

SEQUENCE LISTING

<110> Crescendo Biologics Limited

<120> Binding Molecules

<130> P36323W01

<150> GB1906870.9

<151> 2019-05-15

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<151> 2019-05-15

<160> 39

<170> PatentIn version 3.5

<210> 1

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ala Gly Thr His Ile Tyr Ser Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Pro His Ser Thr Gly Trp Tyr Lys Asp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 2
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 <213> Homo sapiens

<400> 2

Asn Tyr Asn Met Asn
 1 5

<210> 3
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 3

Ser Ile Ser Ser Ala Gly Thr His Ile Tyr Ser Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 4
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 4

Asp Pro His Ser Thr Gly Trp Tyr Lys Asp Phe Asp Tyr
 1 5 10

<210> 5
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 5

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Tyr
 20 25 30

Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ser Gly Arg Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Pro Arg Met Val Gly Asn Pro His Glu Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

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<212> PRT
<213> Homo sapiens

<400> 6

Ser Tyr Thr Met Asn
1 5

<210> 7
<211> 17
<212> PRT
<213> Homo sapiens

<400> 7

Ser Ile Ser Ser Ser Gly Arg Tyr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 8
<211> 13
<212> PRT

<213> Homo sapiens

<400> 8

Asp Pro Arg Met Val Gly Asn Pro His Glu Phe Asp Ile
1 5 10

<210> 9

<211> 609

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
20 25 30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
35 40 45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
100 105 110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115 120 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
130 135 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165 170 175

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
195 200 205

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Gly Leu Lys Cys
210 215 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225 230 235 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
245 250 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
290 295 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305 310 315 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Gly Ser
325 330 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
340 345 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
355 360 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys

370

375

380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385 390 395 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
405 410 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
420 425 430

Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
435 440 445

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
450 455 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Cys Leu Ser Val Phe
465 470 475 480

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
485 490 495

Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Gly Arg Pro Cys Phe
500 505 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
515 520 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
530 535 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545 550 555 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
565 570 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
580 585 590

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
595 600 605

Leu

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> C-terminal extension

<400> 10

Val Thr Val Ser Ser
1 5

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His-tag

<400> 11

His His His His His His
1 5

<210> 12
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Gly Ser linker

<400> 12

Gly Gly Gly Gly Ser
1 5

<210> 13
<211> 10
<212> PRT

<213> Artificial Sequence

<220>

<223> Gly Ser linker

<400> 13

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 14

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Gly Ser linker

<400> 14

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10

<210> 15

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Gly Ser linker

<400> 15

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10

<210> 16

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Gly Ser linker

<400> 16

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 17

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

<220>
<223> Gly Ser linker

<400> 17

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 18
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Gly Ser linker

<400> 18

Gly Gly Ser Gly Ser Gly
1 5

<210> 19
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Gly Ser linker

<400> 19

Gly Gly Ser Gly
1

<210> 20
<211> 366
<212> DNA
<213> Homo sapiens

<400> 20
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tcctgtgcag cctctggatt caccttcagt aactataaca tgaactgggt ccgccaggct 120
ccagggaaga ggctggagtg ggtctcatcg attagtagtg ctggtactca catatactcc 180
gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctactgtat 240

ctgcaaatga acagcctgag agccgaggac acaggtgttt attactgtgc gagagatcct	300
catagcactg gctggtacaa ggactttgac tactggggcc agggaaccct ggtcaccgtc	360
tcctca	366

<210> 21
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 21	
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tcctgtgcag cctctggatt caccgtcagt agctatacca tgaactgggt ccgccaggct	120
ccggggaagg ggctggagtg ggtctcatcc attagtagta gtggtcgtta catatactac	180
gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcattatat	240
ctgcaaatga acagcctgag agccgaggac acagctgtat attattgtgc gagagatccc	300
cgtatggttg ggaaccccca tgaatttgat atctggggcc aagggacaat ggtcaccgtc	360
tcctca	366

<210> 22
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP-814 construct

<400> 22

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1			5					10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Ser	Gly	Tyr
			20					25					30		

Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ala	Tyr	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
165 170 175

Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr Trp Met Asn
180 185 190

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
195 200 205

Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys Gly Arg
210 215 220

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
225 230 235 240

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
245 250 255

Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val Ser Gly Gln
260 265 270

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

275

280

285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu
 290 295 300

Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu
 305 310 315 320

Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Tyr Thr Met Asn Trp
 325 330 335

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser
 340 345 350

Ser Ser Gly Arg Tyr Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe
 355 360 365

Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn
 370 375 380

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro
 385 390 395 400

Arg Met Val Gly Asn Pro His Glu Phe Asp Ile Trp Gly Gln Gly Thr
 405 410 415

Met Val Thr Val Ser Ser
 420

<210> 23
 <211> 1266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP-814 construct

<400> 23
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 tcctgtgcag cctctggatt ctccttcagt ggctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg	300
gcctggggat tacgtttggg ggagtcacgc tcctatgatt ttgatatctg gggccaaggg	360
acaatgggtca ccgtctcctc aggtgggtggc ggttcaggcg gaggtggctc tggaggtgga	420
ggttcaggag gtggtgggtc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag	480
ttagttgaga gcggaggtgg tttagttcag ccggggggct cgcttcgcct gtcgtgcgcc	540
gcctcgggat tcacattatc aaactactgg atgaattggg tccgccaggc tccgggcaaa	600
ggtcttgagt ggggtggcgaa cattaatcag gacgggagcg agcgttatta cgttgattcg	660
gtaaaaggac gtttcactat cagtcgtgac aacgctaaaa attccttgta cttacagatg	720
aactcacttc gtgctgagga caccgcagtg tactactgtg ctgcggtgg tgaaggatac	780
ggcgtcgatc actacggcct tgatgtatca ggacagggga ctacagttac cgtctcttcc	840
ggaggtggag gttcaggagg tgggtggttct ggtggtggcg gttcagggtg aggtggtagt	900
gaggtgcagc tgttggagtc tgggggaggc ctggtcaagc cgggggggtc cctgagactc	960
tcctgtgcag cctctggatt caccgtcagt agctatacca tgaactgggt ccgccaggct	1020
ccggggaagg ggctggagtg ggtctcatcc attagtagta gtggtcgtta catatactac	1080
gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcattatat	1140
ctgcaaatga acagcctgag agccgaggac acagctgtat attattgtgc gagagatccc	1200
cgtatggttg ggaaccccca tgaatttgat atctggggcc aagggacaat ggtcaccgtc	1260
tcctca	1266

<210> 24
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP-712 construct

<400> 24

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Gly Tyr

20

25

30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Tyr Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Ala Trp Gly Leu Arg Leu Gly Glu Ser Ser Ser Tyr
 100 105 110

Asp Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 145 150 155 160

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 165 170 175

Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr Trp Met Asn
 180 185 190

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
 195 200 205

Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val Lys Gly Arg
 210 215 220

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met
 225 230 235 240

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
245 250 255

Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val Ser Gly Gln
260 265 270

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
305 310 315 320

Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
325 330 335

Phe Thr Phe Ser Asn Tyr Asn Met Asn Trp Val Arg Gln Ala Pro Gly
340 345 350

Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ala Gly Thr His Ile
355 360 365

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
370 375 380

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
385 390 395 400

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro His Ser Thr Gly Trp Tyr
405 410 415

Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
420 425 430

<210> 25
<211> 1296
<212> DNA
<213> Artificial Sequence

<220>

<223> TPP-712 construct

<400> 25

gaggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc	60
tcctgtgcag cctctggatt ctccttcagt ggctatggca tgcactgggt ccgccaggct	120
ccaggcaagg gactggagtg ggtggcatat atatcatatg atggaagtaa taaatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagatccg	300
gcctggggat tacgtttggg ggagtcacg tcctatgatt ttgatatctg gggccaaggg	360
acaatggtca ccgtctcctc aggtgggtggc ggttcaggcg gaggtggctc tggaggtgga	420
ggttcaggag gtggtggttc tggcggcggt ggatcgggtg gaggtggtag tgaggtgcag	480
ttagttgaga gcggaggtgg tttagttcag ccggggggct cgcttcgcct gtcgtgcgcc	540
gcctcgggat tcacattatc aaactactgg atgaattggg tccgccaggc tccgggcaaa	600
ggtcttgagt ggggtggcgaa cattaatcag gacgggagcg agcgttatta cgttgattcg	660
gtaaaaggac gtttcactat cagtcgtgac aacgctaaaa attccttgta cttacagatg	720
aactcacttc gtgctgagga caccgcagtg tactactgtg ctgcggttg tgaaggatac	780
ggcgtcgatc actacggcct tgatgtatca ggacagggga ctacagttac cgtctcttcc	840
ggtgggtggcg gttcaggcgg aggtggctct ggaggtggag gttcaggagg tgggtggttct	900
ggcggcggtg gatcgggtgg aggtggtagt gaggtgcagc tgggtggagtc tgggggaggc	960
ctggtcaagc ctggggggtc cctgagactc tcctgtgcag cctctggatt caccttcagt	1020
aactataaca tgaactgggt ccgccaggct ccagggaagg ggctggagtg ggtctcatcg	1080
attagtagtg ctggtactca catatactac gcagactcag tgaagggccg attcaccatc	1140
tccagagaca acgccaagaa ctactgtat ctgcaaatga acagcctgag agccgaggac	1200
acagctgttt attactgtgc gagagatcct catagcactg gctggtacaa ggactttgac	1260
tactggggcc aggggaaccct ggtcaccgtc tcctca	1296

<210> 26

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> TPP-446 construct

<400> 26

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Asp Ala Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Asn
165 170 175

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val Ser
180 185 190

Ser Ile Ser Ser Ala Gly Thr His Ile Tyr Ser Ala Asp Ser Val Lys

195

200

205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Val Tyr Tyr Cys Ala
 225 230 235 240

Arg Asp Pro His Ser Thr Gly Trp Tyr Lys Asp Phe Asp Tyr Trp Gly
 245 250 255

Gln Gly Thr Leu Val Thr Val Ser Ser
 260 265

<210> 27
 <211> 795
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP-446 construct

<400> 27
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
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 ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180
 gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
 ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300
 gtccactggg gccagggaac cctggtcacc gtctcctcag gtggtggcgg ttcaggcgga 360
 ggtggctctg gaggtggagg ttcaggaggt ggtggttctg gcggcggtgg atcgggtgga 420
 ggtggtagtg aggtgcagct gttggagtct gggggaggcc tgggtcaagcc tgggggggtcc 480
 ctgagactct cctgtgcagc ctctggattc accttcagta actataacat gaactgggtc 540
 cgccaggctc cagggaagag gctggagtggt gtctcatcga ttagtagtgc tgggtactcac 600
 atatactccg cagactcagt gaagggccga ttcaccatct ccagagacaa cgccaagaac 660
 tcactgtatc tgcaaatgaa cagcctgaga gccgaggaca caggtgttta ttactgtgcg 720
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gtcaccgtct cctca

795

<210> 28
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-708 construct

<400> 28

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Glu Asn Asp Gly Thr Thr Asp Tyr Ala Asp Ala Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Val His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
145 150 155 160

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Tyr Thr

165

170

175

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 180 185 190

Ser Ile Ser Ser Ser Gly Arg Tyr Ile Tyr Tyr Ala Asp Ser Val Lys
 195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 225 230 235 240

Arg Asp Pro Arg Met Val Gly Asn Pro His Glu Phe Asp Ile Trp Gly
 245 250 255

Gln Gly Thr Met Val Thr Val Ser Ser
 260 265

<210> 29

<211> 795

<212> DNA

<213> Artificial Sequence

<220>

<223> TPP-708 construct

<400> 29

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cagtttttagc agctatgccc tcagttgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcaagt attggtgaga atgatggtac cacagactac 180

gcagacgccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240

ctgcaaatga acagcctgag agtcgaggac acggccgtct attactgtgt gaaagatggt 300

gtccactggg gccagggaac cctggtcacc gtctcctcag gtggtggcgg ttcaggcgga 360

ggtggctctg gaggtggagg ttcaggaggt ggtggttctg gcggcggtgg atcgggtgga 420

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cgccaggctc cggggaaggg gctggagtgg gtctcatcca ttagtagtag tggtcgttac 600
atatactacg cagactcagt gaagggccga ttcaccatct ccagagacaa cgccaagaac 660
tcattatatac tgcaaatgaa cagcctgaga gccgaggaca cagctgtata ttattgtgcg 720
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gtcaccgtct cctca 795

<210> 30
<211> 122
<212> PRT
<213> Homo sapiens

<400> 30

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Ala Gly Thr His Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Pro His Ser Thr Gly Trp Tyr Lys Asp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 31
<211> 366
<212> DNA
<213> Homo sapiens

<400> 31
 gaggtgcagc tgggtggagtc tgggggaggc ctggtcaagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt caccttcagt aactataaca tgaactgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcatcg attagtagtg ctggtactca catatactac 180
 gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240
 ctgcaaatga acagcctgag agccgaggac acagctgttt attactgtgc gagagatcct 300
 catagcactg gctggtacaa ggactttgac tactggggcc agggaaccct ggtcaccgtc 360
 tcctca 366

<210> 32
 <211> 437
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP-1027 construct

<400> 32

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
 100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
145 150 155 160

Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
165 170 175

Ala Ser Gly Phe Thr Phe Ser Asn Tyr Asn Met Asn Trp Val Arg Gln
180 185 190

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ala Gly
195 200 205

Thr His Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
210 215 220

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
225 230 235 240

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro His Ser Thr
245 250 255

Gly Trp Tyr Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
260 265 270

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly
305 310 315 320

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp

325

330

335

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 340 345 350

Val Ser Gly Ile Thr Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser
 355 360 365

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
 370 375 380

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr
 385 390 395 400

Cys Val Arg Asp Lys Tyr Ser Tyr Ala Trp Ser Tyr Asp Asp Phe Asp
 405 410 415

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ala Ala His
 420 425 430

His His His His His
 435

<210> 33
 <211> 437
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TPP-1028 construct

<400> 33

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser
145 150 155 160

Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
165 170 175

Ala Ser Gly Phe Thr Val Ser Ser Tyr Thr Met Asn Trp Val Arg Gln
180 185 190

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Gly
195 200 205

Arg Tyr Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
210 215 220

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
225 230 235 240

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro Arg Met Val
245 250 255

Gly Asn Pro His Glu Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
260 265 270

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly
305 310 315 320

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp
325 330 335

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
340 345 350

Val Ser Gly Ile Thr Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser
355 360 365

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
370 375 380

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr
385 390 395 400

Cys Val Arg Asp Lys Tyr Ser Tyr Ala Trp Ser Tyr Asp Asp Phe Asp
405 410 415

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ala Ala His
420 425 430

His His His His His
435

<210> 34
<211> 437
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP1010 - construct

<400> 34

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Thr Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Arg Asp Lys Tyr Ser Tyr Ala Trp Ser Tyr Asp Asp Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
145 150 155 160

Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
165 170 175

Ala Ser Gly Phe Thr Phe Ser Asn Tyr Asn Met Asn Trp Val Arg Gln
180 185 190

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ala Gly
195 200 205

Thr His Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser

210

215

220

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
 225 230 235 240

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro His Ser Thr
 245 250 255

Gly Trp Tyr Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 260 265 270

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 290 295 300

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
 305 310 315 320

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn
 325 330 335

Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 340 345 350

Val Ala Val Ile Ser Asn Asp Gly Asn Thr Lys Thr Tyr Ala Asp Ser
 355 360 365

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 370 375 380

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 385 390 395 400

Cys Ala Gln Asp Glu Thr Thr Thr Val Thr Ala Ser Tyr Tyr Phe Asp
 405 410 415

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ala Ala His
 420 425 430

His His His His His
435

<210> 35
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> TPP-1246 construct

<400> 35

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Asn Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Arg Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Glu Gly Tyr Gly Val Asp His Tyr Gly Leu Asp Val
100 105 110

Ser Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
145 150 155 160

Gly Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
165 170 175

Ala Ser Gly Phe Thr Phe Ser Asn Tyr Asn Met Asn Trp Val Arg Gln
180 185 190

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ala Gly
195 200 205

Thr His Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
210 215 220

Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
225 230 235 240

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Pro His Ser Thr
245 250 255

Gly Trp Tyr Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
260 265 270

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
275 280 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
290 295 300

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly
305 310 315 320

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp
325 330 335

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
340 345 350

Val Ser Gly Ile Thr Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser
355 360 365

Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu

370

375

380

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr
 385 390 395 400

Cys Val Arg Asp Lys Tyr Ser Tyr Ala Trp Ser Tyr Asp Asp Phe Asp
 405 410 415

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 420 425

<210> 36

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<223> TPP-1246 construct

<400> 36

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 ccgggcaaag gtcttgagtg ggtggcgaac attaatcagg acgggagcga gcgttattac 180
 gttgattcgg taaaaggacg tttcactatc agtcgtgaca acgctaaaaa ttccttgtac 240
 ttacagatga actcacttcg tgctgaggac accgcagtgt actactgtgc tcgcggtggt 300
 gaaggatacg gcgtcgatca ctacggcctt gatgtatcag gacaggggac tacagttacc 360
 gtctcttccg gtgggtggcg ttcaggcgga ggtggctctg gaggtggagg ttcaggaggt 420
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 gactttgact actggggcca gggaaccctg gtcaccgtct cctcaggtgg tggcggttca 840
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ggtggaggtg gtagtgaggt gcagctggtg gagtctgggg gaggtgtggt acggcctggg	960
gggtcccctga gactctcctg tgcagcctct ggattcacct ttgatgatta tgccatgagt	1020
tgggtccgcc aagctccagg gaaggggctg gagtgggtct ctggtattac ttggaatggt	1080
ggtagcacag gttatgcaga ctctgtgaag gaccgattca ccatctccag agacaacgcc	1140
aagaactccc tgtatctgca aatgaacagt ctgagagccg aggacacggc cttgtattac	1200
tgtgtgagag acaagtatag ctatgcctgg tcttatgatg attttgatat ctggggccaa	1260
gggacaatgg tcaccgtctc ctca	1284

<210> 37
 <211> 1311
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP-1010 construct

<400> 37	
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gcagactctg tgaaggaccg attcaccatc tccagagaca acgccaagaa ctccctgtat	240
ctgcaaatga acagtctgag agccgaggac acggccttgt attactgtgt gagagacaag	300
tatagctatg cctgggtctta tgatgatattt gatatctggg gccaaggagc aatggtcacc	360
gtctcctcag gtggtggcgg ttcaggcggg ggtggctctg gaggtggagg ttcaggaggt	420
ggtggttctg gcggcggtgg atcgggtgga ggtggtagtg aggtgcagct ggtggagtct	480
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gccgaggaca cagctgttta ttactgtgcg agagatcctc atagcactgg ctggtacaag	780
gactttgact actggggcca gggaaccctg gtcaccgtct cctcaggcgg aggtggctct	840
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tgggtccgcc aggctccagg caagggcctg gagtgggtgg cagtcatatc aaatgatgga	1080
aataactaaaa cctatgcaga ttccgtgaag ggccgattca ccatctccag agacaattcc	1140
aagaacacgt tatatctgca aatgaacagc ctgagagctg aggacacggc tgtgtattac	1200
tgtgcgcaag atgagacgac tacagtaact gcgtcgtatt actttgacta ctggggccag	1260
ggaaccctgg tcaccgtctc ctgagcggcc gcacaccacc atcatcacca c	1311

<210> 38
 <211> 1311
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TPP-1027 construct

<400> 38	
gaggtgcagt tagttgagag cggaggtgggt ttagttcagc cggggggctc gcttcgcctg	60
tcgtgcgccg cctcgggatt cacattatca aactactgga tgaattgggt ccgccaggct	120
ccgggcaaag gtcttgagtg ggtggcgaac attaatacagg acgggagcga gcgttattac	180
gttgattcgg taaaaggacg ttctactatc agtcgtgaca acgctaaaaa ttccttgtag	240
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gaaggatacg gcgtcgatca ctacggcctt gatgtatcag gacaggggac tacagttacc	360
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ggtagcacag gttatgcaga ctctgtgaag gaccgattca ccatctccag agacaacgcc	1140
aagaactccc tgtatctgca aatgaacagt ctgagagccg aggacacggc cttgtattac	1200
tgtgtgagag acaagtatag ctatgcctgg tcttatgatg attttgatat ctggggccaa	1260
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<210> 39

<211> 1311

<212> DNA

<213> Artificial Sequence

<220>

<223> TPP-1028 construct

<400> 39

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ccgggcaaag gtcttgagtg ggtggcgaac attaatacagg acgggagcga gcgttattac	180
gttgattcgg taaaaggacg tttcactatc agtcgtgaca acgctaataaa ttccttgtag	240
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gggggaggcc tgggtcaagcc ggggggggtc ctgagactct cctgtgcagc ctctggattc	540
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gtctcatcca ttagtagtag tggtcgttac atatactacg cagactcagt gaagggccga	660
ttcaccatct ccagagacaa cgccaagaac tcattatatc tgcaaatgaa cagcctgaga	720
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gaatttgata tctggggcca agggacaatg gtcaccgtct cctcagggtg tggcggttca	840
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gggtccctga gactctcctg tgcagcctct ggattcacct ttgatgatta tgccatgagt	1020
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ggtagcacag gttatgcaga ctctgtgaag gaccgattca ccatctccag agacaacgcc	1140
aagaactccc tgtatctgca aatgaacagt ctgagagccg aggacacggc cttgtattac	1200
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