

SEQUENCE LISTING

<110> Stenmark, Pål

<120> TricepTox

<130> P41705056PCT00

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Hc/TriRecABTox

<400> 1

Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn
1 5 10 15

His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser
20 25 30

Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn
35 40 45

Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr
50 55 60

Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro
65 70 75 80

Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn
85 90 95

Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu
100 105 110

Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val
115 120 125

Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp
130 135 140

Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr
145 150 155 160

Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn
165 170 175

Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp
180 185 190

Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu
195 200 205

Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser
210 215 220

Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro
225 230 235 240

Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile Lys Leu Lys
245 250 255

Lys Asp Ser Pro Val Gly Glu Ile Leu Gly Pro Arg Gly Ser Val Met
260 265 270

Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Glu Lys Phe
275 280 285

Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn Asp Asp Ile Val
290 295 300

Arg Asn Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn Leu Asn Gln Glu
305 310 315 320

Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys Glu Glu Glu Lys Leu
325 330 335

Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe Tyr Asn Thr Ile Gln
340 345 350

Ile Lys Glu Tyr Asp Glu Gln Gly Thr Asn Ser Cys Gln Leu Leu Phe
355 360 365

Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly Ile His
370 375 380

Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr Phe
385 390 395 400

Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn
405 410 415

Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Asp Gly Trp
420 425 430

Gly Glu Arg Pro Leu
435

<210> 2
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<223> Hc/TriRecABTox codon optimised sequence for expression in E. coli

<400> 2
aagaacatta tcaacaccag catcctgaac ctgcgctacg agagcaacca cctgatcgac 60
ctgagccgct acgcgagcaa gattaacatc ggtagcaagg tgaactttga cccgattgat 120
aaaaaccaga tccaactggt caacctggaa agcagcaaga tcgaagtgat tctgaaaaac 180
gcgattgttt ataacagcat gtacgaaaac ttcagcacca gcttttggat ccgtattccg 240
aagtatttta acagcatcag cctgaacaac gaatacacca tcattaactg catggagAAC 300
aacagcgggt ggaaagttag cctgaactac ggcgaaatca tttggaccct gcaggacacc 360
caagagatca agcagcgtgt ggttttcaag tacagccaaa tgatcaacat cagcgattac 420
atcaaccgtt ggattttcgt taccatcacc aacaaccgtc tgaacaacag caagatctac 480
attaacggtc gtctgattga ccagaaaccg atcagcaacc tgggcaacat tcacgcgagc 540
aacaacatca tgttcaagct ggacggttgc cgtgataccc accgttatat ctggattaag 600

tacttcaacc tgtttgataa agagctgaac gaaaaggaga ttaaagacct gtatgataac	660
cagagcaaca gcggtatcct gaaggacttt tggggcgatt atctgcaata cgacaaaccg	720
tactatatgt tcaacgcggg taacaagaac agctacatta aactgaagaa agatagcccg	780
gtgggtgaaa tcctgggtcc gcgtggcagc gttatgacca ccaacatcta tctgaacagc	840
agcctgtacc gtggcgagaa gttcatcatt cgtcgtaaaa gcaacagcca gagcattaac	900
gacgatatcg tgcgtaacga agactacatt tatctggatt tctttaacct gaaccaagag	960
tggcgtgttt acacctacaa gtacttcaag aaagaggaag agaagctgtt cctggcgccg	1020
atcagcgaca gcgatgaatt ctacaacacc atccaaatca aggaatacga cgagcagggt	1080
accaacagct gccaaactgct gttcaagaaa gacgaagaga gcaccgatga aatcgggtctg	1140
atcggcattc accgtttcta cgagagcggc atcgtgttcg aagagtacaa ggattacttc	1200
tgcatcagca agtggatatct gaaagagggt aagcgtaaac cgtacaacct gaaactgggc	1260
tgcaactggc aatttattcc ggtggatgat ggctgggggtg aacgtccgct gtaa	1314

<210> 3

<211> 1311

<212> PRT

<213> Artificial Sequence

<220>

<223> Full-length inactive TriRecABTox with engineered activation site

<400> 3

Met	Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly
1				5				10						15	

Val	Asp	Ile	Ala	Tyr	Ile	Lys	Ile	Pro	Asn	Ala	Gly	Gln	Met	Gln	Pro
		20						25					30		

Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	Glu	Arg
		35					40				45				

Asp	Thr	Phe	Thr	Asn	Pro	Glu	Glu	Gly	Asp	Leu	Asn	Pro	Pro	Pro	Glu
	50					55					60				

Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	Tyr	Leu	Ser	Thr
65					70					75				80	

Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
85 90 95

Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
100 105 110

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
130 135 140

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

Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
165 170 175

Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190

Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205

Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Gln
210 215 220

Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240

Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255

Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
260 265 270

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285

Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300

Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320

Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335

Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350

Asn Phe Val Lys Phe Phe Lys Val Leu Asn Ala Lys Thr Phe Leu Asn
355 360 365

Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380

Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400

Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415

Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430

Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Ile Glu Gly Arg Asp Lys
435 440 445

Gly Tyr Asn Lys Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp
450 455 460

Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn
465 470 475 480

Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu
485 490 495

Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe
500 505 510

Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile
515 520 525

Ile Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly
530 535 540

Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala
545 550 555 560

Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val
565 570 575

Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser
580 585 590

Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu
595 600 605

Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu
610 615 620

Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr
625 630 635 640

Ile Gly Pro Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe
645 650 655

Val Gly Ala Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile
660 665 670

Pro Glu Ile Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr
675 680 685

Ile Ala Asn Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser
690 695 700

Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn
705 710 715 720

Trp Leu Ala Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met
725 730 735

Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn
740 745 750

Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe
755 760 765

Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala
770 775 780

Met Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu
785 790 795 800

Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp
805 810 815

Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly
820 825 830

Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr
835 840 845

Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
850 855 860

Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr
865 870 875 880

Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser
885 890 895

Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro
900 905 910

Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile
915 920 925

Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn
930 935 940

Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile
945 950 955 960

Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser
965 970 975

Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln
980 985 990

Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met
995 1000 1005

Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
1010 1015 1020

Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg
1025 1030 1035

Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala
1040 1045 1050

Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
1055 1060 1065

Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu
1070 1075 1080

Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser
1085 1090 1095

Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys
1100 1105 1110

Pro Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile Lys
1115 1120 1125

Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Gly Pro Arg Gly
1130 1135 1140

Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
1145 1150 1155

Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile
1160 1165 1170

Asn Asp Asp Ile Val Arg Asn Glu Asp Tyr Ile Tyr Leu Asp Phe
1175 1180 1185

Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe
1190 1195 1200

Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser
1205 1210 1215

Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln
1220 1225 1230

Gly Thr Asn Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser
1235 1240 1245

Thr Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser
1250 1255 1260

Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys
1265 1270 1275

Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu
1280 1285 1290

Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
1295 1300 1305

Arg Pro Leu
1310

<210> 4

<211> 3936

<212> DNA

<213> Artificial Sequence

<220>

<223> Full-length inactive TriRecABTox w engineered activation site,
codon optimised sequence for expression in E. coli

<400> 4

atgccgttcg tgaataagca gttcaactac aaagatccgg ttaatggcgt ggacatcgcg	60
tacatcaaaa tcccgaatgc gggtcagatg cagccggtga aggcgttcaa aatccacaac	120
aaaatttggg ttatcccgga gcgtgacacc tttaccaacc cggaggaagg tgatctgaac	180
ccgccgccgg aagcgaaaca agtgccggtt agctactatg acagcaccta tctgagcacc	240
gacaacgaga aggataacta cctgaagggc gtgaccaaac tgttcgaacg tatctacagc	300
accgatctgg gtcgtatgct gctgaccagc attgttcgtg gcatcccgtt ttgggggtggc	360
agcaccatcg acaccgaact gaaagtgatt gataccaact gcattaacgt tatccagccg	420
gatggtagct accgtagcga ggaactgaac ctgggtgatca ttggcccagag cgcggacatc	480
attcagtttg agtgcaagag cttcggtcac gaagttctga acctgaccg taacggttac	540
ggcagcacc aatatatccg tttcagcccg gatttcacct ttggcttcga ggaaagcctg	600
gaagtggaca ccaaccgct gctgggtgcg ggcaagtttg cgaccgacc ggcggttacc	660
ctggcgcacc agctgatcca tgcgggtcac cgtctgtacg gcattgcat caaccgaac	720
cgtgtgttca aagttaacac caacgcgtac tatgagatga gcggtctgga agtgagcttt	780
gaggaactgc gtaccttcgg tggccacgac gcgaagttta tcgatagcct gcaggagaac	840
gaattccgtc tgtactacta caacaagttc aaggacatcg cgagcacct gaacaaggcg	900
aaaagcattg tgggtaccac cgcgagcctg caatacatga agaacgtttt caaggagaag	960
tacctgctga gcgaagatac cagcggcaag tttagcgtgg acaagctgaa attcgataag	1020
ctgtataaaa tgctgaccga gatctacacc gaagataact tcgtgaagtt ctttaaagtt	1080
ctgaacgcga aaacctttct gaacttcgac aaggcggttt ttaaaattaa catcgtgccg	1140
aaggttaact acaccatcta tgatggtttc aacctgcgta acaccaacct ggcggcgaac	1200
tttaacggcc agaacaccga gattaacaac atgaacttta ccaagctgaa aaacttcacc	1260
ggtctgtttg aattctataa actgctgtgc gtgcgtggca tcattaccag caagacaaaa	1320
agcctgatcg aaggctgtga caagggtac aacaaagcgc tgaacgatct gtgcattaaa	1380
gttaacaact gggacctgtt ctttagcccg agcgaggaca acttcaccaa cgatctgaac	1440
aagggcgagg aaatcaccag cgacaccaac attgaagcgg cggaggaaaa catcagcctg	1500

gatctgattc agcaatatta cctgaccttt aacttcgaca acgagccgga aaacattagc	1560
atcgagaacc tgagcagcga catcattggt cagctggagc tgatgccgaa catcgaacgt	1620
ttcccgaacg gcaagaaata cgaactggat aaatatacca tgttccacta cctgcgtgcg	1680
caagagtttg aacacggcaa gagccgtatt gcgctgacca acagcgtgaa cgaggcgctg	1740
ctgaacccga gccgtgttta taccttcttt agcagcgact acgtgaagaa agttaacaaa	1800
gcgaccgagg cggcgatggt cctgggttgg gtggaacagc tggtttacga ctttaccgat	1860
gaaaccagcg aggtgagcac caccgacaaa attgcggata tcaccatcat tatcccgtat	1920
atcgggccgg cgctgaacat tggcaacatg ctgtacaagg acgattttgt ggggtgcgctg	1980
atcttcagcg gcgcggttat cctgctggag ttcattccgg aaattgcgat cccggtgctg	2040
ggtacctttg cgctgggttag ctacatcgcg aacaagggtgc tgaccgttca aaccattgat	2100
aacgcgctga gcaagcgtaa cgagaaatgg gacgaagtgt ataaatacat cgttaccaac	2160
tggctggcga aggttaacac ccagattgac ctgatccgta agaaaatgaa agaggcgctg	2220
gaaaaccaag cggaggcgac caaggcgatt atcaactatc agtacaacca atacaccgag	2280
gaagagaaaa acaacattaa cttcaacatc gacgatctga gcagcaagct gaacgaaagc	2340
atcaacaaag cgatgattaa catcaacaag tttctgaacc agtgcagcgt gagctatctg	2400
atgaacagca tgattccgta cgggtgttaag cgtctggagg acttcgatgc gaggcctgaag	2460
gacgcgctgc tgaaatatat ctacgataac cgtgggtaccc tgattggcca agtggaccgt	2520
ctgaaggata aagttaacaa caccctgagc accgatatcc cgttccagct gagcaaatat	2580
gtggacaacc aacgtctgct gagcaccttt accgagtaca tcaagaacat tatcaacacc	2640
agcattctga acctgcgtta tgaaagcaac cacctgatcg acctgagccg ttacgcgagc	2700
aagattaaca tcggtagcaa agttaacttc gacccgatcg ataaaaacca gattcaactg	2760
tttaacctgg agagcagcaa gattgaagtg atcctgaaaa acgcgatcgt ttacaacagc	2820
atgtatgaga acttttagcac cagcttctgg attcgtatcc cgaaatattt caacagcatt	2880
agcctgaaca acgagtacac cattatcaac tgcattggaaa acaacagcgg ttggaagggtg	2940
agcctgaact acggcgagat tatctggacc ctgcaggaca cccaagaaat caagcagcgt	3000
gtggttttca agtacagcca aatgatcaac atcagcgatt acattaaccg ttggatcttt	3060
gttaccatta ccaacaaccg tctgaacaac agcaaaattt acatcaacgg tcgtctgatc	3120

gaccagaagc cgattagcaa cctgggcaac atccacgcga gcaacaacat tatgttcaag 3180
ctggacgggt gccgtgatac ccaccgttat atttggatca agtacttcaa cctgttcgat 3240
aaggagctga acgagaagga aatcaaagac ctgtatgata accagagcaa cagcgggtatt 3300
ctgaaagact tctggggcga ttacctgcaa tatgacaagc cgtattacat gtttaacgcg 3360
ggtaacaaga acagctacat caaactgaag aaagatagcc cgggtgggtga aattctgggt 3420
ccgcgtggca gcgttatgac caccaacatc tatctgaaca gcagcctgta cctgggcgaa 3480
aagttcatta tccgtcgtaa aagcaacagc cagagcatca acgacgatat tgtgcgtaac 3540
gaggactata tctacctgga tttctttaac ctgaaccaag aatggcgtgt ttacacctac 3600
aagtacttca agaaagaaga ggaaaagctg tttctggcgc cgattagcga cagcgatgaa 3660
ttctataaca ccattcagat caaagagtac gacgaacagg gtaccaacag ctgccaaactg 3720
ctgtttaaga aagacgagga aagcaccgat gagatcggtc tgattggcat ccaccgtttt 3780
tacgaaagcg gcatcgtgtt cgaggaatac aaggattact tctgcatcag caagtgggtat 3840
ctgaaagagg ttaagcgtaa accgtacaac ctgaaactgg gctgcaactg gcaattttatt 3900
ccggtggatg atggctgggg tgaacgtccg ctgtaa 3936

<210> 5

<211> 1311

<212> PRT

<213> Artificial Sequence

<220>

<223> Full-length active TreRecABTox with engineered activation site

<400> 5

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15

Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
20 25 30

Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
35 40 45

Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu
50 55 60

Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
65 70 75 80

Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
85 90 95

Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
100 105 110

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
130 135 140

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

Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
165 170 175

Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
180 185 190

Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
195 200 205

Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
210 215 220

Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
225 230 235 240

Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
245 250 255

Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
260 265 270

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn

275

280

285

Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
 290 295 300

Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
 305 310 315 320

Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
 325 330 335

Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
 340 345 350

Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
 355 360 365

Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
 370 375 380

Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
 385 390 395 400

Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
 405 410 415

Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
 420 425 430

Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Ile Glu Gly Arg Asp Lys
 435 440 445

Gly Tyr Asn Lys Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp
 450 455 460

Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn
 465 470 475 480

Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu
 485 490 495

Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe
500 505 510

Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile
515 520 525

Ile Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly
530 535 540

Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala
545 550 555 560

Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val
565 570 575

Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser
580 585 590

Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu
595 600 605

Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu
610 615 620

Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr
625 630 635 640

Ile Gly Pro Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe
645 650 655

Val Gly Ala Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile
660 665 670

Pro Glu Ile Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr
675 680 685

Ile Ala Asn Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser
690 695 700

Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn

705	710	715	720
Trp Leu Ala Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met	725	730	735
Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn	740	745	750
Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe	755	760	765
Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala	770	775	780
Met Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu	785	790	800
Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp	805	810	815
Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly	820	825	830
Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr	835	840	845
Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln	850	855	860
Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr	865	870	875
Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser	885	890	895
Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro	900	905	910
Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile	915	920	925

Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn
930 935 940

Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile
945 950 955 960

Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser
965 970 975

Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln
980 985 990

Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met
995 1000 1005

Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
1010 1015 1020

Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg
1025 1030 1035

Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala
1040 1045 1050

Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
1055 1060 1065

Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu
1070 1075 1080

Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser
1085 1090 1095

Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys
1100 1105 1110

Pro Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile Lys
1115 1120 1125

Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Gly Pro Arg Gly

1130

1135

1140

Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg
 1145 1150 1155

Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile
 1160 1165 1170

Asn Asp Asp Ile Val Arg Asn Glu Asp Tyr Ile Tyr Leu Asp Phe
 1175 1180 1185

Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe
 1190 1195 1200

Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser
 1205 1210 1215

Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln
 1220 1225 1230

Gly Thr Asn Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser
 1235 1240 1245

Thr Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser
 1250 1255 1260

Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys
 1265 1270 1275

Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu
 1280 1285 1290

Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
 1295 1300 1305

Arg Pro Leu
 1310

<210> 6

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Hc/TAB2.1, optimised loop 360

<400> 6

Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn
1 5 10 15

His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser
20 25 30

Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn
35 40 45

Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr
50 55 60

Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro
65 70 75 80

Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn
85 90 95

Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu
100 105 110

Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val
115 120 125

Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp
130 135 140

Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr
145 150 155 160

Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn
165 170 175

Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp
180 185 190

Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu
195 200 205

Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser
210 215 220

Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro
225 230 235 240

Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile Lys Leu Lys
245 250 255

Lys Asp Ser Pro Val Gly Glu Ile Leu Gly Pro Arg Gly Ser Val Met
260 265 270

Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Glu Lys Phe
275 280 285

Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn Asp Asp Ile Val
290 295 300

Arg Asn Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn Leu Asn Gln Glu
305 310 315 320

Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys Glu Glu Glu Lys Leu
325 330 335

Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe Tyr Asn Thr Ile Gln
340 345 350

Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln Leu Leu Phe
355 360 365

Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly Ile His
370 375 380

Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr Phe
385 390 395 400

Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn

405

410

415

Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Asp Gly Trp
 420 425 430

Gly Glu Arg Pro Leu
 435

<210> 7

<211> 1314

<212> DNA

<213> Artificial Sequence

<220>

<223> Hc/TAB2.1, codon optimised for expression in E. coli

<400> 7

aagaacatta tcaacaccag catcctgaac ctgcgctacg agagcaacca cctgatcgac 60

ctgagccgct acgcgagcaa gattaacatc ggtagcaagg tgaactttga cccgattgat 120

aaaaaccaga tccaactggt caacctggaa agcagcaaga tcgaagtgat tctgaaaaac 180

gcgattgttt ataacagcat gtacgaaaac ttcagcacca gcttttggat ccgtattccg 240

aagtatttta acagcatcag cctgaacaac gaatacacca tcattaactg catggagaac 300

aacagcgggt ggaaagttag cctgaactac ggcgaaatca tttggaccct gcaggacacc 360

caagagatca agcagcgtgt ggttttcaag tacagccaaa tgatcaacat cagcgattac 420

atcaaccgtt ggattttcgt taccatcacc aacaaccgtc tgaacaacag caagatctac 480

attaacgggt gtctgattga ccagaaaccg atcagcaacc tgggcaacat tcacgcgagc 540

aacaacatca tgttcaagct ggacggttgc cgtgataccc accgttatat ctggattaag 600

tacttcaacc tgtttgataa agagctgaac gaaaaggaga ttaaagacct gtatgataac 660

cagagcaaca gcggtatcct gaaggacttt tggggcgatt atctgcaata cgacaaaccg 720

tactatatgt tcaacgcggg taacaagaac agctacatta aactgaagaa agatagcccg 780

gtgggtgaaa tcctgggtcc gcgtggcagc gttatgacca ccaacatcta tctgaacagc 840

agcctgtacc gtggcgagaa gttcatcatt cgtcgtaaaa gcaacagcca gagcattaac 900

gacgatatcg tgcgtaacga agactacatt tatctggatt tctttaacct gaaccaagag 960

tggcgtgttt acacctacaa gtacttcaag aaagaggaag agaagctgtt cctggcgccg 1020

atcagcgaca gcgatgaatt ctacaacacc atccaaatca aggaatacga cgagcagccg 1080
acctatagct gccaaactgct gttcaagaaa gacgaagaga gcaccgatga aatcgggtctg 1140
atcggcattc accgtttcta cgagagcggc atcgtgttcg aagagtacaa ggattacttc 1200
tgcacgagca agtggatatct gaaagagggtt aagcgtaaac cgtacaacct gaaactgggc 1260
tgcaactggc aatttattcc ggtggatgat ggctgggggtg aacgtccgct gtaa 1314

<210> 8
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Hc/TAB2.1.1

<400> 8

Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
1 5 10 15

Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
20 25 30

Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
35 40 45

Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
50 55 60

Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
65 70 75 80

Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
85 90 95

Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
100 105 110

Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
115 120 125

Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile

130

135

140

Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
 145 150 155 160

Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
 165 170 175

Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
 180 185 190

Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
 195 200 205

Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
 210 215 220

Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Phe Asn
 225 230 235 240

Ala Gly Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val
 245 250 255

Gly Glu Ile Leu Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
 260 265 270

Leu Asn Ser Ser Leu Tyr Arg Gly Glu Lys Phe Ile Ile Arg Arg Lys
 275 280 285

Ser Asn Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Asn Glu Asp Tyr
 290 295 300

Ile Tyr Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr
 305 310 315 320

Tyr Lys Tyr Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile
 325 330 335

Ser Asp Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp
 340 345 350

Glu Gln Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu
355 360 365

Ser Thr Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser
370 375 380

Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp
385 390 395 400

Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys
405 410 415

Asn Trp Gln Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
420 425 430

<210> 9
<211> 1299
<212> DNA
<213> Artificial Sequence

<220>
<223> Hc/TAB2.1.1, codon optimised for expression in E. coli

<400> 9
accagcatcc tgaacctgcg ctacgagagc aaccacctga tcgacctgag ccgctacgcg 60
agcaagatta acatcggtag caaggtgaac ttgacccga ttgataaaaa ccagatccaa 120
ctgttcaacc tggaaagcag caagatcgaa gtgattctga aaaacgcgat tgttttataac 180
agcatgtacg aaaacttcag caccagcttt tggatccgta ttccgaagta ttttaacagc 240
atcagcctga acaacgaata caccatcatt aactgcatgg agaacaacag cggttggaaa 300
gtgagcctga actacggcga aatcatttgg accctgcagg acaccaaga gatcaagcag 360
cgtgtgggtt tcaagtacag ccaaagatgc aacatcagcg attacatcaa ccgttggatt 420
ttcgttacca tcaccaacaa ccgtctgaac aacagcaaga tctacattaa cggtcgtctg 480
attgaccaga aaccgatcag caacctgggc aacattcacg cgagcaacaa catcatgttc 540
aagctggacg gttgccgtga taccaccgt tatatctgga ttaagtactt caacctgttt 600
gataaagagc tgaacgaaaa ggagattaaa gacctgtatg ataaccagag caacagcggt 660
atcctgaagg acttttgggg cgattatctg caatacgaca aaccgtacta tatgttcaac 720

gcgggtaaca agaacagcta cattaaactg aagaaagata gcccggtggg tgaaatcctg 780
 ggtccgcgtg gcagcgttat gaccaccaac atctatctga acagcagcct gtaccgtggc 840
 gagaagttca tcattcgtcg taaaagcaac agccagagca ttaacgacga tatcgtgcgt 900
 aacgaagact acatttatct ggatttcttt aacctgaacc aagagtggcg tgtttacacc 960
 tacaagtact tcaagaaaga ggaagagaag ctgttcctgg cgccgatcag cgacagcgat 1020
 gaattctaca acaccatcca aatcaaggaa tacgacgagc agccgaccta tagctgccaa 1080
 ctgctgttca agaaagacga agagagcacc gatgaaatcg gtctgatcgg cattcaccgt 1140
 ttctacgaga gcggcatcgt gttcgaagag tacaaggatt acttctgcat cagcaagtgg 1200
 tatctgaaag aggttaagcg taaaccgtac aacctgaaac tgggctgcaa ctggcaattt 1260
 attccggtgg atgatggctg gggtgaacgt ccgctgtaa 1299

<210> 10
 <211> 424
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hc/TAB2.1.3, increased solubility

<400> 10

Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
 1 5 10 15

Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
 20 25 30

Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
 35 40 45

Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
 50 55 60

Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
 65 70 75 80

Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
 85 90 95

Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
100 105 110

Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
115 120 125

Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
130 135 140

Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
145 150 155 160

Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
165 170 175

Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
180 185 190

Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
195 200 205

Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
210 215 220

Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Phe Asn
225 230 235 240

Ala Gly Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val
245 250 255

Gly Glu Ile Leu Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
260 265 270

Leu Asn Ser Ser Leu Tyr Arg Gly Glu Lys Phe Ile Ile Arg Arg Lys
275 280 285

Ser Asn Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Asn Glu Asp Tyr
290 295 300

Ile Tyr Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr

305		310		315		320									
Tyr	Lys	Tyr	Phe	Lys	Lys	Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Ile
				325					330					335	
Ser	Asp	Ser	Asp	Glu	Phe	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp
			340					345					350		
Glu	Gln	Pro	Thr	Tyr	Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu
		355					360					365			
Ser	Thr	Asp	Glu	Ile	Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Asn	Asn	Lys
	370					375					380				
Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val	Lys	Arg	Lys
385					390					395					400
Pro	Tyr	Asn	Leu	Lys	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Val	Asp
			405						410					415	
Asp	Gly	Trp	Gly	Glu	Arg	Pro	Leu								
			420												

<210> 11
 <211> 1275
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hc/TAB2.1.3, codon optimised for expression in E. coli

<400> 11	
accagcatcc tgaacctgcg ctacgagagc aaccaccta tgcacctgag ccgctacgcg	60
agcaagatta acatcggtag caaggtgaac ttgacccga ttgataaaaa ccagatccaa	120
ctgttcaacc tggaaagcag caagatcgaa gtgattctga aaaacgcatg tgtttataac	180
agcatgtacg aaaacttcag caccagcttt tggatccgta ttccgaagta ttttaacagc	240
atcagcctga acaacgaata caccatcatt aactgcatgg agaacaacag cggttggaag	300
gtgagcctga actacggcga aatcatttgg accctgcagg acaccaaga gatcaagcag	360
cgtgtggttt tcaagtacag ccaaagatgc aacatcagcg attacatcaa ccgttggtatt	420

```

ttcgttacca tcaccaacaa ccgtctgaac aacagcaaga tctacattaa cggtcgtctg      480
attgaccaga aaccgatcag caacctgggc aacattcacg cgagcaacaa catcatgttc      540
aagctggacg gttgccgtga taccaccgtg tatatctgga ttaagtactt caacctgttt      600
gataaagagc tgaacgaaaa ggagattaaa gacctgtatg ataaccagag caacagcggc      660
atcctgaagg acttttgggg cgattatctg caatacgaca aaccgtacta tatgttcaac      720
gcgggtaaca agaacagcta cattaaactg aagaaagata gcccgggtggg tgaaatcctg      780
gggccgcgtg gcagcgttat gaccaccaac atctatctga acagcagcct gtaccgtggc      840
gagaagttca tcattcgtcg taaaagcaac agccagagca ttaacgacga tatcgtgcgt      900
aacgaagact acatttatct ggatttcttt aacctgaacc aagagtggcg tgtttacacc      960
tacaagtact tcaagaaaga ggaagagaag ctgttcctgg cgccgatcag cgacagcgat     1020
gaattctaca acaccatcca aatcaaggaa tacgacgagc agccgaccta tagctgccaa     1080
ctgctgttca agaaagacga agagagcacc gatgaaatcg gtctgatcgg cattcaccgt     1140
ttcaacaaca aggattactt ctgcatcagc aagtggatc tgaaagaggt taagcgtaaa     1200
ccgtacaacc tgaaactggg ctgcaactgg caatttatc cggtggatga tggctggggc     1260
gaacgtccgc tgtaa                                                    1275

```

```

<210> 12
<211> 1343
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> BoNT/TAB2.1.3, full-length active protein

```

```

<400> 12

```

```

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1           5           10          15

```

```

Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
20           25           30

```

```

Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
35           40           45

```

```

Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu

```

50

55

60

Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
 65 70 75 80

Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
 85 90 95

Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
 100 105 110

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
 115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
 130 135 140

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

Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
 165 170 175

Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
 180 185 190

Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
 195 200 205

Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Ala
 210 215 220

Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
 225 230 235 240

Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
 245 250 255

Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
 260 265 270

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
275 280 285

Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
290 295 300

Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
305 310 315 320

Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
325 330 335

Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
340 345 350

Asn Phe Val Lys Phe Phe Lys Val Leu Asn Ala Lys Thr Phe Leu Asn
355 360 365

Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
370 375 380

Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
385 390 395 400

Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
405 410 415

Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
420 425 430

Gly Ile Ile Thr Ser Lys Ala Gly Ala Gly Lys Ser Leu Val Pro Arg
435 440 445

Gly Ser Ala Gly Ala Gly Ala Leu Asn Asp Leu Cys Ile Lys Val Asn
450 455 460

Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp
465 470 475 480

Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala

485

490

495

Glu Glu Asn Ile Ser Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe
 500 505 510

Asn Phe Asp Asn Glu Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser
 515 520 525

Asp Ile Ile Gly Gln Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro
 530 535 540

Asn Gly Lys Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu
 545 550 555 560

Arg Ala Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn
 565 570 575

Ser Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe
 580 585 590

Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met
 595 600 605

Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr
 610 615 620

Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile
 625 630 635 640

Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp
 645 650 655

Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu
 660 665 670

Phe Ile Pro Glu Ile Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val
 675 680 685

Ser Tyr Ile Ala Asn Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala
 690 695 700

Leu Ser Lys Arg Asn Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val
705 710 715 720

Thr Asn Trp Leu Ala Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys
725 730 735

Lys Met Lys Glu Ala Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile
740 745 750

Ile Asn Tyr Gln Tyr Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile
755 760 765

Asn Phe Asn Ile Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn
770 775 780

Lys Ala Met Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser
785 790 795 800

Tyr Leu Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp
805 810 815

Phe Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn
820 825 830

Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn
835 840 845

Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp
850 855 860

Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile
865 870 875 880

Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp
885 890 895

Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe
900 905 910

Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser

915

920

925

Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr
 930 935 940

Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn
 945 950 955 960

Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn
 965 970 975

Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr
 980 985 990

Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser
 995 1000 1005

Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val
 1010 1015 1020

Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
 1025 1030 1035

Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile
 1040 1045 1050

His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp
 1055 1060 1065

Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys
 1070 1075 1080

Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser
 1085 1090 1095

Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr
 1100 1105 1110

Asp Lys Pro Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr
 1115 1120 1125

Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Gly Pro
1130 1135 1140

Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu
1145 1150 1155

Tyr Arg Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln
1160 1165 1170

Ser Ile Asn Asp Asp Ile Val Arg Asn Glu Asp Tyr Ile Tyr Leu
1175 1180 1185

Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys
1190 1195 1200

Tyr Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser
1205 1210 1215

Asp Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp
1220 1225 1230

Glu Gln Gly Thr Asn Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu
1235 1240 1245

Glu Ser Thr Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr
1250 1255 1260

Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile
1265 1270 1275

Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu
1280 1285 1290

Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Asp Gly Trp
1295 1300 1305

Gly Glu Arg Pro Leu Val Pro Arg Gly Ser Ala Asn Ser Ser Ser
1310 1315 1320

Val Asp Lys Leu Trp Ser His Pro Gln Phe Glu Lys Leu Glu His

1325

1330

1335

His His His His His
1340

<210> 13

<211> 4032

<212> DNA

<213> Artificial Sequence

<220>

<223> BoNT/TAB2.1.3, sequence included in pEt29(a) vector for
expression in E. coli

<400> 13

atgccatttg tgaacaagca gtttaactat aaggacccgg tgaacggtgt ggatatcgcg	60
tatatcaaaa tcccgaatgc gggccagatg caaccagtca aggcgttcaa gattcataac	120
aagatttggg ttattccgga acgtgatacc ttcaccaatc cggaagaagg cgacttaaac	180
ccgccgccag aagccaaaca agtgccggtg agctactatg atagcacgta tcttagcacc	240
gataatgaaa aagacaatta cctgaagggc gtgaccaagt tgttcgagcg catctacagt	300
accgacttag gccgcatggt gttgacgagc atcgttcgcg gtatcccggt ctggggcggc	360
tcgaccattg ataccgagtt gaaagtcatt gacacgaact gtatcaatgt tatccaaccg	420
gacggcagtt atcgcagcga ggagttaaatt ttggtcatca tcggtccaag cgcagatatt	480
attcagttcg aatgcaagag cttcggccat gaggtcctga atttgacgcg caacggttac	540
ggcagcacc aatacatccg ctttagcccg gatttcacct ttggcttcga ggagagcttg	600
gaggtggaca ccaaccgct gttaggtgcc ggcaaattcg caaccgacc ggcagtgacg	660
ttggcgcacg cgttgattca tgcgggtcac cgcttatacg gtatcgcgat caatccgaat	720
cgcgtcttta aagtcaatac caacgcgtac tacgaaatga gcggcttaga ggtagcttt	780
gaagaattac gcaccttcgg tggccacgac gccaaattca tcgacagcct gcaggaaaat	840
gagttccgct tgtactatta caataaattc aaggacatcg cgagcacctt aaataaagca	900
aagagcattg tgggcaccac cgcaagcttg cagtacatga agaacgtatt taaggaaaaa	960
tatttgttgt cggaggatac cagcgggaaa ttcagcgtcg ataagctgaa attcgacaaa	1020
ttgtataaaa tgctgaccga gatttacacc gaggataact tcgtcaagtt ttttaaggtg	1080
ttaaatgcga agaccttttt aaactttgat aaagcgggtg ttaaaattaa tatcgtgccg	1140

aaggtgaatt acaccatcta cgatggtttc aattttacgca acacgaatct ggcggcgaat	1200
tttaatggcc aaaacaccga aattaacaac atgaacttta cgaagttaaa gaatttcacg	1260
ggcttattcg aattctacaa gttattatgc gtgcgcggca tcattaccag caaggcaggt	1320
gcgggcaagt ccttggttcc gcgtggcagc gccggcgccg gcgcgctcaa tgatctgtgt	1380
attaaagtca ataactggga cctgttcttc agcccgagcg aggataactt taccaacgac	1440
ttaaacaaag gcgaggagat cacgagcgat acgaacatcg aggcggcgga ggaaaatatt	1500
agcctggacc tcattcagca gtactatctg acgttcaatt ttgacaatga gccggagAAC	1560
atcagcattg aaaatctcag cagcgacatc atcggtcagt tggaactgat gccgaacatt	1620
gaacgctttc cgaacggcaa aaaatatgaa ctggacaagt ataccatgtt ccattactta	1680
cgcgcacagg aatttgagca cggcaagagc cgcattgcgc tgaccaatag cgttaacgag	1740
gccttgtaa atccgagccg tgtctacacg ttcttcagca gcgattatgt caaaaaagtg	1800
aacaaggcga ccgaagccgc gatgtttttg ggctgggtcg agcaattggt ttacgatttt	1860
accgacgaaa ccagcgaggt gagcacgacc gacaaaattg cagatatcac catcatcatt	1920
ccgtacatcg gtccggcgct caatatcggc aatatgttat acaaggacga ctttgtgggc	1980
gcgctgatct ttagcggcgc ggttatctta ttagaattca tcccggagat cgcaatcccg	2040
gtcttgggca ctttgcgtt ggtgagctat atcgcgaata aagtgctcac ggtccaaacc	2100
atcgataacg cgctcagcaa gcgtaatgag aaatgggacg aggtttataa gtatatcgtg	2160
accaactggt tagcaaaagt caatacgagc atcgatctca tccgcaaaaa aatgaaagaa	2220
gccttggaag atcaagcggg ggcaaccaa gccatcatta attaccagta taaccaatat	2280
accgaagaag aaaaaaaca tatcaacttc aatatcgatg atttgagcag caaactgaac	2340
gagagcatta acaaagcgat gattaacatc aacaagttct tgaatcaatg cagcgtgagc	2400
tatctcatga acagcatgat cccgtatggc gtcaaacgct tggaagattt tgacgccagc	2460
ctgaaagatg cgctcctcaa gtatatattat gacaaccgcg gcaccctcat tggccaggtg	2520
gaccgcttga aggataaagt gaacaatacg ctcagcacgg atatcccggt ccagctgagc	2580
aagtacgtcg acaaccagcg ctactgagc acctttaccg agtatatcaa gaacatcatt	2640
aataccagca tcctcaactt gcgctatgag agcaatcacc tgatcgacct cagccgctac	2700
gccagcaaga tcaacatcgg cagcaaggtc aatttcgacc cgatcgataa gaatcagatc	2760

caattgttta acctggaaag cagcaagatc gaggttatct tgaagaacgc gatttgtgtac	2820
aacagcatgt atgagaactt tagcaccagc ttctggattc gtatcccgaa atatttcaac	2880
agcattagcc tgaacaacga gtacaccatt atcaactgca tggaaaacaa cagcggttgg	2940
aaggtgagcc tgaactacgg cgagattatc tggaccctgc aggacacca agaaatcaag	3000
cagcgtgtgg ttttcaagta cagccaaatg atcaacatca gcgattacat taaccgttgg	3060
atctttgtta ccattaccaa caaccgtctg aacaacagca aaattttacat caacggctgt	3120
ctgatcgacc agaagccgat tagcaacctg ggcaacatcc acgcgagcaa caacattatg	3180
ttcaagctgg acggttgccg tgataccac cgttatatct ggatcaagta cttcaacctg	3240
ttcgataagg agctgaacga gaaggaaatc aaagacctgt atgataacca gagcaacagc	3300
ggtatttctga aagacttctg gggcgattac ctgcaatatg acaagccgta ttacatgttt	3360
aacgcgggta acaagaacag ctacatcaaa ctgaagaaag atagcccgtt gggtgaaatt	3420
ctgggtccgc gtggcagcgt tatgaccacc aacatctatc tgaacagcag cctgtaccgt	3480
ggcgaaaagt tcattatccg tcgtaaaagc aacagccaga gcatcaacga cgatattgtg	3540
cgtaacgagg actatatcta cctggatttc tttaacctga accaagaatg gcgtgtttac	3600
acctacaagt acttcaagaa agaagaggaa aagctgtttc tggcgccgat tagcgacagc	3660
gatgaattct ataacacatc tcagatcaaa gactacgacg aacagggtac caacagctgc	3720
caactgctgt ttaagaaaga cgaggaaagc accgatgaga tcggtctgat tggcatccac	3780
cgtttttacg aaagcggcat cgtgttcgag gaatacaagg attacttctg catcagcaag	3840
tggatatctga aagagggtta gcgtaaaccg tacaacctga aactgggctg caactggcaa	3900
tttattccgg tggatgatgg ctggggtgaa cgtccactag tgccacgcgg ttccgcgaat	3960
tcgagctccg tcgacaagct ttggagccac ccgcagttcg aaaaactcga gcaccaccac	4020
caccaccact ga	4032

<210> 14
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hSytI peptide

<400> 14

Gly	Glu	Gly	Lys	Glu	Asp	Ala	Phe	Ser	Lys	Leu	Lys	Glu	Lys	Phe	Met
1				5					10					15	

Asn	Glu	Leu	His	Lys
			20	