100 105 110
 Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
 115 120 125
 Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
 130 135 140 141

<210> 9
 <211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TM2 K141E

<400> 9
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 1 5 10 15
 aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga 96
 Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
 20 25 30
 aag tac ctc tcc aaa gtt ggg gat gtc tac gtg ccc tac cca ctc tct 144
 Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
 35 40 45
 ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
 Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
 50 55 60
 tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg 240
 Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
 65 70 75 80
 agc gga cag ttc ttc tct gag tgc tct cca gtg att ctt act cag tgg 288
 Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
 85 90 95
 ttg ttg tca tgc agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt 336
 Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
 100 105 110
 gtg ggg aat gat tgc ttt aca aag acg gcg ccg act gag cag cag atc 384
 Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
 115 120 125
 gct cat gct caa ctc cat tgt cgc gca ccg agg ttg gag taa 426
 Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Glu
 130 135 140

<210> 10
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TM2 K141E

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

115 120 125
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Glu
130 135 140 141

<210> 11
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> TM2 K33TK37A

<400> 11
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aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga 96
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30
acg tac ctc tcc gca gtt ggg gat gtc tac gtg ccc tac cca ctc tct 144
Thr Tyr Leu Ser Ala Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45
ggg cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60
tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg 240
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80
agc gga cag ttc ttc tct gag tgg tct cca gtg att ctt act cag tgg 288
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95
ttg ttg tca tgg agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt 336
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110
gtg ggg aat gat tgg ttt aca aag acg gcg cgg act gag cag cag atc 384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125
gct cat gct caa ctc cat tgt cgc gca cgg agg ttg aag taa 426
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
130 135 140

<210> 12
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> TM2 K33TK37A

<400> 12
Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
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Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30
Thr Tyr Leu Ser Ala Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
130 135 140 141

<210> 13
 <211> 426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TM2 K33TK37AR104E

<400> 13

atg tca gac gtt caa tct tca ctc acc gga acc tgg tac aat gaa ctc	48
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1 5 10 15	
aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga	96
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly	
20 25 30	
acg tac ctc tcc gca gtt ggg gat gtc tac gtg ccc tac cca ctc tct	144
Thr Tyr Leu Ser Ala Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser	
35 40 45	
ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg	192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly	
50 55 60	
tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg	240
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp	
65 70 75 80	
agc gga cag ttc ttc tct gag tgc tct cca gtg att ctt act cag tgg	288
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp	
85 90 95	
ttg ttg tca tgc agc act gcg gaa ggg gac gta tgg gaa tcc aca ctt	336
Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu	
100 105 110	
gtg ggg aat gat tgc ttt aca aag acg gcg ccg act gag cag cag atc	384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile	
115 120 125	
gct cat gct caa ctc cat tgt cgc gca ccg agg ttg aag taa	426
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys	
130 135 140	

<210> 14
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TM2 K33TK37AR104E

<400> 14

Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu	
1 5 10 15	
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly	
20 25 30	
Thr Tyr Leu Ser Ala Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser	
35 40 45	
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly	
50 55 60	
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp	
65 70 75 80	
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp	
85 90 95	
Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu	
100 105 110	
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile	
115 120 125	
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys	
130 135 140 141	

<210> 15
 <211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> TM2 R104EK141E

<400> 15

atg tca gac gtt caa tct tca ctc acc gga acc tgg tac aat gaa ctc 48
Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1 5 10 15

aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga 96
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30

aag tac ctc tcc aaa gtt ggg gat gtc tac gtg ccc tac cca ctc tct 144
Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45

ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60

tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg 240
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80

agc gga cag ttc ttc tct gag tcg tct cca gtg att ctt act cag tgg 288
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95

ttg ttg tca tgg agc act gcg gaa ggg gac gta tgg gaa tcc aca ctt 336
Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu
100 105 110

gtg ggg aat gat tcg ttt aca aag acg gcg ccg act gag cag cag atc 384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125

gct cat gct caa ctc cat tgt cgc gca ccg agg ttg gag taa 426
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Glu
130 135 140

<210> 16

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> TM2 R104EK141E

<400> 16

Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1 5 10 15

Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30

Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45

Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60

Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80

Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95

Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu
100 105 110

Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125

Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Glu
130 135 140

<210> 17

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> TM2 K19T

<400> 17

atg tca gac gtt caa tct tca ctc acc gga acc tgg tac aat gaa ctc 48
Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1 5 10 15

aac tcc acg atg gaa ttg act gca aac aaa gac ggt act ctc act gga 96
Asn Ser Thr Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30

aag tac ctc tcc aaa gtt ggg gat gtc tac gtg ccc tac cca ctc tct 144
Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45

ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60

tgg cgc gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg 240
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80

agc gga cag ttc ttc tct gag tgg tct cca gtg att ctt act cag tgg 288
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95

ttg ttg tca tgg agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt 336
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110

gtg ggg aat gat tgg ttt aca aag acg gcg cgg act gag cag cag atc 384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125

gct cat gct caa ctc cat tgt cgc gca ccg agg ttg aag taa 426
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
130 135 140

<210> 18

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> TM2 K19T

<400> 18

Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1 5 10 15

Asn Ser Thr Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30

Lys Tyr Leu Ser Lys Val Gly Asp Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45

Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60

Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80

Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95

Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110

Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125

Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
130 135 140

<210> 19

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> TM2 D40N

10

<400> 19

atg tca gac gtt caa tct tca ctc acc gga acc tgg tac aat gaa ctc 48
Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1 5 10 15

aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga 96
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30

aag tac ctc tcc aaa gtt ggg aat gtc tac gtg ccc tac cca ctc tct 144
Lys Tyr Leu Ser Lys Val Gly Asn Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45

ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg 192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60

tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg 240
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80

agc gga cag ttc ttc tct gag tcg tct cca gtg att ctt act cag tgg 288
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95

ttg ttg tca tcg agc act gcg cgt ggg gac gta tgg gaa tcc aca ctt 336
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110

gtg ggg aat gat tcg ttt aca aag acg gcg ccg act gag cag cag atc 384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
115 120 125

gct cat gct caa ctc cat tgt cgc gca ccg agg ttg aag taa 426
Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys
130 135 140

<210> 20

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> TM2 D40N

<400> 20

Met Ser Asp Val Gln Ser Ser Leu Thr Gly Thr Trp Tyr Asn Glu Leu
1 5 10 15
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly
20 25 30
Lys Tyr Leu Ser Lys Val Gly Asn Val Tyr Val Pro Tyr Pro Leu Ser
35 40 45
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
50 55 60
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
65 70 75 80
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
85 90 95
Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
100 105 110
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
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aac tcc aag atg gaa ttg act gca aac aaa gac ggt act ctc act gga					96
Asn Ser Lys Met Glu Leu Thr Ala Asn Lys Asp Gly Thr Leu Thr Gly	20	25	30		
aag tac ctc tcc aaa gtt ggg aat gtc tac gtg ccc tac cca ctc tct					144
Lys Tyr Leu Ser Lys Val Gly Asn Val Tyr Val Pro Tyr Pro Leu Ser	35	40	45		
ggt cgc tat aac ctc caa ccc ccc gcg gga caa ggc gtc gct ctt ggg					192
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly	50	55	60		
tgg gcg gta tcc tgg gag aac agt aaa att cat tcc gct acg aca tgg					240
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp	65	70	75	80	
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Ser Gly Gln Phe Ser Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp	85	90	95		
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Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu	100	105	110		
gtg ggg aat gat tcg ttt aca aag acg gcg ccg act gag cag cag atc					384
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile	115	120	125		
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Ala His Ala Gln Leu His Cys Arg Ala Pro Arg Leu Lys	130	135	140		
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Lys Tyr Leu Ser Lys Val Gly Asn Val Tyr Val Pro Tyr Pro Leu Ser	35	40	45		
Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly	50	55	60		
Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp	65	70	75	80	
Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp	85	90	95		
Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu	100	105	110		
Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile	115	120	125		
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12
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 Lys Tyr Leu Ser Lys Val Gly Asn Val Tyr Val Pro Tyr Pro Leu Ser
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 Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
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 Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
 65 70 75 80
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 Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
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 Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
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 35 40 45
 Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
 50 55 60
 Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
 65 70 75 80
 Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
 85 90 95
 Leu Leu Ser Ser Ser Thr Ala Glu Gly Asp Val Trp Glu Ser Thr Leu
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 Lys Tyr Leu Ser Lys Val Gly Asn Val Tyr Val Pro Tyr Pro Leu Ser
 35 40 45
 Gly Arg Tyr Asn Leu Gln Pro Pro Ala Gly Gln Gly Val Ala Leu Gly
 50 55 60

Trp Ala Val Ser Trp Glu Asn Ser Lys Ile His Ser Ala Thr Thr Trp
 65 70 75 80
 Ser Gly Gln Phe Phe Ser Glu Ser Ser Pro Val Ile Leu Thr Gln Trp
 85 90 95
 Leu Leu Ser Ser Ser Thr Ala Arg Gly Asp Val Trp Glu Ser Thr Leu
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 Val Gly Asn Asp Ser Phe Thr Lys Thr Ala Pro Thr Glu Gln Gln Ile
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<210> 39

<211> 39

<212> DNA

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<400> 39

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