

SEQUENCE LISTING

<110> CODEXIS, INC.

ALEXION PHARMACEUTICALS, INC.

<120> T7 RNA POLYMERASE VARIANTS

<130> CX8-168USP1

<140> NOT YET ASSIGNED

<141> SUBMITTED HEREWITH

<160> 40

<210> 1

<211> 2649

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP Wild Type

<400> 1

```

atgaacacga ttaacatcgc taagaacgac ttctctgaca tcgaactggc tgctatcccc 60
ttcaacactc tggctgacca ttacgggtgag cgtttagctc gcgaacagtt ggcccttgag 120
catgagtctt acgagatggg tgaagcacgc ttccgcaaga tgtttgagcg tcaacttaaa 180
gctggtgagg ttgcggataa cgctgccgcc aagccttctca tcactaccct actccctaag 240
atgattgcac gcatcaacga ctggtttgag gaagtgaag ctaagcgcgg caagcgcccg 300
acagccttcc agttcctgca agaaatcaag ccggaagccg tagcgtagat caccattaag 360
accactctgg cttgcctaac cagtgtgac aatacaaccg ttcaggctgt agcaagcgca 420
atcggtcggg ccattgagga cgaggctcgc ttcggtcgta tccgtgacct tgaagctaag 480
cacttcaaga aaaacgttga ggaacaactc aacaagcgcg tagggcacgt ctacaagaaa 540
gcatttatgc aagttgtcga ggctgacatg ctctctaagg gtctactcgg tggcgaggcg 600
tggtcttcgt ggcataagga agactctatt catgtaggag tacgctgcat cgagatgctc 660
attgagtcaa ccggaatggg tagcttacac cgccaaaatg ctggcgtagt aggtcaagac 720
tctgagacta tcgaactcgc acctgaatac gctgaggcta tcgcaaccgg tgcaggtgcg 780
ctggctggca tctctccgat gttccaacct tgcgtagttc ctcctaagcc gtggactggc 840
attactgggtg gtggctattg ggctaacggg cgtcgtcctc tggcgctggg gcgtactcac 900
agtaagaaaag cactgatgcg ctacgaagac gtttacatgc ctgagggtga caaagcgatt 960
aacattgcgc aaaacaccgc atggaaaatc aacaagaaaag tcctagcggg cgccaacgta 1020
atcaccaagt ggaagcattg tccggtcgag gacatccctg cgattgagcg tgaagaactc 1080
ccgatgaaac cggaagacat cgacatgaat cctgaggctc tcaccgcgtg gaaacgtgct 1140
gccgtgctg tgtaccgcaa ggacaaggct cgcaagtctc gccgtatcag ccttgagttc 1200
atgcttgagc aagccaataa gtttgctaac cataaggcca tctggttccc ttacaacatg 1260
gactggcgcg gtcgtgttta cgctgtgtca atgttcaacc cgcaaggtaa cgatatgacc 1320
aaaggactgc ttacgtggc gaaaggtaaa ccaatcggtg aggaaggtta ctactggctg 1380
aaaatccacg gtgcaaaactg tgcgggtgtc gataagggtt cgttccctga gcgcatcaag 1440
ttcattgagg aaaaccacga gaacatcatg gcttgcgcta agtctccact ggagaacact 1500
tggtgggctg agcaagattc tccgttctgc ttccttgctg tctgctttga gtacgctggg 1560
gtacagcacc acggcctgag ctataactgc tcccttccgc tggcgtttga cgggtcttgc 1620

```

```

tctggcatcc agcacttctc cgcgatgctc cgagatgagg taggtggctc cgcggttaac 1680
ttgcttccta gtgaaaccgt tcaggacatc tacgggattg ttgctaagaa agtcaacgag 1740
attctacaag cagacgcaat caatgggacc gataacgaag tagttaccgt gaccgatgag 1800
aacactgggtg aaatctctga gaaagtcaag ctgggcacta aggcactggc tggatcaatgg 1860
ctggcttacg gtgttactcg cagtgtgact aagcgttcag tcatgacgct ggcttacggg 1920
tccaaagagt tcggcttccg tcaacaagtg ctggaagata ccattcagcc agctattgat 1980
tccggcaagg gtctgatgtt cactcagccg aatcaggctg ctggatacat ggctaagctg 2040
atttgggaat ctgtgagcgt gacggtggtg gctgcggttg aagcaatgaa ctggcttaag 2100
tctgctgcta agctgctggc tgctgaggtc aaagataaga agactggaga gattcttcgc 2160
aagcgttgcg ctgtgcattg ggtaactcct gatggtttcc ctgtgtggca ggaatacaag 2220
aagcctattc agacgcgctt gaacctgatg ttcttcggtc agttccgctt acagcctacc 2280
attaacacca acaaagatag cgagattgat gcacacaaac aggagtctgg tatcgctcct 2340
aactttgtac acagccaaga cggtagccac cttcgtaaga ctgtagtgtg ggcacacgag 2400
aagtacggaa tcgaatcttt tgcactgatt cacgactcct tcggtaccat tccggctgac 2460
gctgcgaacc tgttcaaagc agtgcgcgaa actatggttg acacatatga gtcttgatgat 2520
gtactggctg atttctacga ccagttcgct gaccagttgc acgagtctca attggacaaa 2580
atgccagcac ttccggctaa aggtaacttg aacctccgtg acatcttaga gtcgggacttc 2640
gcgttcgcg                                     2649

```

<210> 2

<211> 883

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP Wild Type

<400> 2

```

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

```

				165				170					175			
Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Leu	Ser	
			180					185					190			
Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	Ser	Ser	Trp	His	Lys	Glu	Asp	
		195					200					205				
Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	Glu	Met	Leu	Ile	Glu	Ser	Thr	
	210					215					220					
Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn	Ala	Gly	Val	Val	Gly	Gln	Asp	
225					230					235					240	
Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu	Tyr	Ala	Glu	Ala	Ile	Ala	Thr	
				245					250						255	
Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser	Pro	Met	Phe	Gln	Pro	Cys	Val	
			260					265					270			
Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile	Thr	Gly	Gly	Gly	Tyr	Trp	Ala	
		275					280					285				
Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val	Arg	Thr	His	Ser	Lys	Lys	Ala	
	290					295					300					
Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met	Pro	Glu	Val	Tyr	Lys	Ala	Ile	
305					310					315					320	
Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys	Ile	Asn	Lys	Lys	Val	Leu	Ala	
				325					330					335		
Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys	His	Cys	Pro	Val	Glu	Asp	Ile	
		340						345					350			
Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro	Met	Lys	Pro	Glu	Asp	Ile	Asp	
		355					360					365				
Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp	Lys	Arg	Ala	Ala	Ala	Ala	Val	
	370					375					380					
Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser	Arg	Arg	Ile	Ser	Leu	Glu	Phe	
385					390					395					400	
Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala	Asn	His	Lys	Ala	Ile	Trp	Phe	
				405					410					415		
Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg	Val	Tyr	Ala	Val	Ser	Met	Phe	
		420						425					430			
Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys	Gly	Leu	Leu	Thr	Leu	Ala	Lys	
		435					440					445				
Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr	Tyr	Trp	Leu	Lys	Ile	His	Gly	
	450					455					460					
Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val	Pro	Phe	Pro	Glu	Arg	Ile	Lys	
465					470					475					480	
Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile	Met	Ala	Cys	Ala	Lys	Ser	Pro	
				485					490					495		
Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln	Asp	Ser	Pro	Phe	Cys	Phe	Leu	
		500						505					510			
Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val	Gln	His	His	Gly	Leu	Ser	Tyr	
		515					520					525				
Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp	Gly	Ser	Cys	Ser	Gly	Ile	Gln	
	530					535					540					
His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu	Val	Gly	Gly	Arg	Ala	Val	Asn	
545					550					555					560	
Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp	Ile	Tyr	Gly	Ile	Val	Ala	Lys	

				565					570				575			
Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp	Ala	Ile	Asn	Gly	Thr	Asp	Asn	
			580					585					590			
Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn	Thr	Gly	Glu	Ile	Ser	Glu	Lys	
		595					600					605				
Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala	Gly	Gln	Trp	Leu	Ala	Tyr	Gly	
	610					615					620					
Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser	Val	Met	Thr	Leu	Ala	Tyr	Gly	
625					630					635					640	
Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln	Val	Leu	Glu	Asp	Thr	Ile	Gln	
			645						650					655		
Pro	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu	Met	Phe	Thr	Gln	Pro	Asn	Gln	
			660					665					670			
Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile	Trp	Glu	Ser	Val	Ser	Val	Thr	
		675					680					685				
Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn	Trp	Leu	Lys	Ser	Ala	Ala	Lys	
	690					695					700					
Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys	Lys	Thr	Gly	Glu	Ile	Leu	Arg	
705					710					715					720	
Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr	Pro	Asp	Gly	Phe	Pro	Val	Trp	
				725					730					735		
Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr	Arg	Leu	Asn	Leu	Met	Phe	Leu	
		740						745					750			
Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile	Asn	Thr	Asn	Lys	Asp	Ser	Glu	
		755					760					765				
Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly	Ile	Ala	Pro	Asn	Phe	Val	His	
	770					775					780					
Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys	Thr	Val	Val	Trp	Ala	His	Glu	
785					790					795					800	
Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu	Ile	His	Asp	Ser	Phe	Gly	Thr	
			805					810						815		
Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe	Lys	Ala	Val	Arg	Glu	Thr	Met	
			820					825					830			
Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val	Leu	Ala	Asp	Phe	Tyr	Asp	Gln	
		835					840					845				
Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln	Leu	Asp	Lys	Met	Pro	Ala	Leu	
	850					855					860					
Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg	Asp	Ile	Leu	Glu	Ser	Asp	Phe	
865					870					875					880	
Ala	Phe	Ala														

<210> 3

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> 6His-T7RNAP

<400> 3

```
atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
atcgaactgg ctgctatccc gttcaacact ctggctgacc attacggtga gcgttttagct 120
cgcgaaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
atgtttgagc gtcaacttaa agctggtgag gttgcggata acgctgccgc caagcctctc 240
atcactaccc tactccctaa gatgattgca cgcatcaacg actggtttga ggaagtgaag 300
gctaagcgcg gcaagcgccc gacagccttc cagttcctgc aagaaatcaa gccggaagcc 360
gtagcgtaga tcaccattaa gaccactctg gcttgccata ccagtgtgta caatacaacc 420
gttcaggctg tagcaagcgc aatcggctcg gccattgagg acgaggctcg cttcggctcg 480
atccgtgacc ttgaagctaa gcacttcaag aaaaacgttg aggaacaact caacaagcgc 540
gtagggcacg tctacaagaa agcatttatg caagttgtcg aggctgacat gctctctaag 600
ggcttactcg gtggcgaggc gtggtcttcg tggcataagg aagactctat tcatgtagga 660
gtacgctgca tcgagatgct cattgagtca accggaatgg ttagcttaca ccgcaaaaat 720
gctggcgtag taggtcaaga ctctgagact atcgaactcg cacctgaata cgctgaggct 780
atcgcaaccc gtgcaggtgc gctggctggc atctctccga tgttccaacc ttgcgtagtt 840
cctcctaagc cgtggactgg cattactggt ggtggctatt gggctaacgg tcgtcgtcct 900
ctggcgctgg tgcgtactca cagtaagaaa gcactgatgc gctacgaaga cgtttacatg 960
cctgagggtg acaaaagcgat taacattgcg caaaacaccg catggaaaat caacaagaaa 1020
gtcctagcgg tcgccaacgt aatcaccaag tggaagcatt gtccggctga ggacatccct 1080
gcgattgagc gtgaagaact cccgatgaaa ccggaagaca tcgacatgaa tcctgaggct 1140
ctcaccgcgt ggaaacgtgc tgccgctgct gtgtaccgca aggacaaggc tcgcaagtct 1200
cgccgtatca gccttgagtt catgcttgag caagccaata agtttgctaa ccataaggcc 1260
atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcgg 1380
aaggaagggt actactggct gaaaatccac ggtgcaaaact gtgcgggtgt cgataagggt 1440
ccgttccctg agcgcatcaa gttcattgag gaaaaccacg agaacatcat ggcttgcgct 1500
aagtctccac tggagaacac ttggtgggct gagcaagatt ctccgttctg cttccttgcg 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgcttg acgggtcttg ctctggcatc cagcacttct ccgcatgct ccgagatgag 1680
gtaggtggtc gcgcggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggt gaaatctctg agaaagtcaa gctgggcact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gcagtgtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaagat 1980
accattcagc cagctattga ttccggcaag ggtctgatgt tcaactcagc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgt agctgcggt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcggttc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcgg 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgcttcgcg taa 2673
```

<210> 4

<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> 6His-T7RNAP

<400> 4

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

Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys			
			340					345					350					
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro			
		355					360					365						
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp			
		370				375					380							
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser			
385					390					395					400			
Arg	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala			
			405						410					415				
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg			
		420						425					430					
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys			
		435					440					445						
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr			
	450					455					460							
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val			
465					470					475					480			
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile			
				485					490					495				
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln			
		500						505					510					
Asp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val			
		515					520				525							
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp			
	530					535					540							
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu			
545					550					555					560			
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp			
				565					570					575				
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp			
			580					585					590					
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn			
		595					600					605						
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala			
	610					615					620							
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser			
625					630					635					640			
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln			
				645					650					655				
Val	Leu	Glu	Asp	Thr	Ile	Gln	Pro	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu			
			660					665					670					
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile			
		675					680					685						
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn			
	690					695					700							
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys			
705					710					715					720			
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr			
				725					730					735				

Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr
			740					745					750		
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile
		755					760					765			
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly
		770				775					780				
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys
785					790					795					800
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu
			805						810						815
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe
			820					825					830		
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val
		835				840						845			
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln
	850				855					860					
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg
865				870						875					880
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala						
			885						890						

<210> 5

<211> 3060

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA template

<400> 5

gatcttcttg	agatcctttt	tttctgcgcg	taatctgctg	cttgcaaaca	aaaaaaccac	60
cgctaccagc	ggtggtttgt	ttgccggatc	aagagctacc	aactcttttt	ccgaaggtaa	120
ctggcttcag	cagagcgcag	ataccaaata	ctgttcttct	agtgtagccg	tagttagccc	180
accacttcaa	gaactctgta	gcaccgccta	catacctcgc	tctgctaata	ctgttaccag	240
tggctgctgc	cagtggcgat	aagtcgtgtc	ttaccgggtt	ggactcaaga	cgatagttac	300
cggataaggc	gcagcggctg	ggctgaacgg	ggggttcgtg	cacacagccc	agcttggagc	360
gaacgacctt	caccgaactg	agatacctac	agcgtgagct	atgagaaagc	gccacgcttc	420
ccgaagggag	aaaggcggac	aggtatccgg	taagcggcag	ggtcggaaca	ggagagcgca	480
cgagggagct	tccaggggga	aacgcctggt	atctttatag	tcctgtcggg	tttcgccacc	540
tctgacttga	gcgtcgattt	ttgtgatgct	cgtcaggggg	gcggagccta	tggaaaaacg	600
ccagcaacgc	ggccttttta	cggttcctgg	ccttttgctg	gccttttgct	cacatgttct	660
ttcctgcgtt	atcccctgat	tctgtggata	accgtattac	cgcttttgag	tgagctgata	720
ccgctcgccg	cagccgaacg	accgagcgca	gcgagtcagt	gagcgaggaa	gcggaaggcg	780
agagtaggga	actgccaggc	atcaaactaa	gcagaaggcc	cctgacggat	ggcctttttg	840
cgtttctaca	aactctttct	gtgttgtaaa	acgacggcca	gtcttaagct	cgggccccct	900
gggcggttct	gataacgagt	aatcgttaat	ccgcaaataa	cgtaaaaacc	cgcttcggcg	960
ggttttttta	tgggggggagt	ttagggaaaag	agcatttgct	agaatattta	agggcgcttg	1020
tcactttgct	tgatatatga	gaattattta	accttataaa	tgagaaaaaa	gcaacgcact	1080
ttaaataaga	tacgttgctt	tttcgattga	tgaacaccta	taattaaact	attcatctat	1140
tatttatgat	tttttgatata	tacaatatat	ctagtttggt	aaagagaatt	aagaaaataa	1200

atctcgaaaa	taataaaggg	aaaatcagtt	tttgatatca	aaattataca	tgtcaacgat	1260
aatacaaaa	ataatacaaa	ctataagatg	ttatcagtat	ttattatgca	tttagaataa	1320
atthttgtgtc	gcccttgtac	ttagtcgctg	aataatacga	ctcactatag	cggaaaccaa	1380
gctaagcgcc	agaactggca	ccttcgggtg	ccagttgacg	aggtgggggtt	tatcgagatt	1440
tcggcggatg	actcccgggtt	gttcatcaca	accgcaagct	tttacttaaa	tcattaaggt	1500
gacttagtgg	acaaagggtga	aagtgtgatg	aaacccgacc	tggacggagg	cgcgcccag	1560
atgagtaggc	tgtcccatca	ggggaggaat	cggggacggc	tgaaaggcga	gggcgccgaa	1620
gcgagcagag	ttcctcccg	tctgcttggc	tgggggtgag	gggaataccc	ttaccactgt	1680
cgcgaaaagc	gagagccgtc	caggatcccc	tcaaaagggc	gacaccccat	aattagcccc	1740
ggcgaaaagg	ccagtctttc	gactgagcct	ttcgttttat	ttgatgcctg	gcagttccct	1800
actctcgcat	ggggagtgccc	cacactacca	tcggcgctac	ggcggtttcac	ttctgagttc	1860
ggcatgggggt	caggtggggac	caccgcgcta	ctgccgccag	gcaaacaagg	ggtgttatga	1920
gccatattca	ggtataaatg	ggctcgcgat	aatgttcaga	attgggtaaat	tgggttgtaac	1980
actgacccct	atttgttttat	ttttctaaat	acattcaa	atgtatccgc	tcatgagaca	2040
ataaccctga	taaatgcttc	aataatattg	aaaaaggaag	aatatgagta	ttcaacattt	2100
ccgtgtcgcc	cttattccct	tttttgcggc	atthttgcctt	cctgtttttg	ctcaccaga	2160
aacgctgggtg	aaagtaaaaag	atgctgaaga	tcagttgggt	gcacgagtgg	gttatatcga	2220
actggatctc	aacagcggta	agatccttga	gagttttcgc	cccgaagaac	gttttccaat	2280
gatgagcact	tttaaagttc	tgctatgtgg	cgcggtatta	ttccgtattg	acgccgggca	2340
agagcaactc	ggtcgccgca	tacactattc	tcagaatgac	ttgggttgagt	actcaccagt	2400
cacagaaaag	catcttacgg	atggcatgac	agtaagagaa	ttatgcagtg	ctgccataac	2460
catgagtgat	aacactgcgg	ccaacttact	tctgacaacg	atcggaggac	cgaaggagct	2520
aaccgctttt	ttgcacaaca	tgggggatca	tgtaactcgc	cttgatcgtt	gggaaccgga	2580
gctgaatgaa	gccataccaa	acgacgagcg	tgacaccacg	atgcctgtag	cgatggcaac	2640
aacgtttgcgc	aaactattaa	ctggcggaact	acttactcta	gcttcccggc	aacaattaat	2700
agactggatg	gaggcgggata	aagttgcagg	accacttctg	cgctcggccc	ttccggctgg	2760
ctggttttatt	gctgataaat	ccggagccgg	tgagcgtgggt	tctcgcggta	tcacgcgagc	2820
gctggggcca	gatggtaagc	cctcccgtat	cgtagtattc	tacacgacgg	ggagtcaggc	2880
aactatggat	gaacgaaata	gacagatcgc	tgagataggt	gcctcactga	ttaagcattg	2940
gtaaaagcag	agcattacgc	tgacttgacg	ggacggcgca	agctcatgac	caaaatccct	3000
taacgtgagt	tacgcgcgcg	tcgttccact	gagcgtcaga	ccccgtagaa	aagatcaaag	3060

<210> 6

<211> 334

<212> RNA

<213> Artificial Sequence

<220>

<223> RNA Transcript

<400> 6

gcggaaccca	agcuaagcgc	cagaacuggc	accuucgggu	gccaguugac	gaggugggggu	60
uuau cgagau	uucggcggau	gacucccggu	uguucaucac	aaccgcaagc	uuuuacuuaa	120
aucauuuagg	ugacuuagug	gacaaaaggug	aaagugugau	gaaacccgac	cuggacggag	180
gcgcgcccga	gaugaguagg	cugucccauc	aggggaggaa	ucggggacgg	cugaaaaggcg	240
agggcgcccga	agcgagcaga	guuccucccg	cucugcuugg	cuggggguga	ggggaauacc	300
cuuaccacug	ucgcgaaagc	ggagagccgu	ccag			334

<210> 7
<211> 16
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA cleavage product

<400> 7
gcggaaccca agcuua

16

<210> 8
<211> 4671
<212> DNA
<213> Artificial Sequence

<220>
<223> Substrate etc

<400> 8
gagttacgcg cgcgtcgttc cactgagcgt cagaccccgt agaaaagatc aaaggatctt 60
cttgagatcc tttttttctg cgcgtaatct gctgcttgca aacaaaaaaaa ccaccgctac 120
cagcgggtggg ttgtttgccg gatcaagagc taccaactct ttttccgaag gtaactggct 180
tcagcagagc gcagatacca aatactgttc ttctagtgtg gccgtagtta gcccaccact 240
tcaagaactc tgtagcaccg cctacatacc tcgctctgct aatcctgtta ccagtggctg 300
ctgccagtgg cgataagtcg tgtcttaccg gggttgactc aagacgatag ttaccggata 360
aggcgcagcg gtcgggctga acgggggggtt cgtgcacaca gccagcttg gagcgaacga 420
cctacaccga actgagatac ctacagcgtg agctatgaga aagcgccacg cttcccgaag 480
ggagaaaaggc ggacaggtat ccggtaaagc gcagggtcgg aacaggagag cgcacgaggg 540
agcttccagg gggaaaacgcc tggatatctt atagtcctgt cgggtttcgc cacctctgac 600
ttgagcgtcg atttttgtga tgctcgtcag gggggcggag cctatggaaa aacgccagca 660
acgcggcctt ttacgggttc ctggcctttt gctggccttt tgctcacatg ttctttcctg 720
cgttatcccc tgattctgtg gataaccgta ttaccgcctt tgagttagct gataccgctc 780
gccgcagccg aacgaccgag cgcagcgagt cagttagcga ggaagcggaa ggcgagagta 840
gggaactgcc aggcatacaa ctaagcagaa ggcccctgac ggatggcctt tttgcgtttc 900
tacaaaactc ttctgtgttg taaaacgacg gccagtctta agctcgggcc ccctgggcgg 960
ttctgataac gagtaatcgt taatccgcaa ataacgtaaa aacccgcttc ggcggggttt 1020
tttatggggg gagtttaggg aaagagcatt tgtcagaata tttaagggcg cctgtcactt 1080
tgcttgatat atgagaatta tttaacctta taaatgagaa aaaagcaacg cactttaaat 1140
aagatacgtt gctttttcga ttgatgaaca cctataatta aactattcat ctattattta 1200
tgattttttg tatatacaat atttctagtt tgttaaagag aattaagaaa ataaatctcg 1260
aaaataataa agggaaaaatc agtttttgat atcaaaatta tacatgtcaa cgataatata 1320
aaatataata caaactataa gatgttatca gtatttatta tgcatttaga atacgtactc 1380
agcgtctggg ttccccatcg gtgatgtcgt ataagagacg tataggagac ctatagtgtc 1440
ttcggggtaa tacgactcac tatagcggaa cccaagcttg gcattccggg actgttggtg 1500
aagccaccat ggaagatgcg aagaacataa agaaaggtcc cgccccattt taccactctg 1560
aggatggaac agctggggag caactgcaca aggccatgaa gcgctatgcg ttggtgccgg 1620
gaaccatcgc gttcaccgac gcacacatcg aagtgaacat cacttacgcc gagtactttg 1680

agatgagcgt	caggctggcc	gaggctatga	agcgatacgg	tctgaacacc	aaccaccgga	1740
tcgtgggtctg	ctctgaaaac	agcctgcagt	tcttcatgcc	ggtcctgggg	gccctgttca	1800
tcggcgtggc	cgtggcaccc	gccaacgata	tctacaacga	gagagaattg	ctgaactcga	1860
tgaacatctc	ccagcctacc	gtgggtgttcg	tgtcgaagaa	ggggttgag	aagatcctga	1920
acgtgcagaa	gaagctgccc	atcattcaaa	agattatcat	tatggattcc	aaaaccgact	1980
accaggggtt	ccagtcaatg	tataccttcg	tgacctcca	tctgccccct	ggcttcaacg	2040
aatacgactt	cgtgcctgaa	agcttcgacc	gcgacaagac	gatcgccctc	atcatgaact	2100
cgtccggctc	gaccgggctg	cccaaaggag	tggccctgcc	acaccggacc	gcttgcggtc	2160
ggttctccca	cggccgggac	cctatttttcg	gcaatcagat	cattccggac	actgccatcc	2220
tgagcgtggt	ccccttccat	cacgggtttg	ggatgtttac	cactctgggc	tacctcatct	2280
gcggattcag	ggtgggtgctg	atgtaccggt	tcgaggaaaga	acttttcctg	cggagcctgc	2340
aggattacaa	gatccagtcc	gccctcctcg	tgccaaccct	cttctcattc	ttcgctaagt	2400
ccactctcat	cgataagtac	gacctgtcga	atctccacga	aattgcgtcc	ggtgggtgcac	2460
cgctgtccaa	ggaggtcggc	gaagccgtgg	ccaagcgctt	ccacctcccg	ggaatacgcc	2520
agggatacgg	cctgactgaa	acgaccagcg	cgattctgat	caccccgag	ggcgacgaca	2580
agccgggtgc	cgtggggaaa	gtgggtccgt	tcttcgaagc	aaaggctgtg	gatctggata	2640
ccggaaaagac	tctgggctg	aaccagagag	gggaactttg	tgtgcgcgga	ccgatgatta	2700
tgtccggata	tgtcaacaac	cccagggcca	ctaattgccct	gatcgacaag	gacggatggt	2760
tgcatagcgg	cgacatcgca	tactgggacg	aggacgagca	ctttttcatt	gtggatcggc	2820
tcaagtccct	gatcaagtac	aagggatacc	aggctgcccc	tgccgaactt	gagtccatcc	2880
tgctgcaaca	tccgaacatt	ttcgacgcgg	gcgtcgctgg	ccttcctgat	gatgacgccg	2940
gagagctgcc	cgcggccgtg	gtgggtgctc	aacacggaaa	aactatgacc	gagaaggaaa	3000
tcgtggacta	cgtggcgtca	caagtcacca	ctgccaagaa	actgcgcggc	ggagtcgtgt	3060
tcgtggacga	ggtgcccgaag	ggcctgaccg	gaaagctgga	cgctagaaaag	atccgggaga	3120
tcctgattaa	ggccaagaag	ggaggaaaagt	ccaagctctg	agatctagag	ggccctattc	3180
tatagtgtca	cctaaatgct	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3240
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3300
gaattcaaaa	gaagaccata	tacgtctcct	ataggtctcg	tatactgctt	cctatacgac	3360
atcaccgatg	gggaacacga	agcgatccag	cccccttat	tagccgggc	gaaaggccca	3420
gtctttcgac	tgagcctttc	gttttatttg	atgcctggca	gttccctact	ctcgcatggg	3480
gagtccccac	actaccatcg	gcgctacggc	gtttcacttc	tgagttcggc	atggggtcag	3540
gtgggaccac	cgcgctactg	ccgccaggca	aacaaggggt	gttatgagcc	atattcaggt	3600
ataaatgggc	tcgcgataat	gttcagaatt	ggttaattgg	ttgtaacact	gaccctatt	3660
tgtttatttt	tctaaataca	ttcaaataatg	tatccgctca	tgagacaata	accctgataa	3720
atgcttcaat	aattattgaaa	aagggaagaat	atgagtattc	aacatttccg	tgtcgccctt	3780
attccctttt	ttgcggcatt	ttgccttcct	gtttttgctc	accagaaac	gctggtgaaa	3840
gtaaaagatg	ctgaagatca	gttgggtgca	cgagtgggtt	acatcgaact	ggatctcaac	3900
agcggtaaga	tccttgagag	ttttcgcccc	gaagaacgtt	ttccaatgat	gagcactttt	3960
aaagtctctg	tatgtggcgc	ggtattatcc	cgtattgacg	ccgggcaaga	gcaactcggg	4020
cgccgcatac	actattctca	gaatgacttg	gttgagtact	caccagtcac	agaaaagcat	4080
cttacggatg	gcatgacagt	aagagaatta	tgcagtgtcg	ccataaccat	gagtataaac	4140
actgcggcca	acttacttct	gacaacgatc	ggaggaccga	aggagctaac	cgcttttttg	4200
cacaacatgg	gggatcatgt	aactcgcctt	gatcgttggg	aaccggagct	gaatgaagcc	4260
ataccaaacg	acgagcgtga	caccacgatg	cctgtagcga	tggaacaac	gttgcgcaaa	4320
ctattaactg	gcgaactact	tactctagct	tcccggaac	aattaataga	ctggatggag	4380
gcggataaaag	ttgcaggacc	acttctgcgc	tcggcccttc	cggctggctg	gtttattgct	4440
gataaatccg	gagccggtga	gcgtgggttct	cgcggtatca	tcgcagcgct	ggggccagat	4500
ggtaagccct	cccgtatcgt	agttatctac	acgacgggga	gtcaggcaac	tatggatgaa	4560
cgaaatagac	agatcgctga	gatagggtgc	tactgatta	agcattggta	agcagagcat	4620
tacgtgact	tgacgggacg	gcgcaagctc	atgacaaaaa	tcccttaacg	t	4671

<210> 9
<211> 1697
<212> RNA
<213> Artificial Sequence

<220>
<223> Substrate etc

<400> 9
gcggaaccca agcuuggcau uccgguacug uugguaaagc caccauggaa gaugcgaaga 60
acauaaagaa aggucccgcc ccauuuuacc cacucgagga uggaacagcu ggggagcaac 120
ugcacaaggc caugaagcgc uaugcguugg ugccgggaac caucgcguuc accgacgcac 180
acaucgaagu gaacaucacu uacgccgagu acuuugagau gagcguagg cuaggcgagg 240
cuaugaagcg auacggucug aacaccaacc accggaucgu ggucugcucu gaaaacagcc 300
ugcaguucuu caugccgguc cuggggggccc uguucaucgg cguggccgug gcacccgcc 360
acgauaucua caacgagaga gaaauugcuga acucgaugaa caucuccag ccuaccgugg 420
uguucguguc gaagaagggg uugcagaaga uccugaacgu gcagaagaag cugcccauca 480
uucaaaagau uaucauuuug gauuccaaaa ccgacuacca ggguuuccag ucaauguaua 540
ccuucgugac cucccaucug ccccuuggcu ucaacgaaua cgacuucgug ccugaaagcu 600
ucgaccgcga caagacgauc gcccucauca ugaacucguc cggcucgacc gggcugccca 660
aaggaguggc ccugccacac cggaccgcuu gcgugcgguu cuccacgccc cgggacccua 720
uuuucggcaa ucagaucuuu ccggacacug ccauccugag cguggucccc uuccaucacg 780
gguuugggau guuuaccacu cugggcuacc ucaucugcgg auucagggug gugcugaugu 840
accgguucga ggaagaacuu uuccugcggg gccugcagga uuacaagau caguccgccc 900
uccucgugcc aaccucuuc ucauuucug cuaaguccac ucucaucgau aaguacgacc 960
ugucgaauuc ccacgaaauu gcguccggug gugcaccgcu guccaaggag gucggcgaag 1020
ccguggccaa gcgcuuccac cuccgggaa uacgccaggg auacggccug acugaaacga 1080
ccagcgcgau ucugaucacc ccggaggggcg acgacaagcc gggugccgug gggaaagugg 1140
ugccguucuu cgaagcaaaag gucguggauc uggauaccgg aaagacucug ggcgugaacc 1200
agagaggggg acuuugugug cgcggaccga ugauuuuguc cggauauguc aacaaccccg 1260
aggccacuaa ugcccuugauc gacaaggacg gaugguugca uagcggcgac aucgcauacu 1320
gggacgagga cgagcacuuu uucauuuggg aucggcucaa gucccuugauc aaguacaagg 1380
gauaccaggu cgcccuugcc gaacuugagu ccauccugcu gcaacauccg aacauuuucg 1440
acgcgggcgug cgcuaggccuu ccugaugaug acgccggaga gcugcccgcg gccguggugg 1500
ugcucgaaca cggaaaaacu augaccgaga aggaaaucgu ggacuacgug gcgucacaag 1560
ucaccacugc caagaaacug cgcggcggag ucguuuucgu ggacgaggug cccaagggcc 1620
ugaccggaaa gcuggacgcu agaaaagaucc gggagauccu gauuaaggcc aagaaggagg 1680
gaaaguccaa gcucuga 1697

<210> 10
<211> 4945
<212> DNA
<213> Artificial Sequence

<220>
<223> Substrate etc

<400> 10

ttaccaatgc	ttaatcagtg	aggcacctat	ctcagcgatc	tgtctatttc	gttcatccat	60
agttgcctga	ctccccgtcg	tgtagataac	tacgatacgg	gagggcttac	catctggccc	120
cagcgctgcg	atgataccgc	gagaaccacg	ctcaccggct	ccggatttat	cagcaataaa	180
ccagccagcc	ggaagggccg	agcgcagaag	tggctctgca	actttatccg	cctccatcca	240
gtctattaat	tgttgccggg	aagctagagt	aagtagttcg	ccagttaata	gtttgcgcaa	300
cgttgttgcc	atcgctacag	gcatcgtggt	gtcacgctcg	tcgtttggta	tggcttcatt	360
cagctccggt	tcccaacgat	caaggcgagt	tacatgatcc	cccatgttgt	gcaaaaaagc	420
ggttagctcc	ttcggtcctc	cgatcgttgt	cagaagtaag	ttggccgcag	tgttatcact	480
catggttatg	gcagcactgc	ataattctct	tactgtcatg	ccatccgtaa	gatgcttttc	540
tgtgactggt	gagtactcaa	ccaagtcatt	ctgagaatag	tgtatgcggc	gaccgagttg	600
ctcttgcccc	gcgtcaatac	gggataatac	cgcgccacat	agcagaactt	taaaagtgtc	660
catcattgga	aaacgttctt	cggggcgaaa	actctcaagg	atcttaccgc	tgttgagatc	720
cagttcgatg	taaccctact	gtgcacccaa	ctgatcttca	gcatctttta	ctttcaccag	780
cgtttctggg	tgagcaaaaa	caggaaggca	aaatgccgca	aaaaagggaa	taagggcgac	840
acggaaatgt	tgaatactca	tattcttcct	ttttcaatat	tattgaagca	tttatcaggg	900
ttattgtctc	atgagcggat	acatatattga	atgtatttag	aaaaataaac	aaataggggt	960
cagtgttaca	accaattaac	caattctgaa	cattatcgcg	agcccattta	tacctgaata	1020
tggctcataa	caccccttgt	ttgcctggcg	gcagtagcgc	ggtggtccca	cctgacccca	1080
tgccgaactc	agaagtgaag	cgccgtagcg	ccgatggtag	tgtggggact	ccccatgcga	1140
gagtagggaa	ctgccaggca	tcaaataaaa	cgaaaggctc	agtcgaaaga	ctgggccttt	1200
cgccggggct	aattatgggg	tgtcgccctt	cgctgaaggg	gtaatacgac	tcactatagg	1260
gaaataagag	agaaaagaag	agtaagaaga	aatataagag	ccaccatgga	agatgcgaag	1320
aacataaaga	aagggtccgc	cccattttac	ccactcgagg	atggaacagc	tggggagcaa	1380
ctgcacaagg	ccatgaagcg	ctatgcgttg	gtgccgggaa	ccatcgcggt	caccgacgca	1440
cacatcgaag	tgaacatcac	ttacgccgag	tactttgaga	tgagcgtcag	gctggccgag	1500
gctatgaagc	gatacggctc	gaacaccaac	caccggatcg	tggctctgctc	tgaaaacagc	1560
ctgcagttct	tcatgccggt	cctggggggc	ctgttcatcg	gcgtggccgt	ggcaccgcc	1620
aacgatatct	acaacgagag	agaattgctg	aactcgatga	acatctcca	gcctaccgtg	1680
gtgttcgtgt	cgaagaaggg	gttgacagaag	atcctgaacg	tgcagaagaa	gctgcccac	1740
attcaaaaga	ttatcattat	ggattccaaa	accgactacc	agggtttcca	gtcaatgtat	1800
accttcgtga	cctcccatct	gccccctggc	ttcaacgaat	acgacttcgt	gcctgaaaagc	1860
ttcgaccgcg	acaagacgat	cgccctcatc	atgaactcgt	ccggctcgac	cgggctgccc	1920
aaaggagtgg	ccctgccaca	ccggaccgct	tgcgtgcggt	tctcccacgc	ccgggaccct	1980
attttcggca	atcagatcat	tccggacact	gccatcctga	gcgtgggtccc	cttccatcac	2040
gggtttggga	tgtttaccac	tctgggctac	ctcatctgcg	gattcaggggt	ggtgctgatg	2100
taccggttcg	aggaagaact	tttcctgcgg	agcctgcagg	attacaagat	ccagtccgcc	2160
ctcctcgtgc	caaccctctt	ctcattcttc	gctaagtcca	ctctcatcga	taagtacgac	2220
ctgtcgaatc	tccacgaaat	tgcgtccggt	ggtgcaccgc	tgtccaagga	ggtcggcgaa	2280
gccgtggcca	agcgtttcca	cctcccggga	attcgccagg	gatacggcct	gactgaaacg	2340
accagcgca	ttctgatcac	cccggagggc	gacgacaagc	cgggtgccgt	ggggaaagtg	2400
gtgccgttct	tcgaagcaaa	ggctcgtggat	ctggataaccg	gaaagactct	gggcgtgaac	2460
cagagagggg	aactttgtgt	gcgcggaccg	atgattatgt	ccggatatgt	caacaacccc	2520
gaggccacta	atgccctgat	cgacaaggac	ggatgggttc	atagcggcga	catcgcatat	2580
tgggacgagg	acgagcactt	tttcattgtg	gatcggctca	agtccttgat	caagtacaag	2640
ggataaccagg	tcgcccctgc	cgaacttgag	tccatcctgc	tgcaacatcc	gaacattttc	2700
gacgcgggcg	tcgctggcct	tcctgatgat	gacgccggag	agctgcccgc	ggccgtgggtg	2760
gtgctcgaac	acggaaaaac	tatgaccgag	aaggaaatcg	tggactacgt	ggcgtcacaa	2820
gtcaccactg	ccaagaaact	gcgcggcgga	gtcgtgttcg	tggacgaggt	gcccgaaggc	2880
ctgaccggaa	agctggacgc	tagaaaagatc	cgggagatcc	tgattaaggc	caagaaggga	2940

ggaaagtcca	agctctgaat	ctgctgcctt	ctgcggggct	tgccttctgg	ccatgccctt	3000
cttctctccc	ttgcacctgt	acctcttggg	ctttgaataa	agcctgagta	ggaagtgagg	3060
gaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3120
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaagga	agagcgctgc	3180
ctccttcaga	gtctgtctac	gagctcgggtc	tcggatcccc	tatacgacat	caccgatggg	3240
gaacacgaag	cgatccagcc	ccccttatta	gcccggggcga	aaggcccagt	ctttcgactg	3300
agcctttcgt	tttatttgat	gcctggcagt	tccctactct	cgcatgggga	gtccccacac	3360
taccatcggc	gctacggcgt	ttcacttctg	agttcggcat	ggggtcagggt	gggaccaccg	3420
cgctactgcc	gccaggcaaa	caaggggtgt	tatgagccat	attcagggtat	aaatgggctc	3480
gcgaaaacgt	caaaaaggcg	acacaaaatt	tattctaaat	gcataataaa	tactgataac	3540
atcttatagt	ttgtattata	ttttgtatta	tcgttgacat	gtataatttt	gatatacaaaa	3600
actgattttc	cctttattat	tttcgagatt	tatttttctta	attctcttta	acaaactaga	3660
aatattgtat	atacaaaaaa	tcataaataa	tagatgaata	gtttaattat	aggtgttcat	3720
caatcgaaaa	agcaacgtat	cttatttaaa	gtgcgttgct	tttttctcat	ttataagggt	3780
aaataattct	catatatcaa	gcaaagtgac	aggcgccctt	aaataattctg	acaaatgctc	3840
tttccctaaa	ctccccccat	aaaaaaaccc	gccgaagcgg	gtttttacgt	tatttgcgga	3900
ttaacgatta	ctcgttatca	gaaccgcccc	ggggggccga	gcttaagact	ggccgtcgtt	3960
ttacaacaca	gaaaagagttt	gtagaaacgc	aaaaaaggcca	tccgtcagggt	gccttctgct	4020
tagtttgatg	cctggcagtt	ccctactctc	gccttccgct	tcttcgctca	ctgactcgct	4080
gcgctcgggtc	gttcggctgc	ggcgagcggt	atcagctcac	tcaaaggcgg	taatacgggt	4140
atccacagaa	tcaggggata	acgcaggaaa	gaacatgtga	gcaaaaaggcc	agcaaaaaggc	4200
caggaaccgt	aaaaaaggccg	cgttgctggc	gtttttccat	aggctccgcc	cccctgacga	4260
gcatcacaaa	aatcgacgct	caagtcagag	gtggcgaaac	ccgacaggac	tataaagata	4320
ccaggcgttt	ccccctggaa	gctccctcgt	gcgctctcct	gttccgaccc	tgccgcttac	4380
cggatacctg	tccgcctttc	tcccttcggg	aagcggtggcg	ctttctcata	gctcacgctg	4440
taggtatctc	agttcgggtg	aggctgttcg	ctccaagctg	ggctgtgtgc	acgaaccccc	4500
cgttcagccc	gaccgctgcg	ccttatccgg	taactatcgt	cttgagtcca	acccggtaag	4560
acacgactta	tcgccactgg	cagcagccac	tggtaacagg	attagcagag	cgaggatatgt	4620
aggcgggtgct	acagagttct	tgaagtgggtg	ggctaactac	ggctacacta	gaagaacagt	4680
atttgggtatc	tgcgctctgc	tgaagccagt	taccttcgga	aaaagagttg	gtagctcttg	4740
atccggcaaaa	caaaccaccg	ctggtagcgg	tggttttttt	gtttgcaagc	agcagattac	4800
gcgcgaaaaa	aaaggatctc	aagaagatcc	tttgatcttt	tctacgggggt	ctgacgctca	4860
gtggaacgac	gcgcgcgtaa	ctcacgttaa	gggatttttg	tcatgagctt	gcgccgtccc	4920
gtcaagtcag	cgtaatgctc	tgctt				4945

<210> 11

<211> 1955

<212> RNA

<213> Artificial Sequence

<220>

<223> Substrate etc

<400> 11

gggaaauaag	agagaaaaaga	agaguaaagaa	gaaauauaag	agccaccaug	gaagaugcga	60
agaacauaaa	gaaaggguccc	gccccauuuu	acccacucga	ggauggaaca	gcuggggagc	120
aacugcacia	ggccaugaag	cgcuauvcgu	uggugccggg	aaccaucgcg	uucaccgacg	180
cacacaucga	agugaacauc	acuuacgccg	aguacuuuga	gaugagcguc	aggcugggccg	240
aggcuauгаа	gcgauacggu	cugaacacca	accaccggau	cguggucugc	ucugaaaaca	300

gccugcaguu	cuucaugccg	guccuggggg	cccuguucau	cggcguggcc	guggcaccgg	360
ccaacgauau	cuacaacgag	agagaaauugc	ugaacucgau	gaacaucucc	cagccuaccg	420
ugguguucgu	gucgaagaag	ggguugcaga	agauccugaa	cuggcagaag	aagcugccca	480
ucauucaaaa	gauuaucauu	auggauucca	aaaccgacua	ccaggguuuc	cagucaaugu	540
auaccuucgu	gaccucccau	cugcccccu	gcuucaacga	auacgacuuc	gugccugaaa	600
gcuucgaccg	cgacaagacg	aucgcccuc	ucaugaacuc	guccggcucg	accgggcugc	660
ccaaaggagu	ggcccugcca	caccggaccg	cuugcgugcg	guucucccac	gcccgggacc	720
cuauuuucgg	caaucagauc	auuccggaca	cugccauccu	gagcgugguc	cccuuccauc	780
acggguuugg	gauguuuacc	acucugggcu	accucaucug	cggauucagg	guggugcuga	840
uguaccgguu	cgaggaagaa	cuuuuccugc	ggagccugca	ggauuacaag	auccaguccg	900
cccuccucgu	gccaaccccuc	uucucauuu	ucgcuaaguc	cacucucauc	gauaaguacg	960
accugucgaa	ucuccacgaa	auugcguccg	guggugcacc	gcuguccaag	gaggucggcg	1020
aagccguggc	caagcgcuuc	caccucccgg	gaauucgcca	gggauacggc	cugacugaaa	1080
cgaccagcgc	gauucugauc	accccggagg	gcgacgacaa	gccgggugcc	gugggggaaag	1140
uggugccguu	cuucgaagca	aaggucgugg	aucuggauac	cggaaagacu	cugggcguga	1200
accagagagg	ggaacuuugu	gugcgcggac	cgaugauuau	guccggauau	gucaacaacc	1260
ccgaggccac	uaaugcccug	aucgacaagg	acggaugguu	gcuaagcggc	gacaucgcau	1320
acugggacga	ggacgagcac	uuuuucauug	uggaucggcu	caagucccug	aucaaguaca	1380
agggauacca	ggucgccccu	gccgaacuug	aguccauccu	gcugcaacau	ccgaacauuu	1440
ucgacgcggg	cgucgcuggc	cuuccugaug	augacgccgg	agagcugccc	gcggccgugg	1500
uggugcucga	acacggaaaa	acuaugaccg	agaaggaaaau	cugggacuac	guggcgucac	1560
aagucaccac	ugccaagaaa	cugcgcggcg	gagucguguu	cugggacgag	gugcccaagg	1620
gccugaccgg	aaagcuggac	gcuagaaaga	uccgggagau	ccugauuaag	gccaagaagg	1680
gaggaaaaguc	caagcucuga	aucugcugcc	uucugcgggg	cuugccuucu	ggccaugccc	1740
uucuuucuc	ccuugcaccu	guaccucuug	gucuuugaau	aaagccugag	uaggaaugua	1800
gggaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	1860
aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaag	gaagagcgcu	1920
gccuccuuca	gagucugcuc	acgagcucgg	ucucg			1955

<210> 12
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Substrate etc

<400> 12
 tctagaggcc agcctggcca taaggagata tacatcggtg ctgttggttaa agccacc 57

<210> 13
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Substrate etc

<400> 13

taatgaggcc aaactggcca ccatcaccat cagagcttgg acttttcctcc

50

<210> 14

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 14

atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
atcgaactgg ctgctatccc gttcaacact ctggctgacc attacggtga gcgttttagct 120
cgcgaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
atgtttgagc gtcaacttaa agctgggtgag gttgcggata acgctgccgc caagcctctc 240
atcactaccc tactccctaa gatgattgca cgcataacg actggtttga ggaagtga 300
gctaagcgcg gcaagcgccc gacagccttc cagttcctgc aagaaatcaa gccggaagcc 360
gtagcgtaca tcaccattaa gaccactctg gcttgcctaa ccagtgtga caatacaacc 420
gttcaggctg tagcaagcgc aatcggctcg gccattgagg acgaggctcg cttcggctcg 480
atccgtgacc ttgaagctaa gcacttcaag aaaaacgttg aggaacaact caacaagcgc 540
gtagggcacg tctacaagaa agcatttatg caagttgtcg aggctgacat gctctctaag 600
ggctactctg gtggcgaggc gtggctcttc tggcataagg aagactctat tcatgtagga 660
gtacgctgca tcgagatgct cattgagtca accggaatgg ttagcttaca ccgcaaaaat 720
gctggcgtag taggtcaaga ctctgagact atcgaactcg cacctgaata cgctgaggct 780
atcgcaaccc gtgcagggtc gctggctggc atctctccga tgttccaacc ttgcgtagtt 840
cctcctaagc cgtggactgg cattactggt ggtggctatt gggctaacgg tcgtcgtcct 900
ctggcgctgg tgcgtactca cagtaagaaa gcactgatgc gctacgaaga cgtttacatg 960
cctgaggtgt acaaagcgat taacattgcg caaaacaccg catggaaaat caacaagaaa 1020
gtcctagcgg tcgccaacgt aatcaccaag tgggaagcatt gtccggctga ggacatccct 1080
gcgattgagc gtgaagaact cccgatgaaa ccggaagaca tcgacatgaa tcctgaggct 1140
ctcaccgctg ggaaacgtgc tgccgctgct gtgtaccgca aggacaaggc tcgcaagtct 1200
cgccgtatca gccttgagtt catgcttgag caagccaata agtttgctaa ccataaggcc 1260
atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcgg 1380
aaggaagggt actactggct gaaaatccac ggtgcaaaact gtgcgggtgt cgataagggt 1440
ccgttccctg agcgcatcaa gttcattgag gaaaaccacg agaacatcat ggcttgcgct 1500
aagtctccac tggagaacac ttgggtgggt gagcaagatt ctccgttctg cttccttgcg 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgtttg acgggtcttg ctctggcatc cagcacttct ccgcatgct ccgagatgag 1680
gtaggtgggtc gcgcgggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggt gaaatctctg agaaagtcaa gctgggcact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gcagtgtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaaagag ttcggcttcc gtcaacaagt gctggaagat 1980
accattcagt gggctattga ttccggcaag ggtctgatgt tcaactcagc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgt agctgcgggt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220

```

cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggc 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgcactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcctag agtcggactt cgcgttcgcg taa 2673

```

<210> 15
 <211> 890
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> T7RNAP variant

<400> 15

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

				245				250					255				
Tyr	Ala	Glu	Ala	Ile	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser		
			260					265					270				
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile		
		275					280					285					
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val		
	290					295					300						
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met		
305					310					315					320		
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys		
				325					330						335		
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys		
			340					345					350				
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro		
		355					360					365					
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp		
	370					375					380						
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser		
385					390					395					400		
Arg	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala		
				405					410					415			
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg		
		420					425					430					
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys		
		435					440					445					
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr		
	450					455					460						
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val		
465					470					475					480		
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile		
				485					490					495			
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln		
			500					505					510				
Asp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val		
		515					520					525					
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp		
	530					535					540						
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu		
545					550					555					560		
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp		
				565					570					575			
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp		
			580					585					590				
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn		
		595					600					605					
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala		
	610					615					620						
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser		
625					630					635					640		
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln		

				645					650					655			
Val	Leu	Glu	Asp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu		
			660					665					670				
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile		
		675					680					685					
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn		
	690					695					700						
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys		
705				710					715						720		
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr		
			725					730					735				
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr		
		740					745					750					
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile		
	755					760					765						
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly		
770						775					780						
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys		
785				790				795							800		
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu		
			805					810						815			
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe		
		820					825					830					
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val		
	835					840					845						
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln		
	850					855				860							
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg		
865				870				875							880		
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala								
			885					890									

<210> 16

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 16

```

atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
atcgaactgg ctgctatccc gttcaacact ctggctgacc attacggtga gcgttttagct 120
cgcgaaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
atgtttgagc gtcaacttaa agctgggtgag gttgcggata acgctgccgc caagcctctc 240
atcactaccc tactccctaa gatgattgca cgcatcaacg actggtttga ggaagtgaaa 300
gctaagcgcg gcaagcgccc gacagccttc cagttcctgc aagaaatcaa gccggaagcc 360
gtacggtaca tcaccattaa gaccactctg gcttgcctaa ccagtgtctga taatacaacc 420
gttcaggctg tagcaagcgc aatcggtcgg gccattgagg acgaggctcg cttcggctcgt 480

```

```

atccgtgacc ttgaagctaa gcacttcaag aaaaacgttg aggaacaact caacaagcgc 540
gtagggcacg tctacaagaa agcatttatg caagttgtcg aggctgacat gctctctaag 600
gggtctactcg gtggcgaggc gtggctcttcg tggcataagg aagactctat tcatgtagga 660
gtacgctgca tcgagatgct cattgagtca accggaatgg ttagcttaca ccgccaaaaat 720
gctggcgtag taggtcaaga ctctgagact atcgaactcg cacctgaata cgctgaggct 780
atcgcaacccc gtgcagggtgc gctggctggc atctctccga tgttccaacc ttgcgtagtt 840
cctcctaagc cgtggactgg cattactggg ggtggctatt gggctaacgg tcgtcgtcct 900
ctggcgctgg tgcgtactca cagtaagaaa gcactgatgc gctacgaaga cgtttacatg 960
cctgaggtgt acaaagcgat taacattgcg caaaacaccg catggaaaat caacaagaaa 1020
gtcctagcgg tcgccaacgt aatcaccaag tggaagcatt gtccggctga ggacatccct 1080
gcgattgagc gtgaagaact cccgatgaaa ccggaagaca tcgacatgaa tcctgaggct 1140
ctcaccgcgt ggaaacgtgc tgccgctgct gtgtaccgca aggacaaggc tcgcaagtct 1200
agacgtatca gccttgagtt catgcttgag caagccaata agtttgctaa ccataaggcc 1260
atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcggg 1380
aagggaaggtt actactggct gaaaatccac ggtgcaaaact gtgcgggtgt cgataaggtt 1440
ccgttccctg agcgcatcaa gttcattgag gaaaaccacg agaacatcat ggcttgcgct 1500
aagtctccac tggagaacac ttgggtgggct gagcaagatt ctccgttctg cttccttgcg 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgtttg acgggtcttg ctctggcatc cagcacttct ccgcatgct ccgagatgag 1680
gtaggtggtc gcgcgggttaa cttgcttccct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggt gaaatctctg agaaagtcaa gctgggcact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gctgggtgac aaagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaaacc 1980
accattcagt gggctattga ttccggcaag ggtctgatgt tcaactcagcc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcgggt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggg 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtag tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

```

<210> 17

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 17

Met His His His His His His Met Asn Thr Ile Asn Ile Ala Lys Asn

1

5

10

15

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

Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg	
			420					425					430			
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys	
		435					440					445				
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr	
	450					455					460					
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val	
465					470				475						480	
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile	
			485						490					495		
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln	
			500					505					510			
Asp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val	
		515					520					525				
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp	
	530					535					540					
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu	
545					550					555					560	
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp	
			565						570					575		
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp	
		580						585					590			
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn	
		595					600					605				
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala	
	610					615					620					
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Trp	Val	Thr	Lys	Arg	Ser	
625					630					635					640	
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln	
			645						650					655		
Val	Leu	Glu	Thr	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu	
			660					665					670			
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile	
		675					680					685				
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn	
	690					695					700					
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys	
705					710					715					720	
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr	
			725						730					735		
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr	
			740					745					750			
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile	
		755					760					765				
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly	
	770					775					780					
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys	
785					790					795					800	
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu	
			805						810					815		

Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe
		820						825					830		
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val
		835					840					845			
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln
		850				855					860				
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg
865					870					875					880
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala						
			885					890							

<210> 18

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 18

atgcaccatc	accatcacca	tatgaacacg	attaacatcg	ctaagaacga	cttctctgac	60
atcgaactgg	ctgctatccc	gttcaacact	ctggctgacc	attacgggtga	gcgttttagct	120
cgcgaacagt	tggcccttga	gcatgagtct	tacgagatgg	gtgaagcacg	cttccgcaag	180
atgtttgagc	gtcaacttaa	agctgggtgag	gttgcgata	acgctgccgc	caagcctctc	240
atcactaccc	tactccctaa	gatgattgca	cgcatcaacg	actggtttga	ggaagtga	300
gctaagcgcg	gcaagcgccc	gacagccttc	cagttcctgc	aagaaatcaa	gccggaagcc	360
gtagcgtaca	tcaccattaa	gaccactctg	gcttgccctaa	ccagtgtctga	taatacaacc	420
gttcaggctg	tagcaagcgc	aatcggctcg	gccattgagg	acgaggctcg	cttcggctcgt	480
atccgtgacc	ttgaagctaa	gcacttcaag	aaaaacgttg	aggaacaact	caacaagcgc	540
gtagggcacg	tctacaagaa	agcatttatg	caagttgtcg	aggctgacat	gctctctaag	600
ggcttactcg	gtggcgaggc	gtggctcttcg	tggcataagg	aagactctat	tcatgtagga	660
gtacgctgca	tcgagatgct	cattgagtca	accggaatgg	ttagcttaca	ccgccaaaat	720
gctggcgtag	taggtcaaga	ctctgagact	atcgaactcg	cacctgaata	cgctgaggct	780
atcgcaacc	gtgcagggtg	gctggctggc	atctctccga	tgttccaacc	ttgcgtagtt	840
cctcctaagc	cgtggactgg	cattactggt	gggtggctatt	gggctaacgg	tcgtcgtcct	900
ctggcgctgg	tgcgtactca	cagtaagaaa	gcactgatgc	gctacgaaga	cgtttacatg	960
cctgagggtg	acaaagcgat	taacattgcg	caaaacaccg	catggaaaat	caacaagaaa	1020
gtcctagcgg	tcgccaacgt	aatcaccaag	tgggaagcatt	gtccgggtcga	ggacatccct	1080
gcgattgagc	gtgaagaact	cccgatgaaa	ccggaagaca	tcgacatgaa	tcctgaggct	1140
ctcaccgcgt	ggaaacgtgc	tgccgctgct	gtgtaccgca	aggacaaggc	tcgcaagtct	1200
cgccgtatca	gccttgagtt	catgcttgag	caagccaata	agtttgctaa	ccataaggcc	1260
atctggttcc	cttacaacat	ggactggcgc	ggctgtgttt	acgctgtgtc	aatgttcaac	1320
ccgcaaggta	acgatatgac	caaaggactg	cttacgctgg	cgaaggta	accaatcgg	1380
aagggaaggt	actactggct	gaaaatccac	ggtgcaaaact	gtgcgggtgt	cgataaggt	1440
ccgttccctg	agcgcatcaa	gttcattgag	gaaaaccacg	agaacatcat	ggcttgcgct	1500
aagtctccac	tggagaacac	ttgggtgggct	gagcaattgt	ctccgttctg	cttccttgcg	1560
ttctgctttg	agtacgctgg	ggtacagcac	cacggcctga	gctataactg	ctcccttccg	1620
ctggcggttg	acgggtcttg	ctctggcatc	cagcacttct	ccgcgatgct	ccgagatgag	1680
gtaggtggct	gcgcggttaa	cttgcttctc	agtgaaccg	ttcaggacat	ctacgggatt	1740

```

gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggg gaaatctctg agaaagtcaa gctgggcact 1860
aaggcactgg ctgggtcaatg gctggccttac ggtgttactc gcagtgtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaatgg 1980
accattcagt gggctattga ttccggcaag ggtctgatgt tcactcagcc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcgggt 2100
gaagcaatga actggcctaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggg 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

```

<210> 19

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 19

```

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

```

			180					185				190			
Val	Glu	Ala	Asp	Met	Leu	Ser	Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp
		195					200					205			
Ser	Ser	Trp	His	Lys	Glu	Asp	Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile
	210					215					220				
Glu	Met	Leu	Ile	Glu	Ser	Thr	Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn
225					230					235					240
Ala	Gly	Val	Val	Gly	Gln	Asp	Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu
				245					250					255	
Tyr	Ala	Glu	Ala	Ile	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser
			260					265					270		
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile
		275					280					285			
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val
	290					295					300				
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met
305					310					315					320
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys
				325					330					335	
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys
			340					345					350		
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro
		355					360					365			
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp
	370					375					380				
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser
385					390					395					400
Arg	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala
				405					410					415	
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg
			420					425					430		
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys
		435					440					445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr
	450					455					460				
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
465					470					475					480
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile
				485					490					495	
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
			500					505					510		
Leu	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val
		515					520					525			
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp
	530					535					540				
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu
545					550					555					560
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp
				565					570					575	
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp

			580					585					590				
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn		
		595					600						605				
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala		
	610					615						620					
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser		
625					630					635					640		
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln		
			645						650					655			
Val	Leu	Glu	Trp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu		
			660					665					670				
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile		
		675					680					685					
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn		
	690					695						700					
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys		
705				710					715						720		
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr		
			725					730						735			
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr		
		740					745						750				
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile		
	755					760						765					
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly		
	770				775						780						
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys		
785				790					795						800		
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu		
			805						810					815			
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe		
		820					825						830				
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val		
		835				840						845					
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln		
	850				855					860							
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg		
865				870					875						880		
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala								
			885				890										

<210> 20

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 20

atgcaccatc	accatcacca	tatgaacacg	attaacatcg	ctaagaacga	cttctctgac	60
atcgaactgg	ctgctatccc	gttcaacact	ctggctgacc	attacggtga	gcgttttagct	120
cgcgaacagt	tggcccttga	gcatgagtct	tacgagatgg	gtgaagcacg	cttccgcaag	180
atgtttgagc	gtcaacttaa	agctgggtgag	gttgcggata	acgctgccgc	caagcctctc	240
atcactaccc	tactccctaa	gatgattgca	cgcatcaacg	actgggtttga	ggaagtgaag	300
gctaagcgcg	gcaagcgccc	gacagccttc	cagttcctgc	aagaaatcaa	gccggaagcc	360
gtagcgtaca	tcaccattaa	gaccactctg	gcttgccctaa	ccagtgcctg	gaatacaacc	420
gttcaggctg	tagcaagcgc	aatcgggtcgg	gccattgagg	acgaggctcg	cttcggctcgt	480
atccgtgacc	ttgaagctaa	gcatttcaag	aaaaacgttg	aggaacaact	caacaagcgc	540
gtagggcacg	tctacaagaa	agcatttatg	caagttgtcg	aggctgacat	gctctctaag	600
ggctctactcg	gtggcgaggc	gtggctcttcg	tggcataagg	aagactctat	tcatgtagga	660
gtacgctgca	tcgagatgct	cattgagtca	accggaatgg	ttagcttaca	ccgccaaaat	720
gctggcgtag	taggtcaaga	ctctgagact	atcgaactcg	cacctgaata	cgctgaggct	780
atcgcaaccc	gtgcagggtgc	gctggctggc	atctctccga	tgttccaacc	ttgcgtagtt	840
cctcctaagc	cgtggactgg	cattactggg	gggtggctatt	gggctaacgg	tcgtcgtcct	900
ctggcgctgg	tgcgtactca	cagtaagaaa	gcactgatgc	gctacgaaga	cgtttacatg	960
cctgagggtg	acaaagcgat	taacattgcg	caaaacaccg	catggaaaat	caacaagaaa	1020
gtcctagcgg	tcgccaacgt	aatcaccaag	tgggaagcatt	gtccgggtcga	ggacatccct	1080
gcgattgagc	gtgaagaact	cccgatgaaa	ccggaagaca	tcgacatgaa	tcctgaggct	1140
ctcaccgcgt	ggaaacgtgc	tgccgctgct	gtgtaccgca	aggacaaggc	tcgcaagtct	1200
agtcgtatca	gccttgagtt	catgcttgag	caagccaata	agtttgctaa	ccataaggcc	1260
atctggttcc	cttacaacat	ggactggcgc	ggctcgtgtt	acgctgtgtc	aatgttcaac	1320
ccgcaaggta	acgatatgac	caaaggactg	cttacgctgg	cgaagggtaa	accaatcggg	1380
aagggaagggt	actactggct	gaaaatccac	gggtgcaaac	gtgcgggtgt	cgataagggt	1440
ccgttccctg	agcgcatcaa	gttcattgag	gaaaaccacg	agaacatcat	ggcttgcgct	1500
aagtctccac	tggagaacac	ttgggtgggct	gagcaacggg	ctccgttctg	cttccttgcg	1560
ttctgctttg	agtacgctgg	ggtagcagcac	cacggcctga	gctataactg	ctcccttccg	1620
ctggcgcttg	acgggtcttg	ctctggcatc	cagcacttct	ccgcgatgct	ccgagatgag	1680
gtaggtgggtc	gcgcgggttaa	cttgcttcct	agtgaaacgg	ttcaggacat	ctacgggatt	1740
gttgctaaga	aagtcaacga	gattctacaa	gcagacgcaa	tcaatgggac	cgataacgaa	1800
gtagttaccg	tgaccgatga	gaacactggg	gaaatctctg	agaaagtcaa	gctgggcact	1860
aaggcactgg	ctgggtcaatg	gctggcttac	gggtgttactc	gcagtgtgac	taagcgttca	1920
gtcatgacgc	tggcttacgg	gtccaaagag	ttcggtctcc	gtcaacaagt	gctggaagat	1980
accattcagt	gggctattga	ttccggcaag	ggctctgatgt	tcactcagcc	gaatcaggct	2040
gctggataca	tggctaagct	gatttgggaa	tctgtgagcg	tgacgggtgg	agctgcgggt	2100
gaagcaatga	actggcttaa	gtctgctgct	aagctgctgg	ctgctgagggt	caaagataag	2160
aagactggag	agattcttcg	caagcgttgc	gctgtgcatt	gggttaactcc	tgatggtttc	2220
cctgtgtggc	aggaatacaa	gaagcctatt	cagacgcgct	tgaacctgat	gttcctcggg	2280
cagttccgct	tacagcctac	cattaacacc	aacaaagata	gcgagattga	tgcacacaaa	2340
caggagtctg	gtatcgctcc	taactttgta	cacagccaag	acggtagcca	ccttcgtaag	2400
actgtagtgt	gggcacacga	gaagtacgga	atcgaatctt	ttgactgat	tcacgactcc	2460
ttcggtagca	ttccggctga	cgctgcgaac	ctgttcaaag	cagtgcgcga	aactatgggt	2520
gacacatatg	agtcttgtag	tgtactggct	gatttctacg	accagttcgc	tgaccagttg	2580
cacgagtctc	aattggacaa	aatgccagca	cttcgggcta	aaggtaactt	gaacctccgt	2640
gacatcttag	agtcggactt	cgcgttcgcg	taa			2673

<210> 21
 <211> 890
 <212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 21

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

His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro
		355					360					365			
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp
	370					375					380				
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser
385					390					395					400
Ser	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala
				405					410					415	
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg
			420					425					430		
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys
		435					440					445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr
	450					455					460				
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
465					470					475					480
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile
				485					490					495	
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
			500					505					510		
Arg	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val
		515					520					525			
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp
	530					535					540				
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu
545					550					555					560
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp
				565					570					575	
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp
			580					585					590		
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn
		595					600					605			
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala
	610					615					620				
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser
625					630					635					640
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln
				645					650					655	
Val	Leu	Glu	Asp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu
			660					665					670		
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile
		675					680					685			
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn
	690					695						700			
Trp	Leu														

Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile
		755					760					765			
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly
		770					775					780			
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys
785					790					795					800
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu
				805					810					815	
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe
			820					825					830		
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val
		835					840						845		
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln
		850				855					860				
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg
865					870					875					880
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala						
				885					890						

<210> 22

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 22

atgcaccatc	accatcacca	tatgaacacg	attaacatcg	ctaagaacga	cttctctgac	60
atcgaactgg	ctgctatccc	gttcaacact	ctggctgacc	attacggtga	gcgttttagct	120
cgcgaaacagt	tggcccttga	gcatgagtct	tacgagatgg	gtgaagcacg	cttccgcaag	180
atgtttgagc	gtcaacttaa	agctgggtgag	gttgcggata	acgctgccgc	caagcctctc	240
atcactaccc	tactccctaa	gatgattgca	cgcatcaacg	actggtttga	ggaagtgaag	300
gctaagcgcg	gcaagcgccc	gacagccttc	cagttcctgc	aagaaatcaa	gccggaagcc	360
gtagcgtaca	tcaccattaa	gaccactctg	gcttgccctaa	ccagtgcctg	gaatacaacc	420
gttcaggctg	tagcaagcgc	aatcgggtcgg	gccattgagg	acgaggctcg	cttcgggtcgt	480
atccgtgacc	ttgaagctaa	gcacttcaag	aaaaacgttg	aggaacaact	caacaagcgc	540
gtagggcacg	tctacaagaa	agcattttatg	caagttgtcg	aggctgacat	gctctctaag	600
ggcttactcg	gtggcgaggc	gtggctcttcg	tggcataaagg	aagactctat	tcatgtagga	660
gtacgctgca	tcgagatgct	cattgagtca	accggaatgg	ttagcttaca	ccgccaaaat	720
gctggcgtag	taggtcaaga	ctctgagact	atcgaactcg	cacctgaata	cgctgaggct	780
atcgcaaccc	gtgcagggtgc	gctggctggc	atctctccga	tgttccaacc	ttgcgtagtt	840
cctcctaagc	cgtggactgg	cattactggg	gggtggctatt	gggctaacgg	tcgtcgtcct	900
ctggcgctgg	tgcgtactca	cagtaagaaa	gcactgatgc	gctacgaaga	cgtttacatg	960
cctgagggtg	acaaagcgat	taacattgctg	caaaacaccg	catggaaaat	caacaagaaa	1020
gtcctagcgg	tcgccaacgt	aatcaccaag	tgggaagcatt	gtccgggtcga	ggacatccct	1080
gcgattgagc	gtgaagaact	cccgatgaaa	ccggaagaca	tcgacatgaa	tcctgaggct	1140
ctcaccgcgt	ggaaacgtgc	tgccgctgct	gtgtaccgca	aggacaaggc	tcgcaagtct	1200
agacgtatca	gccttgagtt	catgcttgag	caagccaata	agtttgctaa	ccataaggcc	1260

```

atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcggg 1380
aaggaagggtt actactggct gaaaatccac ggtgcaaaact gtgcgggtgt cgataagggt 1440
ccgttccctg agcgcacatcaa gttcattgag gaaaaccacg agaacatcat ggcttgcgct 1500
aagtctccac tggagaacac ttggtgggct gagcaatggg ctccgttctg cttccttgcg 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgtttg acgggtcttg ctctggcatc cagcacttct ccgcgatgct ccgagatgag 1680
gtaggtggtc gcgcgggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggg gaaatctctg agaaagtcaa gctggggcact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gcagtgtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaagat 1980
accattcagt gggctattga ttccggcaag ggtctgatgt tcaactcagcc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcgggt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggg 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgcactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

```

<210> 23

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 23

```

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

```

		115					120					125			
Thr	Leu	Ala	Cys	Leu	Thr	Ser	Ala	Trp	Asn	Thr	Thr	Val	Gln	Ala	Val
	130					135					140				
Ala	Ser	Ala	Ile	Gly	Arg	Ala	Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg
145				150						155					160
Ile	Arg	Asp	Leu	Glu	Ala	Lys	His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln
			165					170						175	
Leu	Asn	Lys	Arg	Val	Gly	His	Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val
		180						185					190		
Val	Glu	Ala	Asp	Met	Leu	Ser	Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp
	195					200					205				
Ser	Ser	Trp	His	Lys	Glu	Asp	Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile
	210					215					220				
Glu	Met	Leu	Ile	Glu	Ser	Thr	Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn
225				230						235					240
Ala	Gly	Val	Val	Gly	Gln	Asp	Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu
			245					250						255	
Tyr	Ala	Glu	Ala	Ile	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser
		260					265						270		
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile
	275					280						285			
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val
290					295					300					
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met
305				310					315						320
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys
			325					330						335	
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys
	340					345							350		
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro
	355					360						365			
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp
	370				375					380					
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser
385				390					395						400
Arg	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala
			405					410						415	
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg
		420				425						430			
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys
	435					440						445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr
	450				455					460					
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
465				470					475						480
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile
			485					490						495	
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
	500							505					510		
Trp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val

		515					520				525						
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp		
	530					535					540						
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu		
545				550						555					560		
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp		
			565						570					575			
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp		
		580					585						590				
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn		
	595					600					605						
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala		
	610					615					620						
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser		
625				630						635					640		
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln		
			645						650					655			
Val	Leu	Glu	Asp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu		
		660					665						670				
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile		
	675					680						685					
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn		
	690				695						700						
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys		
705				710					715						720		
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr		
			725						730					735			
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr		
	740						745						750				
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile		
	755					760						765					
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly		
	770				775						780						
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys		
785				790						795					800		
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu		
			805						810					815			
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe		
		820					825					830					
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val		
	835					840					845						
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln		
	850				855					860							
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg		
865				870						875					880		
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala								
			885						890								

<211> 2673
<212> DNA
<213> Artificial Sequence

<220>
<223> T7RNAP variant

<400> 24

atgcaccatc	accatcacca	tatgaacacg	attaacatcg	ctaagaacga	cttctctgac	60
atcgaactgg	ctgctatccc	gttcaacact	ctggctgacc	attacggtga	gcgttttagct	120
cgcgaacagt	tggcccttga	gcatgagtct	tacgagatgg	gtgaagcacg	cttccgcaag	180
atgtttgagc	gtcaacttaa	agctgggtgag	gttgcggata	acgctgccgc	caagcctctc	240
atcactaccc	tactccctaa	gatgattgca	cgcatcaacg	actggtttga	ggaagtgaag	300
gctaagcgcg	gcaagcgccc	gacagccttc	cagttcctgc	aagaaatcaa	gccggaagcc	360
gtagcgtaga	tcaccattaa	gaccactctg	gcttgcctaa	ccagtgcctg	gaatacaacc	420
gttcaggctg	tagcaagcgc	aatcggctcg	gccattgagg	acgaggctcg	cttcggctcg	480
atccgtgacc	ttgaagctaa	gcacttcaag	aaaaacgttg	aggaacaact	caacaagcgc	540
gtagggcacg	tctacaagaa	agcatttatg	caagttgtcg	aggctgacat	gctctctaag	600
ggctctactc	gtggcgaggc	gtggctcttc	tggcataagg	aagactctat	tcatgtagga	660
gtacgctgca	tcgagatgct	cattgagtca	accggaatgg	ttagcttaca	ccgccaaaat	720
gctggcgtag	taggtcaaga	ctctgagact	atcgaactcg	cacctgaata	cgctgaggct	780
atcgcaaccc	gtgcagggtg	gctggctggc	atctctccga	tgttccaacc	ttgcgtagtt	840
cctcctaagc	cgtggactgg	cattactggt	ggtggctatt	gggctaacgg	tcgtcgtcct	900
ctggcgctgg	tgcgtactca	cagtaagaaa	gcactgatgc	gctacgaaga	cgtttacatg	960
cctgagggtg	acaaagcgat	taacattgct	caaaacaccg	catggaaaat	caacaagaaa	1020
gtcctagcgg	tcgccaacgt	aatcaccaag	tgggaagcatt	gtccggctga	ggacatccct	1080
gcgattgagc	gtgaagaact	cccgatgaaa	ccggaagaca	tcgacatgaa	tcctgaggct	1140
ctcaccgcgt	ggaaacgtgc	tgccgctgct	gtgtaccgca	aggacaaggc	tcgcaagtct	1200
agtcgtatca	gccttgagtt	catgcttgag	caagccaata	agtttgctaa	ccataaggcc	1260
atctggttcc	cttacaacat	ggactggcgc	ggctgtgttt	acgctgtgtc	aatgttcaac	1320
ccgcaaggta	acgatatgac	caaaggactg	cttacgctgg	cgaaaggtaa	accaatcggg	1380
aagggaagg	actactggct	gaaaatccac	ggtgcaaaact	gtgcgggtgt	cgataagggt	1440
ccgttccctg	agcgcatcaa	gttcattgag	gaaaaccacg	agaacatcat	ggcttgcgct	1500
aagtctccac	tggagaacac	ttgggtgggt	gagcaatggg	ctccgttctg	cttccttgcg	1560
ttctgctttg	agtacgctgg	ggtacagcac	cacggcctga	gctataactg	ctcccttccg	1620
ctggcgcttg	acgggtcttg	ctctggcatc	cagcacttct	ccgcgatgct	ccgagatgag	1680
gtaggtggtc	gcgcgggtta	cttgcttcct	agtgaacccg	ttcaggacat	ctacgggatt	1740
gttgctaaga	aagtcaacga	gattctacaa	gcagacgcaa	tcaatgggac	cgataacgaa	1800
gtagttaccg	tgaccgatga	gaacactggt	gaaatctctg	agaaaagtcaa	gctggggcact	1860
aaggcactgg	ctggtcaatg	gctggcttac	ggtgttactc	gcagtgtgac	taagcgttca	1920
gtcatgacgc	tggcttacgg	gtccaaagag	ttcggcttcc	gtcaacaagt	gctggaagat	1980
accattcagt	gggctattga	ttccggcaag	ggtctgatgt	tactcagcc	gaatcaggct	2040
gctggataca	tggctaagct	gatttgggaa	tctgtgagcg	tgacgggtgg	agctgcgggt	2100
gaagcaatga	actggcttaa	gtctgctgct	aagctgctgg	ctgctgaggt	caaagataag	2160
aagactggag	agattcttcg	caagcgttgc	gctgtgcatt	gggtaactcc	tgatgggttc	2220
cctgtgtggc	aggaatacaa	gaagcctatt	cagacgcgct	tgaacctgat	gttcctcggt	2280
cagttccgct	tacagcctac	cattaacacc	aacaaagata	gcgagattga	tgacacacaaa	2340
caggagtctg	gtatcgctcc	taactttgta	cacagccaag	acggtagcca	ccttcgtaag	2400
actgtagtgt	gggcacacga	gaagtacgga	atcgaatctt	ttgcactgat	tcacgactcc	2460
ttcgttacca	ttccggctga	cgctgcgaac	ctgttcaaag	cagtgcgcga	aactatgggt	2520

gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

<210> 25
<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> T7RNAP variant

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

Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val
290						295					300				
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met
305					310					315					320
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys
				325					330					335	
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys
			340					345					350		
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro
		355					360					365			
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp
						375					380				
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser
385					390					395					400
Ser	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala
				405					410					415	
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg
			420					425					430		
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys
		435					440					445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr
	450					455					460				
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
465					470					475					480
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile
				485					490					495	
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
			500					505					510		
Trp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val
		515					520					525			
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp
	530					535					540				
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu
545					550					555					560
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp
				565					570					575	
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp
			580					585					590		
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn
		595					600					605			
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala
						615					620				
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser
625					630					635					640
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln
				645					650					655	
Val	Leu	Glu	Asp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu
			660					665					670		
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile
		675					680					685			

Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn
690						695					700				
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys
705				710					715						720
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr
			725						730					735	
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr
		740						745					750		
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile
	755					760						765			
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly
	770					775					780				
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys
785				790						795					800
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu
			805						810					815	
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe
		820					825						830		
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val
	835					840						845			
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln
	850					855				860					
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg
865				870						875					880
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala						
			885					890							

<210> 26
 <211> 2673
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> T7RNAP variant

<400> 26
 atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
 atcgaactgg ctgctatccc gttcaacact ctggctgacc attacggtga gcgttttagct 120
 cgcgaaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
 atgtttgagc gtcaacttaa agctgggtgag gttgcggata acgctgccgc caagcctctc 240
 atcactaccc tactccctaa gatgattgca cgcataacg actggtttga ggaagtgaag 300
 gctaagcgcg gcaagcgccc gacagccttc cagttcctgc aagaaatcaa gccggaagcc 360
 gtagcgtaca tcaccattaa gaccactctg gcttgccctaa ccagtgcctg gaatacaacc 420
 gttcaggctg tagcaagcgc aatcggtcgg gccattgagg acgaggctcg cttcggctcg 480
 atccgtgacc ttgaagctaa gcacttcaag aaaaacgttg aggaacaact caacaagcgc 540
 gtagggcacg tctacaagaa agcatttatg caagttgtcg aggctgacat gctctctaag 600
 ggtctactcg gtggcgaggc gtggctcttcg tggcataagg aagactctat tcatgtagga 660
 gtacgctgca tcgagatgct cattgagtca accggaatgg ttagcttaca ccgcaaaaat 720
 gctggcgtag taggtcaaga ctctgagact atcgaactcg cacctgaata cgctgaggct 780

```

atcgcaaccc gtgcagggtgc gctggctggc atctctccga tgttccaacc ttgcgtagtt 840
cctcctaagc cgtggactgg cattactggg ggtggctatt gggctaacgg tcgtcgtcct 900
ctggcgctgg tgcgtactca cagtaagaaa gcactgatgc gctacgaaga cgtttacatg 960
cctgagggtg acaaagcgat taacattgcg caaaacaccg catggaaaat caacaagaaa 1020
gtcctagcgg tcgccaacgt aatcaccaag tgggaagcatt gtccggtcga ggacatccct 1080
gcgattgagc gtgaagaact cccgatgaaa ccggaagaca tcgacatgaa tcctgaggct 1140
ctcaccgcgt ggaaacgtgc tgccgctgct gtgtaccgca aggacaaggc tcgcaagtct 1200
atacgtatca gccttgagtt catgcttgag caagccaata agtttgctaa ccataaggcc 1260
atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcggg 1380
aagggaagggt actactggct gaaaatccac ggtgcaaaact gtgcgggtgt cgataagggt 1440
ccgttccctg agcgcacatcaa gttcattgag gaaaaccacg agaacatcat ggcttgcgct 1500
aagtctccac tggagaacac ttgggtgggct gagcaagatt ctccgttctg cttccttgcg 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgcttg acgggtcttg ctctggcatc cagcacttct ccgcatgct ccgagatgag 1680
gtagggtgtc gcgcggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggt gaaatctctg agaaagtcaa gctgggcact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gcagtgtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaagat 1980
accattcagt gggctattga ttccggcaag ggtctgatgt tcaactcagcc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcgggt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggg 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgcttcgcg taa 2673

```

<210> 27

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 27

```

Met His His His His His His Met Asn Thr Ile Asn Ile Ala Lys Asn
1           5           10          15
Asp Phe Ser Asp Ile Glu Leu Ala Ala Ile Pro Phe Asn Thr Leu Ala
          20          25          30
Asp His Tyr Gly Glu Arg Leu Ala Arg Glu Gln Leu Ala Leu Glu His
          35          40          45
Glu Ser Tyr Glu Met Gly Glu Ala Arg Phe Arg Lys Met Phe Glu Arg

```

50		55		60	
Gln Leu Lys Ala Gly Glu Val Ala Asp Asn Ala Ala Ala Lys Pro Leu					
65		70		75	80
Ile Thr Thr Leu Leu Pro Lys Met Ile Ala Arg Ile Asn Asp Trp Phe					
	85		90		95
Glu Glu Val Lys Ala Lys Arg Gly Lys Arg Pro Thr Ala Phe Gln Phe					
	100		105		110
Leu Gln Glu Ile Lys Pro Glu Ala Val Ala Tyr Ile Thr Ile Lys Thr					
	115		120		125
Thr Leu Ala Cys Leu Thr Ser Ala Trp Asn Thr Thr Val Gln Ala Val					
	130		135		140
Ala Ser Ala Ile Gly Arg Ala Ile Glu Asp Glu Ala Arg Phe Gly Arg					
145		150		155	160
Ile Arg Asp Leu Glu Ala Lys His Phe Lys Lys Asn Val Glu Glu Gln					
	165		170		175
Leu Asn Lys Arg Val Gly His Val Tyr Lys Lys Ala Phe Met Gln Val					
	180		185		190
Val Glu Ala Asp Met Leu Ser Lys Gly Leu Leu Gly Gly Glu Ala Trp					
	195		200		205
Ser Ser Trp His Lys Glu Asp Ser Ile His Val Gly Val Arg Cys Ile					
	210		215		220
Glu Met Leu Ile Glu Ser Thr Gly Met Val Ser Leu His Arg Gln Asn					
225		230		235	240
Ala Gly Val Val Gly Gln Asp Ser Glu Thr Ile Glu Leu Ala Pro Glu					
	245		250		255
Tyr Ala Glu Ala Ile Ala Thr Arg Ala Gly Ala Leu Ala Gly Ile Ser					
	260		265		270
Pro Met Phe Gln Pro Cys Val Val Pro Pro Lys Pro Trp Thr Gly Ile					
	275		280		285
Thr Gly Gly Gly Tyr Trp Ala Asn Gly Arg Arg Pro Leu Ala Leu Val					
	290		295		300
Arg Thr His Ser Lys Lys Ala Leu Met Arg Tyr Glu Asp Val Tyr Met					
305		310		315	320
Pro Glu Val Tyr Lys Ala Ile Asn Ile Ala Gln Asn Thr Ala Trp Lys					
	325		330		335
Ile Asn Lys Lys Val Leu Ala Val Ala Asn Val Ile Thr Lys Trp Lys					
	340		345		350
His Cys Pro Val Glu Asp Ile Pro Ala Ile Glu Arg Glu Glu Leu Pro					
	355		360		365
Met Lys Pro Glu Asp Ile Asp Met Asn Pro Glu Ala Leu Thr Ala Trp					
	370		375		380
Lys Arg Ala Ala Ala Ala Val Tyr Arg Lys Asp Lys Ala Arg Lys Ser					
385		390		395	400
Ile Arg Ile Ser Leu Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala					
	405		410		415
Asn His Lys Ala Ile Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg					
	420		425		430
Val Tyr Ala Val Ser Met Phe Asn Pro Gln Gly Asn Asp Met Thr Lys					
	435		440		445
Gly Leu Leu Thr Leu Ala Lys Gly Lys Pro Ile Gly Lys Glu Gly Tyr					

450		455		460
Tyr Trp Leu Lys Ile His Gly Ala Asn Cys Ala Gly Val Asp Lys Val				
465		470		480
Pro Phe Pro Glu Arg Ile Lys Phe Ile Glu Glu Asn His Glu Asn Ile				
	485		490	495
Met Ala Cys Ala Lys Ser Pro Leu Glu Asn Thr Trp Trp Ala Glu Gln				
	500		505	510
Asp Ser Pro Phe Cys Phe Leu Ala Phe Cys Phe Glu Tyr Ala Gly Val				
	515		520	525
Gln His His Gly Leu Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp				
	530		535	540
Gly Ser Cys Ser Gly Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu				
545		550		560
Val Gly Gly Arg Ala Val Asn Leu Leu Pro Ser Glu Thr Val Gln Asp				
	565		570	575
Ile Tyr Gly Ile Val Ala Lys Lys Val Asn Glu Ile Leu Gln Ala Asp				
	580		585	590
Ala Ile Asn Gly Thr Asp Asn Glu Val Val Thr Val Thr Asp Glu Asn				
	595		600	605
Thr Gly Glu Ile Ser Glu Lys Val Lys Leu Gly Thr Lys Ala Leu Ala				
	610		615	620
Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser				
625		630		640
Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln				
	645		650	655
Val Leu Glu Asp Thr Ile Gln Trp Ala Ile Asp Ser Gly Lys Gly Leu				
	660		665	670
Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile				
	675		680	685
Trp Glu Ser Val Ser Val Thr Val Val Ala Ala Val Glu Ala Met Asn				
	690		695	700
Trp Leu Lys Ser Ala Ala Lys Leu Leu Ala Ala Glu Val Lys Asp Lys				
705		710		720
Lys Thr Gly Glu Ile Leu Arg Lys Arg Cys Ala Val His Trp Val Thr				
	725		730	735
Pro Asp Gly Phe Pro Val Trp Gln Glu Tyr Lys Lys Pro Ile Gln Thr				
	740		745	750
Arg Leu Asn Leu Met Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile				
	755		760	765
Asn Thr Asn Lys Asp Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly				
	770		775	780
Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly Ser His Leu Arg Lys				
785		790		800
Thr Val Val Trp Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu				
	805		810	815
Ile His Asp Ser Phe Gly Thr Ile Pro Ala Asp Ala Ala Asn Leu Phe				
	820		825	830
Lys Ala Val Arg Glu Thr Met Val Asp Thr Tyr Glu Ser Cys Asp Val				
	835		840	845
Leu Ala Asp Phe Tyr Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln				

850		855		860
Leu Asp Lys Met Pro Ala	Leu Pro Ala Lys Gly	Asn Leu Asn Leu Arg		
865	870	875	880	
Asp Ile Leu Glu Ser Asp	Phe Ala Phe Ala			
885	890			

<210> 28
 <211> 2673
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> T7RNAP variant

<400> 28

atgcaccatc	accatcacca	tatgaacacg	attaacatcg	ctaagaacga	cttctctgac	60
atcgaactgg	ctgctatccc	gttcaacact	ctggctgacc	attacgggtga	gcgttttagct	120
cgcgaaacagt	tggcccttga	gcatgagtct	tacgagatgg	gtgaagcacg	cttccgcaag	180
atgtttgagc	gtcaacttaa	agctgggtgag	gttgccggata	acgctgccgc	caagcctctc	240
atcactaccc	tactccctaa	gatgattgca	cgcatcaacg	actggtttga	ggaagtgaaa	300
gctaagcgcg	gcaagcgccc	gacagccttc	cagttcctgc	aagaaatcaa	gccggaagcc	360
gtagcgtaca	tcaccattaa	gaccactctg	gcttgcctaa	ccagtataga	caatacaacc	420
gttcaggctg	tagcaagcgc	aatcggtcgg	gccattgagg	acgaggctcg	cttcggtcgt	480
atccgtgacc	ttgaagctaa	gcacttcaag	aaaaacgttg	aggaacaact	caacaagcgc	540
gtagggcacg	tctacaagaa	agcatttatg	caagttgtcg	aggctgacat	gctctctaag	600
ggcttactcg	gtggcgaggc	gtggctcttcg	tggcataagg	aagactctat	tcatgtagga	660
gtacgctgca	tcgagatgct	cattgagtca	accggaatgg	ttagcttaca	ccgccaaaat	720
gctggcgtag	taggtcaaga	ctctgagact	atcgaactcg	cacctgaata	cgctgaggct	780
atcgcaaccc	gtgcaggtgc	gctggctggc	atctctccga	tgttccaacc	ttgcgtagtt	840
cctcctaagc	cgtggactgg	cattactggg	gggtggctatt	gggctaacgg	tcgtcgtcct	900
ctggcgctgg	tgcgtactca	cagtaagaaa	gcactgatgc	gctacgaaga	cgtttacatg	960
cctgagggtg	acaaagcgat	taacattgcg	caaaacaccg	catggaaaat	caacaagaaa	1020
gtcctagcgg	tcgccaacgt	aatcaccaag	tgggaagcatt	gtccggtcga	agacatccct	1080
gcgattgagc	gtgaagaact	cccgatgaaa	ccggaagaca	tcgacatgaa	tcctgaggct	1140
ctcaccgcgt	ggaaacgtgc	tgccgctgct	gtgtaccgca	gagacaaggc	tcgcaagtct	1200
cgccgtatct	atcttgagtt	catgcttgag	caagccaata	agtttgctaa	ccataaggcc	1260
atctggttcc	cttacaacat	ggactggcgc	ggtcgtgttt	acgctgtgtc	aatgttcaac	1320
ccgcaaggta	acgattggac	caaaggactg	cttacgctgg	cgaaaggtaa	accaatcggt	1380
aaggaagggt	actactggct	gaaaatccac	ggtgcaaaact	gtgcgggtgt	cgataagggt	1440
ccgttccctg	agcgcatcaa	gttcattgag	gaaaaccacg	agaacatcat	ggcttgcgct	1500
aagtctccac	tggagaacac	ttggtgggct	gagcaagatt	ccccgttctg	cttccttgcg	1560
ttctgctttg	agtacgctgg	ggtacagcac	cacggcctga	gctataactg	ctcccttcg	1620
ctggcgcttg	acgggtcttg	ctctggcatc	cagcacttct	ccgcgatgct	ccgagatgag	1680
gtaggtgggtc	gcgcggttaa	cttgcttcct	agtgaaccg	ttcaggacat	ctacgggatt	1740
gttgctaaga	aagtcaacga	gattctacaa	gcagacgcaa	tcaatgggac	cgataacgaa	1800
gtagttaccg	tgaccgatga	gaacactggt	gaaatctctg	agaaagtcaa	gctgggcact	1860
aaggcactgg	ctggtcaatg	gctggcttac	ggtgttactc	gcagtgtgac	taagcgttca	1920
gtcatgacgc	tggcttacgg	gtccaaagag	ttcggcttcc	gtcaacaagt	gctggaagat	1980
accattcagt	gggctattga	ttccggcaag	ggtctgatgt	tcactcagcc	gaatcaggct	2040

```

gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtggt agctgcggtt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggc 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgcactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

```

<210> 29

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 29

```

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

```

Glu	Met	Leu	Ile	Glu	Ser	Thr	Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn
225					230					235					240
Ala	Gly	Val	Val	Gly	Gln	Asp	Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu
				245						250					255
Tyr	Ala	Glu	Ala	Ile	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser
			260					265						270	
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile
		275					280						285		
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val
	290					295					300				
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met
305					310					315					320
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys
				325					330						335
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys
			340					345						350	
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro
		355					360					365			
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp
	370					375					380				
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Arg	Asp	Lys	Ala	Arg	Lys	Ser
385					390					395					400
Arg	Arg	Ile	Tyr	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala
				405					410						415
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg
			420					425					430		
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Trp	Thr	Lys
		435					440					445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr
	450					455					460				
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
465					470					475					480
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile
				485					490						495
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
		500						505					510		
Asp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val
		515					520					525			
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp
	530					535					540				
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu
545					550					555					560
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp
				565					570						575
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp
			580					585						590	
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn
		595					600					605			
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala
	610					615					620				

Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser
625					630					635					640
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln
				645					650					655	
Val	Leu	Glu	Asp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu
			660					665					670		
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile
		675					680					685			
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn
	690					695					700				
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys
705				710					715						720
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr
			725					730						735	
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr
		740					745						750		
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile
		755					760					765			
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly
	770					775					780				
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys
785				790					795						800
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu
			805						810					815	
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe
		820						825					830		
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val
		835					840					845			
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln
	850					855					860				
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg
865				870					875						880
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala						
			885						890						

<210> 30

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 30

```

atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
atcgaactgg ctgctatccc gttcaacact ctggctgacc attacggtga gcgtttagct 120
cgcgaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
atgtttgagc gtcaacttaa agctgggtgag gttgcggata acgctgccgc caagcctctc 240
atcactaccc tactccctaa gatgattgca cgcatcaacg actggtttga ggaagtgaaa 300

```

gctaagcgcg	gcaagcgccc	gacagccttc	cagttcctgc	aagaaatcaa	gccggaagcc	360
gtagcgtag	tcaccattaa	gaccactctg	gcttgccata	ccagtgtga	caatacaacc	420
gttcaggctg	tagcaagcgc	aatcggctcg	gccattgagg	acgaggctcg	cttcggctcg	480
atccgtgacc	ttgaagctaa	gcacttcaag	aaaaacgttg	aggaacaact	caacaagcgc	540
gtagggcacg	tctacaagaa	agcattttatg	caagttgtcg	aggctgacat	gctctctaag	600
gggtactactg	gtggcgaggc	gtggctcttcg	tggcataagg	aagactctat	tcatgtagga	660
gtacgctgca	tcgagatgct	cattgagtca	accggaatgg	ttagcttaca	ccgcaaaaat	720
gctggcgtag	taggtcaaga	ctctgagact	atcgaactcg	cacctgaata	cgctgaggct	780
atcgcaaccc	gtgcagggtg	gctggctggc	atctctccga	tggtccaacc	ttgcgtagtt	840
cctcctaagc	cgtggactgg	cattactggg	gggtggctatt	gggctaacgg	tcgtcgtcct	900
ctggcgctgg	tgcgtagtca	cagtaagaaa	gcactgatgc	gctacgaaga	cgtttacatg	960
cctgagggtg	acaaagcgat	taacattgctg	caaaacaccg	catggaaaat	caacaagaaa	1020
gtcctagcgg	tcgccaacgt	aatcaccaag	tggaagcatt	gtccggctga	ggacatccct	1080
gcgattgagc	gtgaagaact	cccgatgaaa	ccggaagaca	tcgacatgaa	tcctgaggct	1140
ctcaccgcgt	ggaaacgtgc	tgccgctgct	gtgtaccgca	aggacaaggc	gcgcaagtct	1200
cgccgtatca	gccttgagtt	catgcttgag	caagccaata	agtttgctaa	ccataaggcc	1260
atctggttcc	cttacaacat	ggactggcgc	ggctgtgttt	acgctgtgtc	aatgttcaac	1320
ccgcaaggta	acgatatgac	caaaggactg	cttacgctgg	cgaaaggtaa	accaatcggt	1380
aaggaagggt	actactggct	gaaaatccac	ggtgcaaaact	gtgcgggtgt	cgataagggt	1440
ccgttccctg	agcgcatcaa	gttcattgag	gaaaaccacg	agaacatcat	ggcttgctgc	1500
aagtctccac	tggagaacac	ttgggtgggct	gagcaatggg	ctccgttctg	cttccttgctg	1560
ttctgctttg	agtacgctgg	ggtacagcac	cacggcctga	gctataactg	ctcccttccg	1620
ctggcgcttg	acgggtcttg	ctctggcatc	cagcacttct	ccgcgatgct	ccgagatgag	1680
gtagggtggc	gcgcgggttaa	cttgcttcct	agtgaacccg	ttcaggacat	ctacgggatt	1740
gttgctaaga	aagtcaacga	gattctacaa	gcagacgcaa	tcaatgggac	cgataacgaa	1800
gtagttaccg	tgaccgatga	gaacactggt	gaaatctctg	agaaagtcaa	gctgggcact	1860
aaggcactgg	ctgggtcaatg	gctggcttac	ggtgttactc	gctgggtgac	taagcgttca	1920
gtcatgacgc	tggcttacgg	gtccaaagag	ttcggcttcc	gtcaacaagt	gctggaattc	1980
accattcagc	ctgctattga	ttccggcaag	ggtctgatgt	tcaactcagc	gaatcaggct	2040
gctggataca	tggctaagct	gatttgggaa	tctgtgagcg	tgacgggtgg	agctgcgggt	2100
gaagcaatga	actggcttaa	gtctgctgct	aagctgctgg	ctgctgaggt	caaagataag	2160
aagactggag	agattcttcg	caagcggtgc	gctgtgcatt	gggtaactcc	tgatgggttc	2220
cctgtgtggc	aggaatacaa	gaagcctatt	cagacgcgct	tgaacctgat	gttcctcggt	2280
cagttccgct	tacagcctac	cattaacacc	aacaaagata	gcgagattga	tgacacacaa	2340
caggagtctg	gtatcgctcc	taactttgta	cacagccaag	acggtagcca	ccttcgtaag	2400
actgtagtgt	gggcacacga	gaagtacgga	atcgaatctt	ttgcactgat	tcacgactcc	2460
ttcggtagca	ttccggctga	cgctgcgaac	ctgttcaaag	cagtgcgcga	aactatgggt	2520
gacacatatg	agtcttgtag	tgtactggct	gatttctacg	accagttcgc	tgaccagttg	2580
cacgagtctc	aattggacaa	aatgccagca	cttccggcta	aaggtaactt	gaacctccgt	2640
gacatcttag	agtcggactt	cgcgttcgct	taa			2673

<210> 31

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 31

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

385					390					395					400		
Arg	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala		
				405					410					415			
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg		
				420					425					430			
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys		
				435					440					445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr		
				450					455					460			
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val		
465					470					475					480		
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile		
				485					490					495			
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln		
				500					505					510			
Trp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val		
				515					520					525			
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp		
				530					535					540			
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu		
545					550					555					560		
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp		
				565					570					575			
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp		
				580					585					590			
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn		
				595					600					605			
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala		
				610					615					620			
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Trp	Val	Thr	Lys	Arg	Ser		
625					630					635					640		
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln		
				645					650					655			
Val	Leu	Glu	Phe	Thr	Ile	Gln	Pro	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu		
				660					665					670			
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile		
				675					680					685			
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn		
				690					695					700			
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys		
705					710					715					720		
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr		
				725					730					735			
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr		
				740					745					750			
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile		
				755					760					765			
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly		
				770					775					780			
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys		

785		790		795		800									
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu
				805					810					815	
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe
			820					825					830		
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val
		835					840					845			
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln
	850					855					860				
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg
865				870						875				880	
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala						
				885					890						

<210> 32
 <211> 2673
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> T7RNAP variant

<400> 32

atgcaccatc	accatcacca	tatgaacacg	attaacatcg	ctaagaacga	cttctctgac	60
atcgaactgg	ctgctatccc	gttcaacact	ctggctgacc	attacggtga	gcgttttagct	120
cgcgaacagt	tggcccttga	gcatgagtct	tacgagatgg	gtgaagcacg	cttccgcaag	180
atgtttgagc	gtcaacttaa	agctgggtgag	gttgcgata	acgctgccgc	caagcctctc	240
atcactaccc	tactccctaa	gatgattgca	cgcatacaacg	actggtttga	ggaagtga	300
gctaagcgcg	gcaagcgccc	gacagccttc	cagttcctgc	aagaaatcaa	gccggaagcc	360
gtagcgtaca	tcaccattaa	gaccactctg	gcttgccctaa	ccagtgtgta	caatacaacc	420
gttcaggctg	tagcaagcg	aatcggtcgg	gccattgagg	acgaggctcg	cttcggctcg	480
atccgtgacc	ttgaagctaa	gcacttcaag	aaaaacgttg	aggaacaact	caacaagcg	540
gtagggcacg	tctacaagaa	agcatttatg	caagttgtcg	aggctgacat	gctctctaag	600
ggcttactcg	gtggcgaggc	gtggctcttcg	tggcataagg	aagactctat	tcatgtagga	660
gtacgctgca	tcgagatgct	cattgagtca	accggaatgg	ttagcttaca	ccgcaaaaat	720
gctggcgtag	taggtcaaga	ctctgagact	atcgaactcg	cacctgaata	cgctgaggct	780
atcgcaaccc	gtgcagggtg	gctggctggc	atctctccga	tgttccaacc	ttgcgtagtt	840
cctcctaagc	cgtggactgg	cattactggt	ggtggctatt	gggctaacgg	tcgtcgtcct	900
ctggcgctgg	tcgtactca	cagtaagaaa	gcactgatgc	gctacgaaga	cgtttacatg	960
cctgagggtg	acaaagcgat	taacattgcg	caaaacaccg	catggaaaat	caacaagaaa	1020
gtcctagcgg	tcgccaacgt	aatcaccaag	tgggaagcatt	gtccggctga	ggacatccct	1080
gcgattgagc	gtgaagaact	cccgatgaaa	ccggaagaca	tcgacatgaa	tcctgaggct	1140
ctcaccgcgt	ggaaacgtgc	tgccgctgct	gtgtaccgca	aggacaaggc	gcgcaagtct	1200
cgccgtatca	gccttgagtt	catgcttgag	caagccaata	agtttgctaa	ccataaggcc	1260
atctgggtcc	cttacaacat	ggactggcgc	ggtcgtgttt	acgctgtgtc	aatgttcaac	1320
ccgcaaggta	acgatatgac	caaaggactg	cttacgctgg	cgaaaggtaa	accaatcggt	1380
aaggaagggt	actactggct	gaaaatccac	ggtgcaaaact	gtgcgggtgt	cgataagggt	1440
ccgttccctg	agcgcatcaa	gttcattgag	gaaaaccacg	agaacatcat	ggcttgctgc	1500
aagtctccac	tggagaacac	ttggtgggct	gagcaatatt	ctccgttctg	cttccttgctg	1560

```

ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgtttg acgggtcttg ctctggcatc cagcacttct ccgcgatgct ccgagatgag 1680
gtaggtgggtc gcgcggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggg gaaatctctg agaaagtcaa gctggggcact 1860
aaggcactgg ctgggtcaatg gctggcttac ggtgttactc gctgggtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaatac 1980
accattcagc ctgctattga ttccggcaag ggtctgatgt tcaactcagcc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcggtt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcggttc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggg 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgcaactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

```

<210> 33

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 33

```

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

```

Ile	Arg	Asp	Leu	Glu	Ala	Lys	His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	
				165					170					175		
Leu	Asn	Lys	Arg	Val	Gly	His	Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	
			180					185					190			
Val	Glu	Ala	Asp	Met	Leu	Ser	Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	
		195					200					205				
Ser	Ser	Trp	His	Lys	Glu	Asp	Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	
	210					215					220					
Glu	Met	Leu	Ile	Glu	Ser	Thr	Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn	
225					230					235				240		
Ala	Gly	Val	Val	Gly	Gln	Asp	Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu	
				245					250					255		
Tyr	Ala	Glu	Ala	Ile	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser	
			260					265					270			
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile	
		275					280					285				
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val	
	290					295					300					
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met	
305					310					315					320	
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys	
				325					330					335		
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys	
			340					345					350			
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro	
		355					360					365				
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp	
	370					375					380					
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser	
385					390					395					400	
Arg	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala	
				405					410					415		
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg	
			420					425					430			
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys	
		435					440					445				
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr	
	450					455					460					
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val	
465					470					475					480	
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile	
				485					490					495		
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln	
			500					505					510			
Tyr	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val	
		515					520					525				
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp	
	530					535					540					
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu	
545					550					555					560	

<223> T7RNAP variant

<400> 34

```
atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
atcgaactgg ctgctatccc gttcaacact ctggctgacc attacgggtga gcgttttagct 120
cgcgaaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
atgtttgagc gtcaacttaa agctggtgag gttgcggata acgctgccgc caagcctctc 240
atcactaccc tactccctaa gatgattgca cgcataacg actggtttga ggaagtgaag 300
gctaagcgcg gcaagcgccc gacagccttc cagttcctgc aagaaatcaa gccggaagcc 360
gtagcgtaga tcaccattaa gaccactctg gcttgccata ccagtgcgga caatacaacc 420
gttcaggctg tagcaagcgc aatcgggtcgg gccattgagg acgaggctcg cttcggctcgt 480
atccgtgacc ttgaagctaa gcacttcaag aaaaacgttg aggaacaact caacaagcgc 540
gtagggcacg tctacaagaa agcatttatg caagttgtcg aggctgacat gctctctaag 600
gggtctactcg gtggcgaggc gtggtcttcg tggcataagg aagactctat tcatgtagga 660
gtacgctgca tcgagatgct cattgagtca accggaatgg ttagcttaca ccgccaaaat 720
gctggcgtag taggtcaaga ctctgagact atcgaactcg cacctgaata cgctgaggct 780
atcgcaaccc gtgcagggtg gctggctggc atctctccga tgttccaacc ttgcgtagtt 840
cctcctaagc cgtggactgg cattactggt ggtggctatt gggctaacgg tcgtcgtcct 900
ctggcgctgg tgcgtactca cagtaagaaa gcactgatgc gctacgaaga cgtttacatg 960
cctgaggtgt acaaagcgat taacattgctg caaaacaccg catggaaaat caacaagaaa 1020
gtcctagcgg tcgccaacgt aatcaccaag tgggaagcatt gtccggctga ggacatccct 1080
gcgattgagc gtgaagaact cccgatgaaa ccggaagaca tcgacatgaa tcctgaggct 1140
ctcaccgctg ggaaacgtgc tgccgctgct gtgtaccgca aggacaaggc tcgcaagtct 1200
gttcgtatct atcttgagtt catgcttgag caagccaata agtttgctaa ccataaggcc 1260
atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcggc 1380
aagggaagggt actactggct gaaaatccac ggtgcaaaact gtgcgggtgt cgataagggt 1440
ccgttccctg agcgcatcaa gttcattgag gaaaaccacg agaacatcat ggcttgctg 1500
aagtctccac tggagaacac ttgggtgggt gagcaagatc tcccgttctg cttccttgct 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttcg 1620
ctggcgcttg acgggtcttg ctctggcatc cagcacttct ccgcatgct ccgagatgag 1680
gtaggtgggtc gcgcggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggt gaaatctctg agaaagtcaa gctgggcact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gcagtgtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaagac 1980
accattcagt gggctattga ttccggcaag ggtctgatgt tcaactcagc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcgggt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcggtgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggc 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatggtt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgctg taa 2673
```

<210> 35
<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> T7RNAP variant

<400> 35

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

Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys
			340					345					350		
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro
		355					360					365			
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp
		370				375					380				
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser
385					390					395					400
Val	Arg	Ile	Tyr	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala
			405					410						415	
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg
		420						425					430		
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys
		435					440					445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr
	450					455					460				
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
465				470					475						480
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile
			485						490					495	
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
		500						505					510		
Asp	Leu	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val
		515					520				525				
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp
	530					535					540				
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu
545				550					555						560
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp
			565						570					575	
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp
		580						585					590		
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn
		595					600						605		
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala
	610					615					620				
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser
625				630					635						640
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln
			645						650					655	
Val	Leu	Glu	Asp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu
		660						665					670		
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile
		675					680					685			
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn
	690					695					700				
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys
705				710						715					720
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr

				725					730					735					
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr				
			740					745					750						
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile				
		755					760					765							
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly				
		770				775					780								
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys				
785					790					795					800				
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu				
			805						810					815					
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe				
			820					825					830						
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val				
		835				840						845							
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln				
		850				855					860								
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg				
865				870						875					880				
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala										
			885					890											

<210> 36

<211> 2673

<212> DNA

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 36

```

atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
atcgaactgg ctgctatccc gttcaacact ctggctgacc attacggtga gcgttttagct 120
cgcgaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
atgtttgagc gtcaacttaa agctggtgag gttgcggata acgctgccgc caagcctctc 240
atcactaccc tactccctaa gatgattgca cgcataacg actggtttga ggaagtga 300
gctaagcgcg gcaagcgccc gacagccttc cagttcctgc aagaaatcaa gccggaagcc 360
gtagcgtaga tcaccattaa gaccactctg gcttgcctaa ccagtgcgga caatacaacc 420
gttcaggctg tagcaagcgc aatcggctcg gccattgagg acgaggctcg cttcggctcg 480
atccgtgacc ttgaagctaa gcacttcaag aaaaacgttg aggaacaact caacaagcgc 540
gtagggcacg tctacaagaa agcatttatg caagttgtcg aggctgacat gctctctaag 600
ggctactctg gtggcgaggc gtggtcttcg tggcataagg aagactctat tcatgtagga 660
gtacgctgca tcgagatgct cattgagtca accggaatgg ttagcttaca ccgcaaaaat 720
gctggcgtag taggtcaaga ctctgagact atcgaactcg cacctgaata cgctgaggct 780
atcgcaaccc gtgcaggctg gctggctggc atctctccga tgttccaacc ttgcgtagtt 840
ctcctaagc cgtggactgg cattactggt ggtggctatt gggctaacgg tcgtcgtcct 900
ctggcgctgg tgcgtactca cagtaagaaa gcactgatgc gctacgaaga cgtttacatg 960
cctgaggtgt acaaagcgat taacattgcg caaaacaccg catggaaaat caacaagaaa 1020
gtcctagcgg tcgccaacgt aatcaccaag tggaagcatt gtccgggtcc ggacatccct 1080

```

```

gcgattgagc gtgaagaact cccgatgaaa ccggaagaca tcgacatgaa tcctgaggct 1140
ctcaccgcgt ggaaacgtgc tgccgctgct gtgtaccgca gagacaaggc tcgcaagtct 1200
gttcgtatct atcttgagtt catgcttgag caagccaata agtttgctaa ccataaggcc 1260
atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcggc 1380
aaggaagggt actactggct gaaaatccac ggtgcaaact gtgcgggtgt cgataagggt 1440
ccgttccctg agcgcacaa gttcattgag gaaaaccacg agaacatcat ggcttgcgct 1500
aagtctccac tggagaacac ttgggtgggt gagcaagatc tcccgttctg cttccttgcg 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgcttg acgggtcttg ctctggcatc cagcacttct ccgcatgct ccgagatgag 1680
gtagggtggc gcgcgggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggt gaaatctctg agaaagtcaa gctgggcact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gcagtgtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaagat 1980
actattcagt gggctattga ttccggcaag ggtctgatgt tctctcagcc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcgggt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggc 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340
caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ctttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgcaactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

```

<210> 37

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 37

```

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

```

Glu	Glu	Val	Lys	Ala	Lys	Arg	Gly	Lys	Arg	Pro	Thr	Ala	Phe	Gln	Phe	100	105	110
Leu	Gln	Glu	Ile	Lys	Pro	Glu	Ala	Val	Ala	Tyr	Ile	Thr	Ile	Lys	Thr	115	120	125
Thr	Leu	Ala	Cys	Leu	Thr	Ser	Ala	Asp	Asn	Thr	Thr	Val	Gln	Ala	Val	130	135	140
Ala	Ser	Ala	Ile	Gly	Arg	Ala	Ile	Glu	Asp	Glu	Ala	Arg	Phe	Gly	Arg	145	150	155
Ile	Arg	Asp	Leu	Glu	Ala	Lys	His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	165	170	175
Leu	Asn	Lys	Arg	Val	Gly	His	Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	180	185	190
Val	Glu	Ala	Asp	Met	Leu	Ser	Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	195	200	205
Ser	Ser	Trp	His	Lys	Glu	Asp	Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	210	215	220
Glu	Met	Leu	Ile	Glu	Ser	Thr	Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn	225	230	235
Ala	Gly	Val	Val	Gly	Gln	Asp	Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro	Glu	245	250	255
Tyr	Ala	Glu	Ala	Ile	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser	260	265	270
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile	275	280	285
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val	290	295	300
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met	305	310	315
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys	325	330	335
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys	340	345	350
His	Cys	Pro	Val	Arg	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro	355	360	365
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp	370	375	380
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Arg	Asp	Lys	Ala	Arg	Lys	Ser	385	390	395
Val	Arg	Ile	Tyr	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala	405	410	415
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg	420	425	430
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys	435	440	445
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr	450	455	460
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val	465	470	475
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile	485	490	495

Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
			500					505					510		
Asp	Leu	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val
		515					520					525			
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp
	530					535					540				
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu
545					550					555					560
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp
			565						570					575	
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp
			580					585					590		
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn
		595					600					605			
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala
	610					615					620				
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser
625					630					635					640
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln
				645					650					655	
Val	Leu	Glu	Asp	Thr	Ile	Gln	Trp	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu
			660					665					670		
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile
		675					680					685			
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn
	690					695					700				
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys
705				710					715						720
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr
				725					730					735	
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr
			740					745					750		
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile
		755					760					765			
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly
	770					775					780				
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys
785					790					795					800
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu
				805					810					815	
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe
			820					825					830		
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val
		835					840					845			
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln
	850					855					860				
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg
865					870					875					880
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala						
				885					890						

<210> 38
<211> 2673
<212> DNA
<213> Artificial Sequence

<220>
<223> T7RNAP variant

<400> 38
atgcaccatc accatcacca tatgaacacg attaacatcg ctaagaacga cttctctgac 60
atcgaactgg ctgctatccc gttcaacact ctggctgacc attacggtga gcgttttagct 120
cgcgaacagt tggcccttga gcatgagtct tacgagatgg gtgaagcacg cttccgcaag 180
atgtttgagc gtcaacttaa agctggtgag gttgcggata acgctgccgc caagcctctc 240
atcactaccc tactccctaa gatgattgca cgcatacaac actggtttga ggaagtga 300
gctaagcgcg gcaagcgccc gacagccttc cagttcctgc aagaaatcaa gccggaagcc 360
gtagcgtaga tcaccattaa gaccactctg gcttgcttaa ccagtgtga caatacaacc 420
gttcaggctg tagcaagcgc aatcggctcg gccattgagg acgaggctcg cttcggctcg 480
atccgtgacc ttgaagctaa gcacttcaag aaaaacgttg aggaacaact caacaagcgc 540
gtagggcacg tctacaagaa agcatttatg caagttgtcg aggctgacat gctctctaag 600
ggctactctg gtggcgaggc gtggtcttcg tggcataagg aagactctat tcatgtagga 660
gtacgctgca tcgagatgct cattgagtca accggaatgg ttagcttaca ccgccaaaat 720
gctggcgtag taggtcaaga ctctgagact atcgaactcg cacctgaata cgctgaggct 780
atcgcaaccc gtgcagggtg gctggctggc atctctccga tgttccaacc ttgcgtagtt 840
cctcctaagc cgtggactgg cattactggt ggtggctatt gggctaacgg tcgtcgtcct 900
ctggcgctgg tgcgtactca cagtaagaaa gcactgatgc gctacgaaga cgtttacatg 960
cctgagggtg acaaagcgat taacattgcg caaaacaccg catggaaaat caacaagaaa 1020
gtcctagcgg tcgccaacgt aatcaccaag tgggaagcatt gtccggctga ggacatccct 1080
gcgattgagc gtgaagaact cccgatgaaa ccggaagaca tcgacatgaa tcctgaggct 1140
ctcaccgcgt ggaaacgtgc tgccgctgct gtgtaccgca aggacaaggc gcgcaagtct 1200
cgccgtatca gccttgagtt catgcttgag caagccaata agtttgctaa ccataaggcc 1260
atctggttcc cttacaacat ggactggcgc ggtcgtgttt acgctgtgtc aatgttcaac 1320
ccgcaaggta acgatatgac caaaggactg cttacgctgg cgaaaggtaa accaatcggc 1380
aagggaagggt actactggct gaaaatccac ggtgcaact gtgcgggtgt cgataagggt 1440
ccgttccctg agcgcatcaa gttcattgag gaaaaccacg agaacatcat ggcttgcgct 1500
aagtctccac tggagaacac ttggtgggct gagcaatatt ctccgttctg cttccttgcg 1560
ttctgctttg agtacgctgg ggtacagcac cacggcctga gctataactg ctcccttccg 1620
ctggcgcttg acgggtcttg ctctggcatc cagcacttct ccgcatgct ccgagatgag 1680
gtaggtggct gcgcgggttaa cttgcttcct agtgaaaccg ttcaggacat ctacgggatt 1740
gttgctaaga aagtcaacga gattctacaa gcagacgcaa tcaatgggac cgataacgaa 1800
gtagttaccg tgaccgatga gaacactggt gaaatctctg agaaagtcaa gctgggact 1860
aaggcactgg ctggtcaatg gctggcttac ggtgttactc gctgggtgac taagcgttca 1920
gtcatgacgc tggcttacgg gtccaaagag ttcggcttcc gtcaacaagt gctggaattc 1980
accattcagc ctgctattga ttccggcaag ggtctgatgt tctactcagc gaatcaggct 2040
gctggataca tggctaagct gatttgggaa tctgtgagcg tgacgggtgg agctgcggtt 2100
gaagcaatga actggcttaa gtctgctgct aagctgctgg ctgctgaggt caaagataag 2160
aagactggag agattcttcg caagcgttgc gctgtgcatt gggtaactcc tgatggtttc 2220
cctgtgtggc aggaatacaa gaagcctatt cagacgcgct tgaacctgat gttcctcggt 2280
cagttccgct tacagcctac cattaacacc aacaaagata gcgagattga tgcacacaaa 2340

```

caggagtctg gtatcgctcc taactttgta cacagccaag acggtagcca ccttcgtaag 2400
actgtagtgt gggcacacga gaagtacgga atcgaatctt ttgcactgat tcacgactcc 2460
ttcggtagca ttccggctga cgctgcgaac ctgttcaaag cagtgcgcga aactatgggt 2520
gacacatatg agtcttgtga tgtactggct gatttctacg accagttcgc tgaccagttg 2580
cacgagtctc aattggacaa aatgccagca cttccggcta aaggtaactt gaacctccgt 2640
gacatcttag agtcggactt cgcgttcgcg taa 2673

```

<210> 39

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> T7RNAP variant

<400> 39

```

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

```

			260				265				270				
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Thr	Gly	Ile
		275					280					285			
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro	Leu	Ala	Leu	Val
	290					295					300				
Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met
305				310						315					320
Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala	Gln	Asn	Thr	Ala	Trp	Lys
				325					330					335	
Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala	Asn	Val	Ile	Thr	Lys	Trp	Lys
			340					345					350		
His	Cys	Pro	Val	Glu	Asp	Ile	Pro	Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro
		355					360					365			
Met	Lys	Pro	Glu	Asp	Ile	Asp	Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp
	370					375					380				
Lys	Arg	Ala	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser
385				390						395					400
Arg	Arg	Ile	Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala
			405					410						415	
Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg
		420						425					430		
Val	Tyr	Ala	Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys
	435					440						445			
Gly	Leu	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr
	450					455					460				
Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
465				470					475						480
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn	Ile
			485					490					495		
Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala	Glu	Gln
		500						505					510		
Tyr	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val
		515					520					525			
Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp
	530					535					540				
Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu
545				550						555					560
Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Glu	Thr	Val	Gln	Asp
			565					570						575	
Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val	Asn	Glu	Ile	Leu	Gln	Ala	Asp
		580						585					590		
Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu	Val	Val	Thr	Val	Thr	Asp	Glu	Asn
		595					600					605			
Thr	Gly	Glu	Ile	Ser	Glu	Lys	Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala
	610					615					620				
Gly	Gln	Trp	Leu	Ala	Tyr	Gly	Val	Thr	Arg	Trp	Val	Thr	Lys	Arg	Ser
625				630						635					640
Val	Met	Thr	Leu	Ala	Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln
			645						650					655	
Val	Leu	Glu	Phe	Thr	Ile	Gln	Pro	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu

			660					665				670					
Met	Phe	Thr	Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile		
			675					680				685					
Trp	Glu	Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn		
			690					695				700					
Trp	Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys		
705						710				715					720		
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val	Thr		
				725					730						735		
Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile	Gln	Thr		
			740					745						750			
Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln	Pro	Thr	Ile		
			755					760						765			
Asn	Thr	Asn	Lys	Asp	Ser	Glu	Ile	Asp	Ala	His	Lys	Gln	Glu	Ser	Gly		
			770				775					780					
Ile	Ala	Pro	Asn	Phe	Val	His	Ser	Gln	Asp	Gly	Ser	His	Leu	Arg	Lys		
785					790					795					800		
Thr	Val	Val	Trp	Ala	His	Glu	Lys	Tyr	Gly	Ile	Glu	Ser	Phe	Ala	Leu		
				805					810						815		
Ile	His	Asp	Ser	Phe	Gly	Thr	Ile	Pro	Ala	Asp	Ala	Ala	Asn	Leu	Phe		
			820					825						830			
Lys	Ala	Val	Arg	Glu	Thr	Met	Val	Asp	Thr	Tyr	Glu	Ser	Cys	Asp	Val		
			835					840					845				
Leu	Ala	Asp	Phe	Tyr	Asp	Gln	Phe	Ala	Asp	Gln	Leu	His	Glu	Ser	Gln		
			850			855					860						
Leu	Asp	Lys	Met	Pro	Ala	Leu	Pro	Ala	Lys	Gly	Asn	Leu	Asn	Leu	Arg		
865					870					875					880		
Asp	Ile	Leu	Glu	Ser	Asp	Phe	Ala	Phe	Ala								
				885					890								

<210> 40

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Substrate etc

<400> 40

tttttttttt tttttttttt ttttt