

SEQUENCE LISTING

<110> Xbrane Biopharma AB

<120> NOVEL COMBINATION OF TIS SEQUENCE AND SIGNAL PEPTIDE SEQUENCE FOR EXPRESSING A RECOMBINANT PROTEIN

<130> 2020Q105-2

<160> 14

<170> BiSSAP 1.3.6

<210> 1

<211> 11

<212> DNA

<213> Artificial Sequence

<220>

<223> Kozak sequence - DNA

<400> 1

tcggtcatgg c

11

<210> 2

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Signal peptide - DNA sequence

<400> 2

atggctctgc tgcacaagaa catgaagcac ctgtggttct ttctgctgct ggtggccgct

60

cctagatggg tgctgtct

78

<210> 3

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Signal peptide aa sequence

<400> 3

Met Ala Leu Leu His Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu

1

5

10

15

Leu Val Ala Ala Pro Arg Trp Val Leu Ser

<210> 4
 <211> 1326
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nivolumab - heavy chain - DNA sequence

<400> 4
 caggtgcagc tggttgaatc tgggtggcgga gtggtgcagc ctggcagatc tctgagactg 60
 gattgcaagg cctccggcat caccttctcc aactctggca tgcactgggt ccgacaggcc 120
 cctggaaaag gactggaatg ggtcgccgtg atttggtacg acggctctaa gcggtactac 180
 gccgactccg tgaagggcag attcaccatc tctcgggaca actccaagaa caccctgttt 240
 ctgcagatga actccctgag agccgaggac accgccgtgt actactgtgc caccaacgat 300
 gattattggg gccagggcac actggtcacc gtgtcctctg cttctaccaa gggaccctct 360
 gtgttccctc tggctccttg ctccagatcc acctctgagt ctaccgtgc tctgggctgc 420
 ctgggtcaagg attactttcc tgagcctgtg accgtgtctt ggaactctgg tgctctgacc 480
 tccggcgtgc acacatttcc agctgtgctg cagtcctccg gcctgtactc tctgtcctct 540
 gtcgtgaccg tgccttctag ctctctgggc accaagacct acacctgtaa cgtggaccac 600
 aagccttcca acaccaaggt ggacaagcgc gtggaatcta agtacggccc tccttgtcct 660
 ccatgtcctg ctccagaatt cctcggcgga ccttccgtgt tcctgtttcc tccaaagcct 720
 aaggacaccc tgatgatctc tcggaccct gaagtgcct gcgtgggtgg ggatgtgtct 780
 caagaggacc ccgaggtgca gttcaattgg tacgtggacg gcgtggaagt gcacaacgcc 840
 aagaccaagc ctagagagga acagttcaac tccacctaca gagtgggtgtc cgtgctgacc 900
 gtgctgcacc aggattggct gaacggcaaa gagtacaagt gcaaggtgtc caacaagggc 960
 ctgccttcca gcatcgaata gaccatctcc aaggctaagg gccagcctcg ggaacctcag 1020
 gtttacaccc tgcctccaag ccaagaggaa atgaccaaga accaggtgtc cctgacctgc 1080
 ctctgtaagg gattctaccc ttccgatatc gccgtggaat gggagtccaa tggccagcct 1140
 gagaacaact acaagacaac ccctcctgtg ctggactccg acggctcctt ctttctgtat 1200
 tccgcctga ccgtggacaa gtctagatgg caagagggca acgtgttctc ctgctctgtg 1260

atgcacgagg ccctgcacaa ccactacacc cagaagtccc tgtctctgtc cctgggcaaa 1320
 tgatag 1326

<210> 5
 <211> 440
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Nivolumab - heavy chain - protein sequence

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

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

<210> 6

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<223> Nivolumab - light chain - DNA sequence

<400> 6

gagatcgtgc tgaccagtc tcctgccaca ttgtctctga gtcctggcga gagagctacc	60
ctgtcttgca gagcttccca gtccgtgtcc tcctacctgg cctggtatca gcagaaacct	120
ggacaggccc ctcggctgct gatctacgat gcctctaata gagccacagg catccccgcc	180
agattctctg gctctggatc tggcaccgac ttcaccctga ccatctctag cctggaacct	240
gaggacttcg ccgtgtacta ctgccagcag tcctccaact ggcctagaac ctttggccag	300
ggcaccaagg tggaaatcaa gagaaccgtg gctgcccctt ccgtgttcat cttcccacca	360
tctgacgagc agctgaagtc cggcacagct tctgtcgtgt gcctgctgaa caacttctac	420
cctcgggaag ccaaggtgca gtggaagggtg gacaatgccc tgcagtccgg caactcccaa	480
gagtctgtga ccgagcagga ctccaaggac tctacctaca gcctgtcctc cacactgacc	540
ctgtctaagg ccgactacga gaagcacaag gtgtacgcct gtgaagtgac ccaccaggga	600
ctgtctagcc ccgtgaccaa gtctttcaac agaggcgagt gctgatag	648

<210> 7

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Nivolumab - light chain - protein sequence

<400> 7

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

<210> 8

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<223> Kozak - SP - protein heavy chain - DNA

<400> 8

```
tcggtcatgg ccctgctgca caagaacatg aagcacctgt gggtctttct gctgctggtg      60
gccgctccta gatgggtggt gtctcaggtg cagctgggtg aatctgggtg cggagtgggt      120
cagcctggca gatctctgag actggattgc aaggcctccg gcatcacctt ctccaactct      180
ggcatgcact ggggtccgaca ggcccctgga aaaggactgg aatgggtcgc cgtgatttgg      240
```

tacgacggct ctaagcggt a ctacgccgac tccgtgaagg gcagattcac catctctcgg	300
gacaactcca agaacaccct gtttctgcag atgaactccc tgagagccga ggacaccgcc	360
gtgtactact gtgccaccaa cgatgattat tggggccagg gcacactggg caccgtgtcc	420
tctgcttcta ccaagggacc ctctgtgttc cctctggctc cttgctccag atccacctct	480
gagtctaccg ctgctctggg ctgcctgggc aaggattact ttcctgagcc tgtgaccgtg	540
tcttggaact ctgggtgctct gacctccggc gtgcacacat ttccagctgt gctgcagtcc	600
tccggcctgt actctctgtc ctctgtcgtg accgtgcctt ctagctctct gggcaccaag	660
acctacacct gtaacgtgga ccacaagcct tccaacacca aggtggacaa gcgcgtggaa	720
tctaagtagc gccctccttg tcctccatgt cctgctccag aattcctcgg cggaccttcc	780
gtgttcctgt ttcctccaaa gcctaaggac accctgatga tctctcggac ccctgaagtg	840
acctgcgtgg tgggtggatgt gtctcaagag gaccccgagg tgcagttcaa ttggtacgtg	900
gacggcgtgg aagtgcacaa cgccaagacc aagcctagag aggaacagtt caactccacc	960
tacagagtgg tgtccgtgct gaccgtgctg caccaggatt ggctgaacgg caaagagtac	1020
aagtgcaagg tgtccaacaa gggcctgcct tccagcatcg aaaagaccat ctccaaggct	1080
aagggccagc ctcggaacc tcaggtttac accctgcctc caagccaaga ggaaatgacc	1140
aagaaccagg tgtccctgac ctgcctcgtg aagggtattct acccttccga tatcgccgtg	1200
gaatgggagt ccaatggcca gcctgagaac aactacaaga caaccctcc tgtgctggac	1260
tccgacggct ctttctttct gtattcccgc ctgaccgtgg acaagtctag atggcaagag	1320
ggcaacgtgt tctcctgctc tgtgatgcac gaggccctgc acaaccacta caccagaag	1380
tccctgtctc tgtccctggg caaatgatag	1410

<210> 9

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Kozak - SP - protein light chain - DNA

<400> 9

tcggtcatgg ccctgctgca caagaacatg aagcacctgt gggtctttct gctgctgggtg	60
gccgctccta gatgggtgct gtctgagatc gtgctgaccc agtctcctgc cacattgtct	120

ctgagtcctg gcgagagagc taccctgtct tgcagagctt cccagtcctg gtcctcctac	180
ctggcctggt atcagcagaa acctggacag gccctcggc tgctgatcta cgatgcctct	240
aatagagcca caggcatccc cgccagattc tctggctctg gatctggcac cgacttcacc	300
ctgaccatct ctagcctgga acctgaggac ttcgccgtgt actactgcca gcagtcctcc	360
aactggccta gaacctttgg ccagggcacc aaggtggaaa tcaagagaac cgtggctgcc	420
ccttccgtgt tcatcttccc accatctgac gagcagctga agtccggcac agcttctgtc	480
gtgtgcctgc tgaacaactt ctaccctcgg gaagccaagg tgcagtggaa ggtggacaat	540
gccctgcagt ccggcaactc ccaagagtct gtgaccgagc aggactccaa ggactctacc	600
tacagcctgt cctccacact gaccctgtct aaggccgact acgagaagca caaggtgtac	660
gcctgtgaag tgaccaccca gggactgtct agccccgtga ccaagtcttt caacagaggc	720
gagtgtgat ag	732

<210> 10
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SP - protein heavy chain - protein

<400> 10

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

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 165 170 175
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205
 Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
 210 215 220
 Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
 225 230 235 240
 Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
 245 250 255
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 260 265 270
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
 275 280 285
 Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 290 295 300
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
 305 310 315 320
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
 340 345 350
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 355 360 365
 Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 370 375 380
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 385 390 395 400
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 405 410 415
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
 420 425 430
 Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
 435 440 445
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
 450 455 460
 Gly Lys
 465

<210> 11

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> SP - protein light chain - protein

<400> 11

Met Ala Leu Leu His Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu
 1 5 10 15
 Leu Val Ala Ala Pro Arg Trp Val Leu Ser Glu Ile Val Leu Thr Gln

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

<210> 12

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> Restriction site - SP - protein heavy chain - DNA

<400> 12

ggtacctcgg tcatggccct gctgcacaag aacatgaagc acctgtggtt ctttctgctg 60

ctggtggccg ctctagatg ggtgttgtct caggtgcagc tggttgaatc tggtggcgga 120

gtggtgcagc ctggcagatc tctgagactg gattgcaagg cctccggcat caccttctcc 180

aactctggca tgcactgggt cgcacaggcc cctggaaaag gactggaatg ggctgccgtg 240

atttggtacg acggctctaa gcggtactac gccgactccg tgaagggcag attcaccatc 300

tctcgggaca actccaagaa caccctgttt ctgcagatga actccctgag agccgaggac 360

accgccgtgt actactgtgc caccaacgat gattattggg gccagggcac actggtcacc 420

gtgtcctctg cttctaccaa gggaccctct gtgttccttc tggctccttg ctccagatcc	480
acctctgagt ctaccgctgc tctgggctgc ctgggtcaagg attactttcc tgagcctgtg	540
accgtgtctt ggaactctgg tgctctgacc tccggcgtgc acacatttcc agctgtgctg	600
cagtcctccg gcctgtactc tctgtcctct gtcgtgaccg tgccttctag ctctctgggc	660
accaagacct acacctgtaa cgtggaccac aagccttcca acaccaaggt ggacaagcgc	720
gtggaatcta agtacggccc tccttgtcct ccatgtcctg ctccagaatt cctcggcgga	780
ccttccgtgt tcctgtttcc tccaaagcct aaggacaccc tgatgatctc tcggaccctt	840
gaagtgacct gcgtgggtgt ggatgtgtct caagaggacc ccgaggtgca gttcaattgg	900
tacgtggacg gcgtggaagt gcacaacgcc aagaccaagc ctagagagga acagttcaac	960
tccacctaca gagtgggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaaa	1020
gagtacaagt gcaagggtgtc caacaagggc ctgccttcca gcatcgaaaa gaccatctcc	1080
aaggctaagg gccagcctcg ggaacctcag gtttacaccc tgcctccaag ccaagaggaa	1140
atgaccaaga accaggtgtc cctgacctgc ctctgaagg gattctaccc ttccgatatc	1200
gccgtggaat gggagtccaa tggccagcct gagaacaact acaagacaac ccctcctgtg	1260
ctggactccg acggctcctt ctttctgtat tcccgcctga ccgtggacaa gtctagatgg	1320
caagagggca acgtgttctc ctgctctgtg atgcacgagg ccctgcacaa ccactacacc	1380
cagaagtccc tgtctctgtc cctgggcaaa tgatagaagc tt	1422

<210> 13

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Restriction site - SP - light chain - DNA

<400> 13

ggatcctcgg tcatggccct gctgcacaag aacatgaagc acctgtggtt ctttctgctg	60
ctgggtggccg ctcttagatg ggtgctgtct gagatcgtgc tgaccagtc tcctgccaca	120
ttgtctctga gtcctggcga gagagctacc ctgtcttgca gagcttcca gtccgtgtcc	180
tcctacctgg cctggtatca gcagaaacct ggacaggccc ctcggctgct gatctacgat	240
gcctctaata gagccacagg catccccgcc agattctctg gctctggatc tggcaccgac	300

ttcacccctga ccattctctag cctggaacct gaggacttcg ccgtgtacta ctgccagcag	360
tcctccaact ggcctagaac ctttggccag ggcaccaagg tggaaatcaa gagaaccgtg	420
gctgcccctt ccgtgttcat cttcccacca tctgacgagc agctgaagtc cggcacagct	480
tctgtcgtgt gcctgctgaa caacttctac cctcggaag ccaaggtgca gtggaaggtg	540
gacaatgccc tgcagtccgg caactcccaa gagtctgtga ccgagcagga ctccaaggac	600
tctacctaca gcctgtcctc cacactgacc ctgtctaagg ccgactacga gaagcacaag	660
gtgtacgcct gtgaagtac ccaccaggga ctgtctagcc ccgtgaccaa gtctttcaac	720
agaggcgagt gctgatagct cgag	744

<210> 14
 <211> 11
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> TIS RNA

<400> 14 ucggucaugg c	11
--------------------------	----