

SEQUENCE LISTING

<110> New England Biolabs, Inc.
 <120> Enzymatic RNA Capping Method
 <130> NEB-423
 <150> 62/890,821
 <151> 2019-08-23
 <160> 21
 <170> PatentIn version 3.5
 <210> 1
 <211> 844
 <212> PRT
 <213> Vaccinia virus
 <220>
 <221> misc_feature
 <223> FL VCE capping enzyme; >YP_232988.1 large subunit of mRNA capping enzyme

<400> 1

Met Asp Ala Asn Val Val Ser Ser Ser Thr Ile Ala Thr Tyr Ile Asp
 1 5 10 15

Ala Leu Ala Lys Asn Ala Ser Glu Leu Glu Gln Arg Ser Thr Ala Tyr
 20 25 30

Glu Ile Asn Asn Glu Leu Glu Leu Val Phe Ile Lys Pro Pro Leu Ile
 35 40 45

Thr Leu Thr Asn Val Val Asn Ile Ser Thr Ile Gln Glu Ser Phe Ile
 50 55 60

Arg Phe Thr Val Thr Asn Lys Glu Gly Val Lys Ile Arg Thr Lys Ile
 65 70 75 80

Pro Leu Ser Lys Val His Gly Leu Asp Val Lys Asn Val Gln Leu Val
 85 90 95

Asp Ala Ile Asp Asn Ile Val Trp Glu Lys Lys Ser Leu Val Thr Glu
 100 105 110

Asn Arg Leu His Lys Glu Cys Leu Leu Arg Leu Ser Thr Glu Glu Arg
115 120 125

His Ile Phe Leu Asp Tyr Lys Lys Tyr Gly Ser Ser Ile Arg Leu Glu
130 135 140

Leu Val Asn Leu Ile Gln Ala Lys Thr Lys Asn Phe Thr Ile Asp Phe
145 150 155 160

Lys Leu Lys Tyr Phe Leu Gly Ser Gly Ala Gln Ser Lys Ser Ser Leu
165 170 175

Leu His Ala Ile Asn His Pro Lys Ser Arg Pro Asn Thr Ser Leu Glu
180 185 190

Ile Glu Phe Thr Pro Arg Asp Asn Glu Thr Val Pro Tyr Asp Glu Leu
195 200 205

Ile Lys Glu Leu Thr Thr Leu Ser Arg His Ile Phe Met Ala Ser Pro
210 215 220

Glu Asn Val Ile Leu Ser Pro Pro Ile Asn Ala Pro Ile Lys Thr Phe
225 230 235 240

Met Leu Pro Lys Gln Asp Ile Val Gly Leu Asp Leu Glu Asn Leu Tyr
245 250 255

Ala Val Thr Lys Thr Asp Gly Ile Pro Ile Thr Ile Arg Val Thr Ser
260 265 270

Asn Gly Leu Tyr Cys Tyr Phe Thr His Leu Gly Tyr Ile Ile Arg Tyr
275 280 285

Pro Val Lys Arg Ile Ile Asp Ser Glu Val Val Val Phe Gly Glu Ala
290 295 300

Val Lys Asp Lys Asn Trp Thr Val Tyr Leu Ile Lys Leu Ile Glu Pro
305 310 315 320

Val Asn Ala Ile Asn Asp Arg Leu Glu Glu Ser Lys Tyr Val Glu Ser
325 330 335

Lys Leu Val Asp Ile Cys Asp Arg Ile Val Phe Lys Ser Lys Lys Tyr
340 345 350

Glu Gly Pro Phe Thr Thr Thr Ser Glu Val Val Asp Met Leu Ser Thr
355 360 365

Tyr Leu Pro Lys Gln Pro Glu Gly Val Ile Leu Phe Tyr Ser Lys Gly
370 375 380

Pro Lys Ser Asn Ile Asp Phe Lys Ile Lys Lys Glu Asn Thr Ile Asp
385 390 395 400

Gln Thr Ala Asn Val Val Phe Arg Tyr Met Ser Ser Glu Pro Ile Ile
405 410 415

Phe Gly Glu Ser Ser Ile Phe Val Glu Tyr Lys Lys Phe Ser Asn Asp
420 425 430

Lys Gly Phe Pro Lys Glu Tyr Gly Ser Gly Lys Ile Val Leu Tyr Asn
435 440 445

Gly Val Asn Tyr Leu Asn Asn Ile Tyr Cys Leu Glu Tyr Ile Asn Thr
450 455 460

His Asn Glu Val Gly Ile Lys Ser Val Val Val Pro Ile Lys Phe Ile
465 470 475 480

Ala Glu Phe Leu Val Asn Gly Glu Ile Leu Lys Pro Arg Ile Asp Lys
485 490 495

Thr Met Lys Tyr Ile Asn Ser Glu Asp Tyr Tyr Gly Asn Gln His Asn
500 505 510

Ile Ile Val Glu His Leu Arg Asp Gln Ser Ile Lys Ile Gly Asp Ile
515 520 525

Phe Asn Glu Asp Lys Leu Ser Asp Val Gly His Gln Tyr Ala Asn Asn
530 535 540

Asp Lys Phe Arg Leu Asn Pro Glu Val Ser Tyr Phe Thr Asn Lys Arg
545 550 555 560

Thr Arg Gly Pro Leu Gly Ile Leu Ser Asn Tyr Val Lys Thr Leu Leu
565 570 575

Ile Ser Met Tyr Cys Ser Lys Thr Phe Leu Asp Asp Ser Asn Lys Arg
580 585 590

Lys Val Leu Ala Ile Asp Phe Gly Asn Gly Ala Asp Leu Glu Lys Tyr
595 600 605

Phe Tyr Gly Glu Ile Ala Leu Leu Val Ala Thr Asp Pro Asp Ala Asp
610 615 620

Ala Ile Ala Arg Gly Asn Glu Arg Tyr Asn Lys Leu Asn Ser Gly Ile
625 630 635 640

Lys Thr Lys Tyr Tyr Lys Phe Asp Tyr Ile Gln Glu Thr Ile Arg Ser
645 650 655

Asp Thr Phe Val Ser Ser Val Arg Glu Val Phe Tyr Phe Gly Lys Phe
660 665 670

Asn Ile Ile Asp Trp Gln Phe Ala Ile His Tyr Ser Phe His Pro Arg
675 680 685

His Tyr Ala Thr Val Met Asn Asn Leu Ser Glu Leu Thr Ala Ser Gly
690 695 700

Gly Lys Val Leu Ile Thr Thr Met Asp Gly Asp Lys Leu Ser Lys Leu
705 710 715 720

Thr Asp Lys Lys Thr Phe Ile Ile His Lys Asn Leu Pro Ser Ser Glu
725 730 735

Asn Tyr Met Ser Val Glu Lys Ile Ala Asp Asp Arg Ile Val Val Tyr
740 745 750

Asn Pro Ser Thr Met Ser Thr Pro Met Thr Glu Tyr Ile Ile Lys Lys
755 760 765

Asn Asp Ile Val Arg Val Phe Asn Glu Tyr Gly Phe Val Leu Val Asp
770 775 780

Asn Val Asp Phe Ala Thr Ile Ile Glu Arg Ser Lys Lys Phe Ile Asn
785 790 795 800

Gly Ala Ser Thr Met Glu Asp Arg Pro Ser Thr Arg Asn Phe Phe Glu
805 810 815

Leu Asn Arg Gly Ala Ile Lys Cys Glu Gly Leu Asp Val Glu Asp Leu
820 825 830

Leu Ser Tyr Tyr Val Val Tyr Val Phe Ser Lys Arg
835 840

<210> 2
<211> 60
<212> PRT
<213> Faustovirus

<220>
<221> MISC_FEATURE
<223> Fausto_CR_01

<400> 2

Phe Asp Lys Leu Lys Pro Asp Gly Glu Ile Thr Thr Thr Met Arg Val
1 5 10 15

Ser Asn Ala Asp Gly Met Ala Arg Glu Ile Thr Phe Gly Gly Gly Val
20 25 30

Lys Thr Gly Glu Met Phe Val Lys Lys Gln Asn Ile Cys Val Phe Asp
35 40 45

Val Val Asp Ile Phe Ser Tyr Lys Val Ala Val Ser
50 55 60

<210> 3
<211> 111

<212> PRT
<213> Faustovirus

<220>
<221> misc_feature
<223> Fausto_CR_03

<400> 3

Gly Phe Tyr Gly Asn Asn Tyr Lys Ile Ala Ser Asp Ile Tyr Leu Asn
1 5 10 15

Tyr Ile Asp Val Phe Asn Phe Asp Asp Leu Trp Lys Tyr Asn Pro Gly
20 25 30

Tyr Phe Glu Lys Asn Lys Ser Asp Ile Tyr Ile Ala Pro Asn Lys Tyr
35 40 45

Arg Arg Tyr Leu Ile Lys Ser Leu Phe Asn Lys Tyr Ile Lys Asn Ala
50 55 60

Lys Trp Val Ile Asp Ala Ala Ala Gly Arg Gly Ala Asp Leu His Leu
65 70 75 80

Tyr Lys Ala Glu Cys Val Glu Asn Leu Leu Ala Ile Asp Ile Asp Pro
85 90 95

Thr Ala Ile Ser Glu Leu Ile Arg Arg Arg Asn Glu Ile Thr Gly
100 105 110

<210> 4
<211> 60
<212> PRT
<213> Faustovirus

<220>
<221> MISC_FEATURE
<223> Fausto_CR_05

<400> 4

Lys Tyr Ser Ile Lys Arg Leu Tyr Asp Ser Asp Lys Leu Thr Lys Thr
1 5 10 15

Gly Gln Lys Ile Ala Val Leu Leu Pro Met Ser Gly Glu Met Lys Glu
 20 25 30

Glu Pro Leu Cys Asn Ile Lys Asn Ile Ile Ser Met Ala Arg Lys Met
 35 40 45

Gly Leu Asp Leu Val Glu Ser Ala Asn Phe Ser Val
 50 55 60

<210> 5
 <211> 67
 <212> PRT
 <213> Mimivirus

<220>
 <221> MISC_FEATURE
 <223> 5: mimi_CR_03

<400> 5

Ile Asn Asp Asn Thr Val Val Glu Phe Ile Phe Asp Asn Phe Lys Ile
 1 5 10 15

Asp Met Asp Asp Pro Tyr Lys Trp Ile Pro Ile Arg Thr Arg Tyr Asp
 20 25 30

Lys Thr Glu Ser Val Gln Lys Tyr His Lys Lys Tyr Gly Asn Asn Leu
 35 40 45

His Ile Ala Asn Arg Ile Trp Lys Thr Ile Thr Asn Pro Ile Thr Glu
 50 55 60

Asp Ile Ile
 65

<210> 6
 <211> 111
 <212> PRT
 <213> Mimivirus

<220>
 <221> MISC_FEATURE
 <223> mimi_CR_04

<400> 6

Tyr Tyr Gln Lys Asn Thr Ser Asn Ala Ala Gly Met Arg Ala Phe Asn
1 5 10 15

Asn Phe Ile Lys Ser Asn Met Ile Thr Thr Tyr Cys Lys Asp Gly Asp
20 25 30

Lys Val Leu Asp Ile Gly Cys Gly Arg Gly Gly Asp Leu Ile Lys Phe
35 40 45

Ile His Ala Gly Ile Glu Glu Tyr Val Gly Ile Asp Ile Asp Asn Asn
50 55 60

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

Lys Lys Thr Ile Lys Asn Ile Pro Pro Met Thr Phe Ile Asn Ala Asp
85 90 95

Ala Arg Gly Leu Phe Asn Leu Glu Ala Gln Glu Lys Ile Leu Pro
100 105 110

<210> 7

<211> 873

<212> PRT

<213> Faustovirus

<220>

<221> MISC_FEATURE

<223> Faustovirus D5b RNA capping enzyme Genbank accession no. AMN83561

<400> 7

Met Ala Lys Arg Leu Gln Arg Cys Gln Asp Val Asn Gln Val Cys Glu
1 5 10 15

Ile Tyr Asn Ser Lys Gly Gly Ile Gly Glu Leu Glu Leu Arg Phe Asp
20 25 30

Lys Leu Pro Gln Asn Leu Phe Ala Gly Val Phe Asp Lys Leu Lys Pro
35 40 45

Asp Gly Glu Ile Gln Thr Thr Met Arg Val Ser Asn Arg Asp Gly Val
50 55 60

Ala Arg Glu Ile Thr Phe Gly Gly Gly Val Lys Thr Asn Glu Ile Phe
65 70 75 80

Val Lys Lys Gln Asn Ile Cys Val Phe Asp Val Val Asp Ile Phe Ser
85 90 95

Tyr Lys Val Ala Val Ser Thr Glu Glu Thr Val Val Glu Lys Pro Thr
100 105 110

Met Glu Thr Thr Ala Gly Val Arg Phe Lys Ile Arg Leu Ser Val Glu
115 120 125

Asp Val Val Lys Asp Trp Arg Ile Asp Leu Thr Ala Val Lys Thr Ala
130 135 140

Glu Leu Gly Lys Ile Ala Gln His Thr Ala Ser Ile Val Gln Arg Thr
145 150 155 160

Phe Pro Asp Asn Leu Leu Lys Leu Thr Gly Ala Glu Val Ala Lys Leu
165 170 175

Ala Ala Asp Ser Tyr Glu Leu Glu Leu Glu Tyr Thr Gly Lys Ser Pro
180 185 190

Ala Thr Asn Glu Lys Val Asn Val Ala Ala Lys Tyr Ala Val Glu Leu
195 200 205

Leu Ser Ser Val Arg Asn Ala Asn Ser Thr Ala Ala Ala Ser Phe Gly
210 215 220

Glu Ser Val Ser Asp Leu Cys Arg Val Ala Lys Ile Ile His Thr His
225 230 235 240

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

Pro Gln Val Val Ser Leu Thr Lys Ser Ser Tyr Tyr Gly Gly Leu Tyr
260 265 270

Pro Pro Glu Asn Leu Trp Leu Ala Gly Lys Thr Asp Gly Val Arg Ala
 275 280 285

Leu Val Val Cys Glu Asp Gly Val Ala Lys Val Ile Thr Ala Glu Ser
 290 295 300

Val Asp Ile Thr His Gly Val Cys Ser Ala Thr Thr Ile Leu Asp Cys
 305 310 315 320

Glu Leu Asn Val Asp Ala Lys Ile Leu Tyr Val Phe Asp Val Ile Ile
 325 330 335

Ser Asn Asn Thr Gln Val Tyr Thr Gln Pro Phe Ser Thr Arg Ile Thr
 340 345 350

Thr Asp Ile Ser Asp Ile Lys Ile Asp Gly Tyr Lys Ile Glu Met Lys
 355 360 365

Pro Phe Val Lys Val Val Lys Ala Asp Glu Ala Thr Phe Lys Ser Ala
 370 375 380

Tyr Lys Ala Pro His Asn Glu Gly Leu Ile Met Ile Glu Asp Gly Ala
 385 390 395 400

Ala Tyr Ala Ala Thr Lys Thr Tyr Lys Trp Lys Pro Leu Ser His Asn
 405 410 415

Thr Ile Asp Phe Leu Ile Lys Ala Cys Pro Lys Gln Leu Ile Asn Val
 420 425 430

Asp Pro Tyr Lys Pro Arg Ala Gly Tyr Lys Leu Trp Leu Leu Phe Thr
 435 440 445

Thr Ile Ser Leu Asp Gln Gln Arg Glu Leu Gly Ile Glu Phe Ile Pro
 450 455 460

Ala Trp Lys Ile Leu Phe Thr Asp Ile Asn Met Phe Gly Ser Arg Val
 465 470 475 480

Pro Ile Gln Phe Gln Pro Ala Ile Asn Pro Leu Ala Tyr Val Cys Tyr
485 490 495

Leu Pro Glu Asp Val Asn Val Asn Asp Gly Asp Ile Val Glu Met Arg
500 505 510

Ala Val Asp Gly Tyr Asp Thr Ile Pro Lys Trp Glu Leu Val Arg Ser
515 520 525

Arg Asn Asp Arg Lys Asn Glu Pro Gly Phe Tyr Gly Asn Asn Tyr Lys
530 535 540

Ile Ala Ser Asp Ile Tyr Leu Asn Tyr Ile Asp Val Phe His Phe Glu
545 550 555 560

Asp Leu Tyr Lys Tyr Asn Pro Gly Tyr Phe Glu Lys Asn Lys Ser Asp
565 570 575

Ile Tyr Val Ala Pro Asn Lys Tyr Arg Arg Tyr Leu Ile Lys Ser Leu
580 585 590

Phe Gly Arg Tyr Leu Arg Asp Ala Lys Trp Val Ile Asp Ala Ala Ala
595 600 605

Gly Arg Gly Ala Asp Leu His Leu Tyr Lys Ala Glu Cys Val Glu His
610 615 620

Leu Leu Ala Ile Asp Ile Asp Pro Thr Ala Ile Ser Glu Leu Val Arg
625 630 635 640

Arg Arg Asn Glu Ile Thr Gly Tyr Asn Lys Ser His Arg Gly Gly Arg
645 650 655

Asn Met His Ser His Arg Gly Gln Ser His Cys Ala Lys Ser Thr Ser
660 665 670

Leu His Ala Leu Val Ala Asp Leu Arg Glu Asn Pro Asp Val Leu Ile
675 680 685

Pro Lys Ile Ile Gln Ser Arg Pro His Glu Arg Cys Tyr Asp Ala Ile
690 695 700

Val Ile Asn Phe Ala Ile His Tyr Leu Cys Asp Thr Asp Glu His Ile
705 710 715 720

Arg Asp Phe Leu Ile Thr Val Ser Arg Leu Leu Ala Pro Asn Gly Val
725 730 735

Phe Ile Phe Thr Thr Met Asp Gly Glu Ser Ile Val Lys Leu Leu Ala
740 745 750

Asp His Lys Val Arg Pro Gly Glu Ala Trp Thr Ile His Thr Gly Asp
755 760 765

Val Asn Ser Pro Asp Ser Thr Val Pro Lys Tyr Ser Ile Arg Arg Leu
770 775 780

Tyr Asp Ser Asp Lys Leu Thr Lys Thr Gly Gln Gln Ile Glu Val Leu
785 790 795 800

Leu Pro Met Ser Gly Glu Met Lys Ala Glu Pro Leu Cys Asn Ile Lys
805 810 815

Asn Ile Ile Ser Met Ala Arg Lys Met Gly Leu Asp Leu Val Glu Ser
820 825 830

Ala Asn Phe Ser Val Leu Tyr Glu Ala Tyr Ala Arg Asp Tyr Pro Asp
835 840 845

Ile Tyr Ala Arg Met Thr Pro Asp Asp Lys Leu Tyr Asn Asp Leu His
850 855 860

Thr Tyr Ala Val Phe Lys Arg Lys Lys
865 870

<210> 8
<211> 890
<212> PRT
<213> Faustovirus

<220>
<221> MISC_FEATURE

<223> Faustovirus E12 RNA capping enzyme; Genbank accession no.
AIB52055

<400> 8

Met Arg Arg Val Phe Asn Ser Ala Lys Lys Gln Gln Arg Cys Asp Ser
1 5 10 15

Val Glu Gln Val Cys Glu Phe Tyr Asn Ala Asp Asn Lys Thr Asn Glu
20 25 30

Leu Glu Leu Arg Phe Asp Lys Leu Asn Arg Glu Leu Phe Val Val Leu
35 40 45

Phe Asp Lys Leu Lys Pro Asp Gly Glu Ile Thr Thr Thr Met Arg Val
50 55 60

Ser Asn Ala Asp Gly Met Ala Arg Glu Ile Thr Phe Gly Gly Gly Val
65 70 75 80

Lys Thr Gly Glu Met Phe Val Lys Lys Gln Asn Ile Cys Val Phe Asp
85 90 95

Val Val Asp Val Phe Ser Tyr Lys Val Ala Val Ser Ser Glu Asp Glu
100 105 110

Ile Lys Asp Lys Pro Lys Met Asp Thr Asn Ala Ser Val Arg Phe Lys
115 120 125

Ile Arg Leu Ser Cys Asp Thr Leu Ile Pro Asp Trp Arg Ile Asp Leu
130 135 140

Thr Ala Val Lys Val Ala Asp Leu Gly Lys Ile Ala Gln His Thr Ser
145 150 155 160

Thr Val Val Leu Gln Thr Phe Pro Glu Asn Leu Leu Arg Met Lys Gly
165 170 175

Ala Glu Val Ala Ala Leu Ala Thr Asn Ser Tyr Glu Leu Glu Leu Glu
180 185 190

Tyr Ile Gly Lys Ser Ala Ala Ser Lys Glu Lys Val Leu Ala Ala Ala

195	200	205
Glu Tyr Ala Met Glu Leu Leu Thr Asn Ser Arg Asn Ala Ile Ser Pro 210 215 220		
Ala Ala Ala Thr Leu Gly Glu Ser Val Ser Asp Ile Cys Arg Ile Ala 225 230 235 240		
Lys Leu Ile His Pro Ala Glu Tyr Ala Asn Val Ile Cys Arg Thr Pro 245 250 255		
Ser Phe Lys Asn Leu Leu Pro Gln Val Ile Ser Leu Thr Lys Ser Ser 260 265 270		
Tyr Tyr Gly Gly Ile Tyr Pro Pro Val Asp Met Tyr Ile Ala Gly Lys 275 280 285		
Thr Asp Gly Val Arg Ala Leu Val Leu Cys Glu Asn Gly Val Ala Lys 290 295 300		
Ile Ile Thr Ala Thr Thr Val Asp Thr Thr Thr Val Gly Asn Thr Pro 305 310 315 320		
Ile Thr Ile Leu Asp Cys Glu Leu Ser Thr Ser Gly His Asn Gly Ala 325 330 335		
Thr Asp Asn Lys His Leu Tyr Ile Phe Asp Val Ile Met Asn Arg Gly 340 345 350		
Val His Ser His Arg Glu Gly Phe Asn Lys Arg Ile Asp Ile Asp Leu 355 360 365		
Ser Asp Leu Thr Pro Ala Gly Tyr Thr Leu Glu Leu Lys Pro Phe Thr 370 375 380		
Lys Leu Val Asp Ala Ala Ser Val Asn Glu Thr Thr Phe Lys Ser Val 385 390 395 400		
Phe Lys Pro Pro His Asn Glu Gly Leu Val Leu Val Glu Ser Gly Pro 405 410 415		

Pro Tyr Ala Leu Thr Lys Thr Tyr Lys Trp Lys Pro Ile Thr His Asn
420 425 430

Thr Ile Asp Phe Leu Ile Lys Ala Cys Pro Lys Gln Leu Ile Asn Val
435 440 445

Asp Pro Phe Lys Pro Arg Asn Gly His Asp Leu Trp Leu Leu Phe Thr
450 455 460

Thr Ile Ser Leu Asp Gln Gln Arg Glu Leu Gly Ile Asp Leu Ile Pro
465 470 475 480

Ala Trp Lys Leu Leu Phe Thr Asp Val Asn Leu Phe Gly Asn Lys Ile
485 490 495

Pro Ile Gln Phe Met Pro Ala Ile Asn Pro Leu Ala Tyr Ile Cys Tyr
500 505 510

Leu Pro Ser Ser Thr Gly Val Asn Asp Gly Asp Ile Val Glu Met Arg
515 520 525

Ala Val Asp Gly Phe Asp Gly Ile Pro Thr Trp Glu Leu Val Arg Thr
530 535 540

Arg Pro Asp Arg Lys Asp Glu Arg Gly Phe Tyr Gly Asn Asn Tyr Lys
545 550 555 560

Ile Ala Ser Asp Ile Tyr Leu Asn Tyr Ile Asp Val Phe Asn Phe Asp
565 570 575

Asp Leu Trp Lys Tyr Asn Pro Gly Tyr Phe Glu Lys Asn Lys Ser Asp
580 585 590

Ile Tyr Ile Ala Pro Asn Lys Tyr Arg Arg Tyr Leu Ile Lys Ser Leu
595 600 605

Phe Asn Lys Tyr Ile Lys Asn Ala Lys Trp Val Ile Asp Ala Ala Ala
610 615 620

Gly Arg Gly Ala Asp Leu His Leu Tyr Lys Gln Glu Cys Val Glu Asn

625		630		635		640
Leu	Leu	Ala	Ile	Asp	Ile	Arg
			645			655
Arg	Arg	Asn	Glu	Ile	Thr	Gly
		660			665	670
Thr	Arg	His	Asn	Ala	Arg	His
		675			680	685
Leu	His	Ala	Leu	Val	Ala	Asp
	690				695	700
Pro	Lys	Ile	Ile	Gln	Ser	Arg
705				710		715
Val	Ile	Asn	Phe	Ala	Ile	His
			725			730
Arg	Asn	Phe	Leu	Ile	Thr	Val
		740			745	750
Phe	Ile	Phe	Thr	Thr	Met	Asp
	755				760	765
Glu	His	Lys	Val	Ala	Pro	Gly
770				775		780
Asn	Ala	Asn	Ala	Thr	Asp	Ala
785				790		795
Leu	Tyr	Asp	Ser	Asp	Lys	Leu
			805			810
Leu	Leu	Pro	Met	Ser	Gly	Glu
		820			825	830
Lys	Asn	Ile	Val	Ser	Met	Ala
	835				840	845

Ser Ala Asn Phe Ser Val Leu Tyr Gly Ala Tyr Ala Lys Asp Tyr Pro
850 855 860

Glu Ile Tyr Ala Lys Leu Thr Pro Asp Asp Lys Leu Tyr Asn Asp Leu
865 870 875 880

His Ala Phe Ala Val Phe Lys Arg Lys Lys
885 890

<210> 9
<211> 894
<212> PRT
<213> Faustovirus

<220>
<221> MISC_FEATURE
<223> Faustovirus ST1 RNA capping enzyme; Genbank accession no.
SME65026

<400> 9

Met Arg Arg Val Ser Asn Ser Ala Lys Lys Gln Gln Arg Cys Asp Ser
1 5 10 15

Val Glu Gln Val Cys Glu Phe Tyr Asn Ala Asp Asn Lys Thr Asn Glu
20 25 30

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

Phe Asp Lys Leu Lys Pro Asp Gly Glu Ile Thr Thr Thr Met Arg Val
50 55 60

Ser Asn Ala Asp Gly Met Ala Arg Glu Ile Thr Phe Gly Gly Gly Val
65 70 75 80

Lys Thr Gly Glu Met Phe Val Lys Lys Gln Asn Ile Cys Val Phe Asp
85 90 95

Val Val Asp Val Phe Ser Tyr Lys Val Ala Val Ser Ser Glu Asp Glu
100 105 110

Val Lys Asp Lys Pro Lys Met Asp Thr Asn Ala Ser Val Arg Phe Lys
115 120 125

Ile Arg Leu Ser Cys Asp Thr Leu Ile Pro Asp Trp Arg Ile Asp Leu
130 135 140

Thr Ala Val Lys Val Ala Asp Leu Gly Lys Ile Ala Gln His Thr Ser
145 150 155 160

Thr Val Val Leu Gln Thr Phe Pro Glu Asn Leu Leu Arg Met Lys Gly
165 170 175

Ala Glu Val Ala Ala Leu Ala Thr Asn Ser Tyr Glu Leu Glu Leu Glu
180 185 190

Tyr Ile Gly Lys Ser Thr Ala Gly Lys Glu Lys Val Leu Lys Ala Ala
195 200 205

Glu Tyr Ala Ile Glu Leu Leu Thr Asn Leu Arg Asn Ala Val Ser Pro
210 215 220

Val Ala Ala Thr Leu Gly Glu Ser Val Ser Asp Ile Cys Arg Ile Ala
225 230 235 240

Lys Leu Ile His Pro Ala Glu Tyr Ala Asn Val Ile Cys Arg Thr Pro
245 250 255

Ser Phe Lys Asn Leu Leu Pro Gln Val Ile Ser Leu Thr Lys Ser Ser
260 265 270

Tyr Tyr Gly Gly Ile Tyr Pro Pro Val Asp Met Tyr Ile Thr Gly Lys
275 280 285

Thr Asp Gly Val Arg Ala Leu Val Leu Cys Glu Asn Gly Val Ala Lys
290 295 300

Ile Ile Thr Ala Thr Thr Val Asp Thr Thr Thr Val Gly Asp Thr Pro
305 310 315 320

Ile Thr Ile Leu Asp Cys Glu Leu Ser Thr Ser Gly His Asn Gly Ala
325 330 335

Thr Asp Asn Lys His Leu Tyr Val Phe Asp Val Ile Met Asn Arg Gly
340 345 350

Ala His Ser His Arg Asp Gly Phe Asn Lys Arg Ile Asp Ile Asp Leu
355 360 365

Ser Asp Leu Thr Pro Ala Gly Tyr Thr Leu Glu Leu Lys Pro Phe Thr
370 375 380

Lys Val Ala Asp Ala Ala Ser Val Asn Glu Thr Thr Phe Lys Ser Val
385 390 395 400

Phe Lys Pro Pro His Asn Glu Gly Leu Val Leu Val Glu Ser Gly Pro
405 410 415

Pro Tyr Ala Leu Thr Lys Thr Tyr Lys Trp Lys Pro Ile Thr His Asn
420 425 430

Thr Ile Asp Phe Leu Ile Lys Ala Cys Pro Lys Gln Leu Ile Asn Val
435 440 445

Asp Pro Phe Lys Pro Arg Asn Gly His Asp Leu Trp Leu Leu Phe Thr
450 455 460

Thr Ile Ser Leu Asp Gln Gln Arg Glu Leu Gly Ile Asp Leu Ile Pro
465 470 475 480

Ala Trp Lys Leu Leu Phe Thr Asp Val Asn Leu Phe Gly Asn Lys Ile
485 490 495

Pro Ile Gln Phe Met Pro Ala Ile Asn Pro Leu Ala Tyr Ile Cys Tyr
500 505 510

Leu Pro Ser Ser Thr Gly Val Asn Asp Gly Asp Ile Val Glu Met Arg
515 520 525

Ala Val Asp Gly Phe Asp Gly Ile Pro Thr Trp Glu Leu Val Arg Thr
530 535 540

Arg Pro Asp Arg Lys Asp Glu Arg Gly Phe Tyr Gly Asn Asn Tyr Lys
 545 550 555 560

Ile Ala Ser Asp Ile Tyr Leu Asn Tyr Ile Asp Val Phe Asn Phe Asp
 565 570 575

Asp Leu Trp Lys Tyr Asn Pro Gly Tyr Phe Glu Lys Asn Lys Ser Asp
 580 585 590

Ile Tyr Ile Ala Pro Asn Lys Tyr Arg Arg Tyr Leu Ile Lys Ser Leu
 595 600 605

Phe Asn Lys Tyr Ile Lys Asn Ala Lys Trp Val Ile Asp Ala Ala Ala
 610 615 620

Gly Arg Gly Ala Asp Leu His Leu Tyr Lys Gln Glu Cys Val Glu Asn
 625 630 635 640

Leu Leu Ala Ile Asp Ile Asp Pro Thr Ala Ile Ser Glu Leu Ile Arg
 645 650 655

Arg Arg Asn Glu Ile Thr Gly Trp Gln Gln Arg Gly Arg Gly Gly Asn
 660 665 670

Met His His Asn Ser Arg His Asn Thr Arg His Asn Thr His Cys Ala
 675 680 685

Ser Ser Thr Ser Leu His Ala Leu Val Ala Asp Leu Arg Thr Glu Pro
 690 695 700

Asn Met Leu Ile Pro Lys Ile Ile Gln Ser Arg Pro Pro Glu Arg Gly
 705 710 715 720

Tyr Asp Ala Leu Val Ile Asn Phe Ala Ile His Tyr Leu Cys Glu Thr
 725 730 735

Asp Asp Tyr Ile Arg Asn Phe Leu Ile Thr Val Ser Arg Leu Leu Ala
 740 745 750

His Asp Gly Val Phe Ile Phe Thr Thr Met Asp Gly Glu Ala Ile Val
 755 760 765

Asn Leu Leu Thr Glu His Lys Val Ala Pro Gly Ala Ser Trp Val Val
 770 775 780

His Thr Asp Gly Asn Thr Asn Ala Thr Asp Ala Asn Val Val Lys Tyr
 785 790 795 800

Ser Ile Lys Arg Leu Tyr Asp Ser Asp Lys Leu Thr Lys Thr Gly Gln
 805 810 815

Lys Ile Ala Val Leu Leu Pro Met Ser Gly Glu Met Arg Glu Glu Pro
 820 825 830

Leu Cys Asn Ile Lys Asn Ile Val Ser Met Ala Arg Lys Met Gly Leu
 835 840 845

Asp Leu Val Glu Ser Ala Asn Phe Ser Val Leu Tyr Gly Ala Tyr Ala
 850 855 860

Lys Asp Tyr Pro Glu Ile Tyr Ala Lys Leu Thr Pro Asp Asp Lys Leu
 865 870 875 880

Tyr Asn Asp Leu His Ala Phe Ala Val Phe Lys Arg Lys Lys
 885 890

<210> 10
 <211> 901
 <212> PRT
 <213> Faustovirus

<220>
 <221> MISC_FEATURE
 <223> Faustovirus ST1 RNA capping enzyme; Genbank accession no.
 SMH63629

<400> 10

Leu Glu Tyr Gln Tyr Tyr Lys Tyr Ile Leu Val Asn Ile Met Ser Arg
 1 5 10 15

Arg Leu Gln Arg Cys Arg Asp Val Asp Gln Val Cys Glu Tyr Tyr Asn
 20 25 30

Ala Lys Gly Ala Ile Gly Glu Leu Glu Leu Arg Phe Asp Lys Leu Thr
35 40 45

Pro Asp Leu Phe Ala His Val Phe Asp Lys Leu Lys Pro Asp Gly Glu
50 55 60

Ile Ser Thr Thr Met Arg Val Ser Asn Ser Asp Gly Thr Ala Arg Glu
65 70 75 80

Ile Thr Phe Gly Gly Gly Val Lys Thr Gly Glu Thr Phe Val Arg Lys
85 90 95

Gln Asn Ile Cys Val Phe Asp Val Val Asp Ile Phe Ser Tyr Lys Val
100 105 110

Ala Val Ser Thr Glu Glu Thr Leu Val Asp Lys Pro Ala Met Glu Lys
115 120 125

Asp Ala Ser Val Arg Phe Lys Ile Arg Met Ser Val Glu Gly Ala Val
130 135 140

Pro Asn Trp Arg Ile Asp Leu Thr Ala Val Lys Thr Ala Glu Leu Gly
145 150 155 160

Lys Ile Ala Gln His Thr Ala Ser Leu Val Leu Gln Thr Phe Pro Pro
165 170 175

Asn Leu Leu Lys Met Ser Gly Ala Glu Val Ala Lys Leu Ala Asn Asn
180 185 190

Ser Tyr Glu Leu Glu Leu Glu Tyr Ile Gly Lys Thr Pro Ala Thr Lys
195 200 205

Glu Arg Val Asp Ala Ala Ala Lys Tyr Ala Val Asp Leu Leu Ala Gly
210 215 220

Ile Lys Asn Ala Asn Ser Ala Val Gly Ala Val Leu Gly Glu Ser Ile
225 230 235 240

Ser Asp Ile Cys Arg Val Ala Lys Val Ile His Thr Pro Asp Tyr Ala

255

Asp Pro Tyr Lys Pro Arg Pro Gly His Lys Leu Trp Leu Leu Phe Thr
450 455 460

Thr Ile Ser Leu Asp Gln Gln Arg Glu Leu Gly Ile Glu Phe Ile Pro
 465 470 475 480

Ala Trp Lys Met Leu Phe Thr Asp Ile Asn Leu Phe Gly Ser Arg Val
 485 490 495

Pro Ile Gln Phe Met Pro Ala Ile Asn Pro Leu Ala Tyr Ile Cys Tyr
 500 505 510

Leu Pro Glu Ala Ala Thr Cys Ala Asn Gly Asp Ala Ile Asn Asp Gly
 515 520 525

Asp Ile Val Glu Met Arg Ala Val Asp Gly Phe Asp Thr Val Pro Lys
 530 535 540

Trp Glu Pro Ile Arg Val Arg Ser Asp Arg Lys Asp Glu Pro Gly Phe
 545 550 555 560

Tyr Gly Asn Asn Tyr Lys Ile Ala Ser Asp Ile Tyr Leu Asn Tyr Ile
 565 570 575

Asp Ile Phe Gln Phe Glu Asp Leu Tyr Lys Tyr Asn Pro Gly Tyr Phe
 580 585 590

Glu Lys Asn Lys Ser Asp Ile Tyr Val Ala Pro Asn Lys Tyr Arg Arg
 595 600 605

Phe Leu Ile Lys Asn Ile Phe Ser Lys Tyr Leu Lys Asn Ala Lys Trp
 610 615 620

Val Ile Asp Ala Ala Ala Gly Arg Gly Ala Asp Leu His Leu Tyr Lys
 625 630 635 640

Ala Glu Cys Val Glu Asn Leu Leu Ala Ile Asp Ile Asp Pro Thr Ala
 645 650 655

Ile Ser Glu Leu Val Arg Arg Arg Asn Glu Ile Thr Gly Tyr Asn Arg
 660 665 670

Gly His Arg Gly His Arg Gly Gly Ser Met Arg Ala His Met Gly Ala

675	680	685																	
Ser	His	His	Gly	Ala	Gln	Asn	Cys	Ala	Lys	Ser	Thr	Thr	Leu	His	Ala				
690						695					700								
Leu	Val	Ala	Asp	Leu	Arg	Thr	Asp	Pro	Asp	Val	Leu	Ile	Pro	Lys	Ile				
705					710					715					720				
Ile	Gln	Ser	Arg	Pro	Pro	Glu	Arg	Gly	Tyr	Asp	Ala	Ile	Val	Ile	Asn				
				725					730					735					
Phe	Ala	Ile	His	Tyr	Leu	Cys	Asp	Thr	Asp	Glu	His	Ile	Arg	Asp	Phe				
			740					745					750						
Leu	Ile	Thr	Val	Ser	Arg	Leu	Leu	Ala	Pro	Asn	Gly	Ile	Phe	Met	Phe				
		755					760					765							
Thr	Thr	Met	Asp	Gly	Glu	Ser	Ile	Val	Lys	Leu	Leu	Glu	Thr	His	Lys				
		770				775						780							
Val	Lys	Ser	Gly	Glu	Ser	Trp	Thr	Val	His	Thr	Gly	Ala	Asp	Asp	Pro				
785					790					795					800				
Glu	Ala	Gly	Val	Ile	Lys	Tyr	Ser	Ile	Arg	Arg	Leu	Tyr	Asp	Ser	Asp				
				805					810					815					
Lys	Leu	Thr	Lys	Thr	Gly	Gln	Gln	Ile	Ala	Val	Leu	Leu	Pro	Met	Ser				
			820					825					830						
Gly	Glu	Met	Lys	Thr	Glu	Pro	Leu	Cys	Asn	Ile	Lys	Asn	Ile	Ile	Ser				
		835					840					845							
Ile	Ala	Arg	Lys	Met	Gly	Leu	Asp	Leu	Val	Glu	Ser	Ala	Asp	Phe	Ser				
	850					855					860								
Val	Met	Tyr	Asp	Ala	Phe	Ala	Arg	Ala	Tyr	Pro	Glu	Ile	Ser	Ala	Arg				
865					870					875					880				
Leu	Thr	Pro	Asp	Asp	Lys	Leu	Tyr	Asn	Asp	Leu	His	Ser	Tyr	Ala	Val				
				885					890					895					

Phe Lys Arg Lys Lys
900

<210> 11
<211> 1170
<212> PRT
<213> Acanthamoeba polyphaga

<220>
<221> MISC_FEATURE
<223> mimivirus RNA capping enzyme; Genbank accession no. AAV50651

<400> 11

Met Gly Thr Lys Leu Lys Lys Ser Asn Asn Asp Ile Thr Ile Phe Ser
1 5 10 15

Glu Asn Glu Tyr Asn Glu Ile Val Glu Met Leu Arg Asp Tyr Ser Asn
20 25 30

Gly Asp Asn Leu Glu Phe Glu Val Ser Phe Lys Asn Ile Asn Tyr Pro
35 40 45

Asn Phe Met Arg Ile Thr Glu His Tyr Ile Asn Ile Thr Pro Glu Asn
50 55 60

Lys Ile Glu Ser Asn Asn Tyr Leu Asp Ile Ser Leu Ile Phe Pro Asp
65 70 75 80

Lys Asn Val Tyr Arg Val Ser Leu Phe Asn Gln Glu Gln Ile Gly Glu
85 90 95

Phe Ile Thr Lys Phe Ser Lys Ala Ser Ser Asn Asp Ile Ser Arg Tyr
100 105 110

Ile Val Ser Leu Asp Pro Ser Asp Asp Ile Glu Ile Val Tyr Lys Asn
115 120 125

Arg Gly Ser Gly Lys Leu Ile Gly Ile Asp Asn Trp Ala Ile Thr Ile
130 135 140

Lys Ser Thr Glu Glu Ile Pro Leu Val Ala Gly Lys Ser Lys Ile Ser

145		150		155		160									
Lys	Pro	Lys	Ile	Thr	Gly	Ser	Glu	Arg	Ile	Met	Tyr	Arg	Tyr	Lys	Thr
			165						170					175	
Arg	Tyr	Ser	Phe	Thr	Ile	Asn	Lys	Asn	Ser	Arg	Ile	Asp	Ile	Thr	Asp
			180					185					190		
Val	Lys	Ser	Ser	Pro	Ile	Ile	Trp	Lys	Leu	Met	Thr	Val	Pro	Ser	Asn
		195					200					205			
Tyr	Glu	Leu	Glu	Leu	Glu	Leu	Ile	Asn	Lys	Ile	Asp	Ile	Asn	Thr	Leu
	210						215				220				
Glu	Ser	Glu	Leu	Leu	Asn	Val	Phe	Met	Ile	Ile	Gln	Asp	Thr	Lys	Ile
225					230					235					240
Pro	Ile	Ser	Lys	Ala	Glu	Ser	Asp	Thr	Val	Val	Glu	Glu	Tyr	Arg	Asn
				245					250					255	
Leu	Leu	Asn	Val	Arg	Gln	Thr	Asn	Asn	Leu	Asp	Ser	Arg	Asn	Val	Ile
			260					265					270		
Ser	Val	Asn	Ser	Asn	His	Ile	Ile	Asn	Phe	Ile	Pro	Asn	Arg	Tyr	Ala
		275					280					285			
Val	Thr	Asp	Lys	Ala	Asp	Gly	Glu	Arg	Tyr	Phe	Leu	Phe	Ser	Leu	Asn
	290					295					300				
Ser	Gly	Ile	Tyr	Leu	Leu	Ser	Ile	Asn	Leu	Thr	Val	Lys	Lys	Leu	Asn
305					310					315					320
Ile	Pro	Val	Leu	Glu	Lys	Arg	Tyr	Gln	Asn	Met	Leu	Ile	Asp	Gly	Glu
				325					330					335	
Tyr	Ile	Lys	Thr	Thr	Gly	His	Asp	Leu	Phe	Met	Val	Phe	Asp	Val	Ile
			340					345					350		
Phe	Ala	Glu	Gly	Thr	Asp	Tyr	Arg	Tyr	Asp	Asn	Thr	Tyr	Ser	Leu	Pro
		355					360					365			

Lys Arg Ile Ile Ile Ile Asn Asn Ile Ile Asp Lys Cys Phe Gly Asn
 370 375 380

Leu Ile Pro Phe Asn Asp Tyr Thr Asp Lys His Asn Asn Leu Glu Leu
 385 390 395 400

Asp Ser Ile Lys Thr Tyr Tyr Lys Ser Glu Leu Ser Asn Tyr Trp Lys
 405 410 415

Asn Phe Lys Asn Arg Leu Asn Lys Ser Thr Asp Leu Phe Ile Thr Arg
 420 425 430

Lys Leu Tyr Leu Val Pro Tyr Gly Ile Asp Ser Ser Glu Ile Phe Met
 435 440 445

Tyr Ala Asp Met Ile Trp Lys Leu Tyr Val Tyr Asn Glu Leu Thr Pro
 450 455 460

Tyr Gln Leu Asp Gly Ile Ile Tyr Thr Pro Ile Asn Ser Pro Tyr Leu
 465 470 475 480

Ile Arg Gly Gly Ile Asp Ala Tyr Asp Thr Ile Pro Met Glu Tyr Lys
 485 490 495

Trp Lys Pro Pro Ser Gln Asn Ser Ile Asp Phe Tyr Ile Arg Phe Lys
 500 505 510

Lys Asp Val Ser Gly Ala Asp Ala Val Tyr Tyr Asp Asn Ser Val Glu
 515 520 525

Arg Ala Glu Gly Lys Pro Tyr Lys Ile Cys Leu Leu Tyr Val Gly Leu
 530 535 540

Asn Lys Gln Gly Gln Glu Ile Pro Ile Gln Phe Lys Val Asn Gly Val
 545 550 555 560

Glu Gln Thr Ala Asn Ile Tyr Thr Lys Asp Gly Glu Ala Thr Asp Ile
 565 570 575

Asn Gly Asn Ala Ile Asn Asp Asn Thr Val Val Glu Phe Val Phe Asp

580	585	590
Thr Leu Lys Ile Asp Met Asp Asp Ser Tyr Lys Trp Ile Pro Ile Arg		
595	600	605
Thr Arg Tyr Asp Lys Thr Glu Ser Val Gln Lys Tyr His Lys Arg Tyr		
610	615	620
Gly Asn Asn Leu Gln Ile Ala Asn Arg Ile Trp Lys Thr Ile Thr Asn		
625	630	635
Pro Ile Thr Glu Asp Ile Ile Ser Ser Leu Gly Asp Pro Thr Thr Phe		
	645	650
Asn Lys Glu Ile Thr Leu Leu Ser Asp Phe Arg Asp Thr Lys Tyr Asn		
	660	665
Lys Gln Ala Leu Thr Tyr Tyr Gln Lys Asn Thr Ser Asn Ala Ala Gly		
	675	680
Met Arg Ala Phe Asn Asn Trp Ile Lys Ser Asn Met Ile Thr Thr Tyr		
	690	695
Cys Arg Asp Gly Ser Lys Val Leu Asp Ile Gly Cys Gly Arg Gly Gly		
705	710	715
Asp Leu Ile Lys Phe Ile Asn Ala Gly Val Glu Phe Tyr Val Gly Ile		
	725	730
Asp Ile Asp Asn Asn Gly Leu Tyr Val Ile Asn Asp Ser Ala Asn Asn		
	740	745
Arg Tyr Lys Asn Leu Lys Lys Thr Ile Gln Asn Ile Pro Pro Met Tyr		
	755	760
Phe Ile Asn Ala Asp Ala Arg Gly Leu Phe Thr Leu Glu Ala Gln Glu		
	770	775
Lys Ile Leu Pro Gly Met Pro Asp Phe Asn Lys Ser Leu Ile Asn Lys		
785	790	795
		800

Tyr Leu Val Gly Asn Lys Tyr Asp Thr Ile Asn Cys Gln Phe Thr Ile
805 810 815

His Tyr Tyr Leu Ser Asp Glu Leu Ser Trp Asn Asn Phe Cys Lys Asn
820 825 830

Ile Asn Asn Gln Leu Lys Asp Asn Gly Tyr Leu Leu Ile Thr Ser Phe
835 840 845

Asp Gly Asn Leu Ile His Asn Lys Leu Lys Gly Lys Gln Lys Leu Ser
850 855 860

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

Asn Lys Ile Tyr Ser Asp Thr Asp Lys Val Gly Leu Gly Met Ala Ile
885 890 895

Asp Leu Tyr Asn Ser Leu Ile Ser Asn Pro Gly Thr Tyr Ile Arg Glu
900 905 910

Tyr Leu Val Phe Pro Glu Phe Leu Glu Lys Ser Leu Lys Glu Lys Cys
915 920 925

Gly Leu Glu Leu Val Glu Ser Asp Leu Phe Tyr Asn Ile Phe Asn Thr
930 935 940

Tyr Lys Asn Tyr Phe Lys Lys Thr Tyr Asn Glu Tyr Gly Met Thr Asp
945 950 955 960

Val Ser Ser Lys Lys His Ser Glu Ile Arg Glu Phe Tyr Leu Ser Leu
965 970 975

Glu Gly Asn Ala Asn Asn Asp Ile Glu Ile Asp Ile Ala Arg Ala Ser
980 985 990

Phe Lys Leu Ala Met Leu Asn Arg Tyr Tyr Val Phe Arg Lys Thr Ser
995 1000 1005

Thr Ile Asn Ile Thr Glu Pro Ser Arg Ile Val Asn Glu Leu Asn

1010	1015	1020
Asn Arg Ile Asp Leu Gly Lys Phe Ile Met Pro Tyr Phe Arg Thr 1025 1030 1035		
Asn Asn Met Phe Ile Asp Leu Asp Asn Val Asp Thr Asp Ile Asn 1040 1045 1050		
Arg Val Tyr Arg Asn Ile Arg Asn Lys Tyr Arg Thr Thr Arg Pro 1055 1060 1065		
His Val Tyr Leu Ile Lys His Asn Ile Asn Glu Asn Arg Leu Glu 1070 1075 1080		
Asp Ile Tyr Leu Ser Asn Asn Lys Leu Asp Phe Ser Lys Ile Lys 1085 1090 1095		
Asn Gly Ser Asp Pro Lys Val Leu Leu Ile Tyr Lys Ser Pro Asp 1100 1105 1110		
Lys Gln Phe Tyr Pro Leu Tyr Tyr Gln Asn Tyr Gln Ser Met Pro 1115 1120 1125		
Phe Asp Leu Asp Gln Ile Tyr Leu Pro Asp Lys Lys Lys Tyr Leu 1130 1135 1140		
Leu Asp Ser Asp Arg Ile Ile Asn Asp Leu Asn Ile Leu Ile Asn 1145 1150 1155		
Leu Thr Glu Lys Ile Lys Asn Ile Pro Gln Leu Ser 1160 1165 1170		

<210> 12
 <211> 1162
 <212> PRT
 <213> Acanthamoeba polyphaga

<220>
 <221> misc_feature
 <223> mousmouvirus RNA capping enzyme; Genbank accession no.
 YP_007354410

<400> 12

Met Val Thr Lys Asn Lys Ser Glu Asn Ile Arg Asp Ile Leu Gly Ser
1 5 10 15

Asp Asn Val Ser Arg Val Glu Glu Met Ile Asn Asn Phe Arg Lys Asn
20 25 30

Arg Asn Thr Glu Phe Glu Ile Ser Val Arg Lys Ile Asn Tyr Ser Asn
35 40 45

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

Gln Val Thr Ser Leu Asp Ile Ser Ile Ile Leu Glu Asp Gly Asn Thr
65 70 75 80

Tyr Arg Val Ser Phe Leu Asn Glu Asn Leu Ile Asn Asp Phe Leu Ser
85 90 95

Lys Tyr Ser Asn Met Lys Tyr Gly Asp Ile Val Lys Tyr Ile Leu Ala
100 105 110

Leu Asn Pro Asn Asp Asp Ile Glu Ile Ile Tyr Lys Asn Arg Gly Ser
115 120 125

Ala Asp Arg Leu Ser Ile Glu Asp Leu Asn Leu Val Val Lys Leu Thr
130 135 140

Glu Glu Val Pro Val Leu Asn Asn Thr Thr Lys Pro Lys Leu Ser Gly
145 150 155 160

Arg Glu Lys Ile Leu Tyr Arg Tyr Lys Asn Arg Tyr Ser Phe Ile Ile
165 170 175

Asp Asp Ile Thr Arg Ile Asp Ile Thr Asp Val Lys Glu Thr Pro Asn
180 185 190

Ile Trp Glu Leu Ser Arg Lys Ile Ser Asn Tyr Glu Ile Glu Leu Glu
195 200 205

Phe Thr Asn Asn Lys Ile Lys Ser Asn Gln Val Phe Glu Lys Ile Phe
 210 215 220

Asp Leu Leu Arg Ile Val Gln Asn Thr Glu Ile Pro Ile Gly Ile Arg
 225 230 235 240

Glu Ser Lys Gln Val Ile Thr Asp Tyr Gln Asn Leu Leu Asn Leu Arg
 245 250 255

Ser Ser Asn His Leu Asp Ser Arg Asn Val Val Ser Ile Glu Thr Gln
 260 265 270

His Ile Val Lys Phe Val Pro Asn Arg Tyr Ala Ile Thr Asp Lys Ala
 275 280 285

Asp Gly Glu Arg Tyr Phe Leu Phe Ser Thr Pro Asn Gly Val Tyr Leu
 290 295 300

Leu Ser Thr Asn Leu Thr Val Lys Lys Val Asn Ile Pro Val Leu Gln
 305 310 315 320

Lys Asp Phe Gln Asn Met Leu Leu Asp Gly Glu Leu Ile Asp Ile Asp
 325 330 335

Gly Lys Glu Leu Phe Met Val Phe Asp Val Val Tyr His Asn Gly Ile
 340 345 350

Asp Tyr Arg Tyr Asp Thr Asn Tyr Thr Leu Thr His Arg Ile Ile Ile
 355 360 365

Ile Asn Asp Ile Ile Asp Lys Ala Phe Asn Asn Leu Ile Pro Phe Thr
 370 375 380

Asp Tyr Thr Asp Lys Tyr Asn Asn Leu Glu Leu Asp Lys Ile Lys Glu
 385 390 395 400

Phe Tyr Ser Asn Glu Ile Lys Thr Tyr Trp Lys Asn Phe Ser Lys Lys
 405 410 415

Leu Lys Asn Tyr Ser Gly Leu Phe Ile Ser Arg Lys Leu Tyr Phe Val
 420 425 430

Pro Tyr Gly Ile Asp Ser Ser Glu Val Phe Met Tyr Ala Asp Leu Val
435 440 445

Trp Lys Leu Cys Val Tyr Asp Gln Leu Thr Pro Tyr Lys Leu Asp Gly
450 455 460

Ile Ile Tyr Thr Pro Ile Ala Ser Pro Tyr Met Ile Lys Thr Ser Ala
465 470 475 480

Asn Glu Leu Asp Ser Val Pro Met Glu Tyr Lys Trp Lys Pro Pro Ser
485 490 495

Gln Asn Ser Ile Asp Phe Tyr Val Lys Phe Asp Lys Asp Ala Arg Gly
500 505 510

Asn Glu Ala Ile Tyr Tyr Asp Asn Ala Val Val Arg Gly Glu Gly Arg
515 520 525

Pro Tyr Lys Val Cys Gly Leu Phe Val Gly Leu Asn Lys Gly Gly Glu
530 535 540

Glu Lys Pro Ile Ala Phe Lys Val Ala Gly Val Glu Gln Lys Ala Phe
545 550 555 560

Ile Tyr Leu Thr Asn Asp Glu Ala Leu Asp Leu Ser Gly Asn Val Ile
565 570 575

Asn Asp Asn Thr Val Val Glu Phe Ile Phe Asp Asn Phe Lys Thr Asp
580 585 590

Met Asp Asp Pro Tyr Lys Trp Ile Pro Val Arg Thr Arg Tyr Asp Lys
595 600 605

Thr Glu Ser Val Gln Lys Tyr Arg Lys Lys Tyr Gly Asn Asn Leu His
610 615 620

Ile Ala Thr Arg Ile Trp Arg Thr Ile Thr Asn Pro Val Thr Glu Glu
625 630 635 640

Ile Ile Ala Ala Leu Gly Asn Ala Ser Thr Phe Glu Lys Glu Met Ser
645 650 655

Lys Leu Val Lys Met Asn Glu Ser Tyr Asn Lys Gln Ser Phe Ser Tyr
660 665 670

Tyr Gln Lys Asn Thr Ser Asn Ala Ile Gly Met Arg Ala Phe Asn Asn
675 680 685

Phe Ile Lys Ser Asn Met Ile Thr Thr Tyr Cys Lys Asp Lys Asp Ser
690 695 700

Val Leu Asp Ile Gly Cys Gly Arg Gly Gly Asp Leu Ile Lys Phe Ile
705 710 715 720

His Ala Asn Ile Arg Glu Tyr Val Gly Leu Asp Ile Asp Asn Asn Gly
725 730 735

Leu Tyr Val Ile Asn Asp Ser Ala Phe Asn Arg Tyr Lys Asn Leu Lys
740 745 750

Lys Thr Asn Lys Asn Val Pro Pro Met Thr Phe Ile Asn Ala Asp Ala
755 760 765

Arg Gly Leu Phe Asn Val Glu Ala Gln Glu Lys Ile Leu Pro Asn Met
770 775 780

Ser Glu Ser Asn Lys Lys Leu Ile Asn Asn Tyr Leu Ser Ser Asn Lys
785 790 795 800

Lys Tyr Asp Ala Ile Asn Cys Gln Phe Thr Ile His Tyr Tyr Leu Ser
805 810 815

Asp Asp Ile Ser Trp Asn Asn Phe Cys Gln Asn Ile Asn Asn His Ile
820 825 830

Lys Asp Asn Gly Tyr Leu Leu Ile Thr Cys Phe Asp Gly Gln Leu Ile
835 840 845

Tyr Asp Lys Leu Lys Gly Lys Gln Lys Tyr Ser Ser Ser Tyr Thr Asp
850 855 860

Asn Phe Gly Lys Lys Asn Ile Phe Phe Glu Ile Asn Lys Ile Tyr Ser
865 870 875 880

Asp Glu Glu Ile Lys Pro Val Gly Met Ala Ile Asp Ile Tyr Asn Ser
885 890 895

Leu Ile Ser Asn Pro Gly Thr Tyr Gln Arg Glu Tyr Leu Val Phe Pro
900 905 910

Asp Phe Leu Gln Lys Ser Leu Lys Asp Gln Cys Gly Leu Glu Leu Val
915 920 925

Glu Thr Asp Met Phe Tyr Asn Ile Phe Asn Leu Tyr Arg Asn Tyr Phe
930 935 940

Thr Ile Asn Asn Gly Thr Phe Ser Thr Gly Glu Ile Ser Ser Lys Arg
945 950 955 960

Tyr Asn Glu Ile Lys Asp Phe Tyr Leu Ala Leu Glu Gly Lys Ser Ser
965 970 975

Ser Val Thr Glu Ser Asp Ile Ala Phe Ala Ser Phe Lys Leu Ala Met
980 985 990

Leu Asn Arg Tyr Tyr Ile Phe Lys Lys Lys Thr Val Ile Asn Ile Thr
995 1000 1005

Glu Pro Ser His Ile Val Ser Gly Val Asn Lys Lys Thr Asp Leu
1010 1015 1020

Gly Lys Val Leu Met Pro Tyr Phe Ile Thr Asn Asn Met Ile Ile
1025 1030 1035

Asp Tyr Ser Leu Gly Asn Asn Asp Val Asn Lys Ile Tyr His Phe
1040 1045 1050

Ile Arg Lys Lys Tyr Ser Pro Ile Lys Pro Ser Val Tyr Leu Val
1055 1060 1065

Arg His Asn Ile Ile Asp Asn Pro Met Asp Gly Ile Thr Phe Ser
 1070 1075 1080

Arg Asn Lys Leu Glu Phe Ile Lys Ile Lys Asn Gly Thr Asp Pro
 1085 1090 1095

Lys Val Leu Leu Ile Tyr Lys Ser Pro Glu Lys Ile Phe Tyr Pro
 1100 1105 1110

Phe Tyr Tyr Gln Arg Leu Glu Asn His Asp Tyr Ser Glu Asp Tyr
 1115 1120 1125

Leu Lys Asn Asn Ile Tyr Leu Lys Asp Asn Gly Thr Tyr Leu Leu
 1130 1135 1140

Asp Ser Asn Lys Ile Ile Asn Asp Leu Asn Met Leu Val Asn Ile
 1145 1150 1155

Ser Gly Lys Val
 1160

<210> 13
 <211> 25
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>
 <221> misc_feature
 <223> RNA1

<400> 13
 guagaacuuc gucgaguacg cucaa

25

<210> 14
 <211> 23
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>
 <221> misc_feature
 <223> RNA2

 <400> 14
 gcaagucuuc gucgaguacu ugc 23

 <210> 15
 <211> 24
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic construct

 <220>
 <221> misc_feature
 <223> RNA3

 <400> 15
 ggcaagucuu cgucgaguac uugc 24

 <210> 16
 <211> 25
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic construct

 <220>
 <221> misc_feature
 <223> RNA4

 <400> 16
 gggcaagucu ucgucgagua cuugc 25

 <210> 17
 <211> 150
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic construct

 <400> 17
 gggagucuuc gccgagaggg ccaucgccag uugccgcaac cugugggaau uucucuucca 60
 guuuauccgg augcucaacg gugacuuuaa uuccgguauc uuucucgaau uucuuaccga 120

cuucagcgag cuggacaaug cucuuccua 150

<210> 18
 <211> 1753
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>
 <221> misc_feature
 <223> Sequence of the fluc transcript

<400> 18
 gggucuagaa auauuuuuugu uuaacuuuaa gaaggagaua uaaccaugaa aaucgaagaa 60
 gguaaagguc accaucacca ucaccacgga uccauggaag acgccaaaaa cauaaagaaa 120
 ggcccggcgc cauucuaucc ucuagaggau ggaaccgcug gagagcaacu gcauaaggcu 180
 augaagagau acgcccuggu uccuggaaca auugcuuuua cagaugcaca uaucgaggug 240
 aacaucacgu acgcggaaua cuucgaaaug uccguucggu uggcagaagc uaugaaacga 300
 uaugggcuga auacaaaucagaagaucguc guaugcagug aaaacucucu ucaauucuuu 360
 augccggugu ugggcgcggu auuuauucgga guugcaguug cgcccgcgaa cgacauuuau 420
 aaugaacgug aaauugcucaa caguaugaac auuucgcagc cuaccguagu guuuguuuucc 480
 aaaaaggggu ugcaaaaaau uuugaacgug caaaaaaaau uaccaauaau ccagaaaaau 540
 auuaucaugg auucuaaaac ggauuaccag ggauuucagu cgauguacac guucgucaca 600
 ucucaucuac cucccgguuu uaaugaauac gauuuuguac cagaguccuu ugaucgugac 660
 aaaacaauug cacugauaau gaauuccucu ggauucuacug gguuaccuaa ggguguggcc 720
 cuuccgcaua gaacugccug cgucagauuc ucgcaugcca gagauccuau uuuuggcaau 780
 caaaucuuuc cggauacugc gauuuuaagu guuguuccau uccaucacgg uuuuggaau 840
 uuuacuacac ucggauuuu gauaugugga uuucgagucg ucuaaauua uagauuugaa 900
 gaagagcugu uuuuacgauc ccuucaggau uacaaaauuc aaagugcguu gcuaguacca 960
 acccuuuuuu cauucuuucg caaaagcacu cugauugaca aaucgauuu aucuaauuuu 1020
 cacgaaaauug cuucuggggg cgaccucuu ucgaaagaag ucggggaagc gguugcaaaa 1080

cgcuuccauc uuccagggau acgacaagga uaugggcuca cugagacuac aucagcuauu	1140
cugauuacac ccgaggggga ugauaaaccg ggcgcggucg guaaaguugu uccauuuuuu	1200
gaagcgaagg uuguggaucu ggauaccggg aaaacgcugg gcguuaauca gagaggcgaa	1260
uuauugugua gaggaccuau gauuaugucc gguuauguaa acaauccgga agcgaccaac	1320
gccuugauug acaaggauug auggcuacau ucuggagaca uagcuuacug ggacgaagac	1380
gaacacuucu ucauaguuga ccgcuugaag ucuuuauua aaucacaaagg auaucaggug	1440
gccccgcug aauggauc gauauuguua caacacccca acaucuucga cgcgggcgug	1500
gcaggucuuc ccgacgauga cgccggugaa cuuccgccg ccguuguugu uuuggagcac	1560
ggaaagacga ugacggaaaa agagaucgug gauuacgucg ccagucaagu aacaaccgcg	1620
aaaaaguugc gcggaggagu uguguuugug gacgaaguac cgaaaggucu uaccggaaaa	1680
cucgacgcaa gaaaaaucag agagauccuc auaaaggcca agaagggcgg aaaguccaaa	1740
cucgaguaag guu	1753

<210> 19
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>
 <221> misc_feature
 <223> Targeting oligo for fluc transcript

<220>
 <221> misc_feature
 <222> (44)..(44)
 <223> C is TEG-desthiobiotin

<400> 19	
gttaaarcra rarararuru rarurururc rurargrarc rcrc	44

<210> 20
 <211> 1778
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>

<221> MISC_FEATURE

<223> The amino acid sequence of H3C2:T7 RNA polymerase fusion protein

<400> 20

Met Lys Ile Glu Glu His His His His His His His His Gly Ala Ser
1 5 10 15

Thr Ala Lys Arg Leu Gln Arg Cys Gln Asp Val Asn Gln Val Cys Glu
20 25 30

Ile Tyr Asn Ser Lys Gly Gly Ile Gly Glu Leu Glu Leu Arg Phe Asp
35 40 45

Lys Leu Pro Gln Asn Leu Phe Ala Gly Val Phe Asp Lys Leu Lys Pro
50 55 60

Asp Gly Glu Ile Gln Thr Thr Met Arg Val Ser Asn Arg Asp Gly Val
65 70 75 80

Ala Arg Glu Ile Thr Phe Gly Gly Gly Val Lys Thr Asn Glu Ile Phe
85 90 95

Val Lys Lys Gln Asn Ile Cys Val Phe Asp Val Val Asp Ile Phe Ser
100 105 110

Tyr Lys Val Ala Val Ser Thr Glu Glu Thr Val Val Glu Lys Pro Thr
115 120 125

Met Glu Thr Thr Ala Gly Val Arg Phe Lys Ile Arg Leu Ser Val Glu
130 135 140

Asp Val Val Lys Asp Trp Arg Ile Asp Leu Thr Ala Val Lys Thr Ala
145 150 155 160

Glu Leu Gly Lys Ile Ala Gln His Thr Ala Ser Ile Val Gln Arg Thr
165 170 175

Phe Pro Asp Asn Leu Leu Lys Leu Thr Gly Ala Glu Val Ala Lys Leu
180 185 190

Ala Ala Asp Ser Tyr Glu Leu Glu Leu Glu Tyr Thr Gly Lys Ser Pro
195 200 205

Ala Thr Asn Glu Lys Val Asn Val Ala Ala Lys Tyr Ala Val Glu Leu
210 215 220

Leu Ser Ser Val Arg Asn Ala Asn Ser Thr Ala Ala Ala Ser Phe Gly
225 230 235 240

Glu Ser Val Ser Asp Leu Cys Arg Val Ala Lys Ile Ile His Thr His
245 250 255

Glu Tyr Ala Asn Val Val Cys Arg Thr Pro Ser Phe Lys Met Leu Leu
260 265 270

Pro Gln Val Val Ser Leu Thr Lys Ser Ser Tyr Tyr Gly Gly Leu Tyr
275 280 285

Pro Pro Glu Asn Leu Trp Leu Ala Gly Lys Thr Asp Gly Val Arg Ala
290 295 300

Leu Val Val Cys Glu Asp Gly Val Ala Lys Val Ile Thr Ala Glu Ser
305 310 315 320

Val Asp Ile Thr His Gly Val Cys Ser Ala Thr Thr Ile Leu Asp Cys
325 330 335

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

Ser Asn Asn Thr Gln Val Tyr Thr Gln Pro Phe Ser Thr Arg Ile Thr
355 360 365

Thr Asp Ile Ser Asp Ile Lys Ile Asp Gly Tyr Lys Ile Glu Met Lys
370 375 380

Pro Phe Val Lys Val Val Lys Ala Asp Glu Ala Thr Phe Lys Ser Ala
385 390 395 400

Tyr Lys Ala Pro His Asn Glu Gly Leu Ile Met Ile Glu Asp Gly Ala
405 410 415

Ala Tyr Ala Ala Thr Lys Thr Tyr Lys Trp Lys Pro Leu Ser His Asn
420 425 430

Thr Ile Asp Phe Leu Ile Lys Ala Cys Pro Lys Gln Leu Ile Asn Val
435 440 445

Asp Pro Tyr Lys Pro Arg Ala Gly Tyr Lys Leu Trp Leu Leu Phe Thr
450 455 460

Thr Ile Ser Leu Asp Gln Gln Arg Glu Leu Gly Ile Glu Phe Ile Pro
465 470 475 480

Ala Trp Lys Ile Leu Phe Thr Asp Ile Asn Met Phe Gly Ser Arg Val
485 490 495

Pro Ile Gln Phe Gln Pro Ala Ile Asn Pro Leu Ala Tyr Val Cys Tyr
500 505 510

Leu Pro Glu Asp Val Asn Val Asn Asp Gly Asp Ile Val Glu Met Arg
515 520 525

Ala Val Asp Gly Tyr Asp Thr Ile Pro Lys Trp Glu Leu Val Arg Ser
530 535 540

Arg Asn Asp Arg Lys Asn Glu Pro Gly Phe Tyr Gly Asn Asn Tyr Lys
545 550 555 560

Ile Ala Ser Asp Ile Tyr Leu Asn Tyr Ile Asp Val Phe His Phe Glu
565 570 575

Asp Leu Tyr Lys Tyr Asn Pro Gly Tyr Phe Glu Lys Asn Lys Ser Asp
580 585 590

Ile Tyr Val Ala Pro Asn Lys Tyr Arg Arg Tyr Leu Ile Lys Ser Leu
595 600 605

Phe Gly Arg Tyr Leu Arg Asp Ala Lys Trp Val Ile Asp Ala Ala Ala
610 615 620

Gly Arg Gly Ala Asp Leu His Leu Tyr Lys Ala Glu Cys Val Glu His
625 630 635 640

Leu Leu Ala Ile Asp Ile Asp Pro Thr Ala Ile Ser Glu Leu Val Arg
645 650 655

Arg Arg Asn Glu Ile Thr Gly Tyr Asn Lys Ser His Arg Gly Gly Arg
660 665 670

Asn Met His Ser His Arg Gly Gln Ser His Cys Ala Lys Ser Thr Ser
675 680 685

Leu His Ala Leu Val Ala Asp Leu Arg Glu Asn Pro Asp Val Leu Ile
690 695 700

Pro Lys Ile Ile Gln Ser Arg Pro His Glu Arg Cys Tyr Asp Ala Ile
705 710 715 720

Val Ile Asn Phe Ala Ile His Tyr Leu Cys Asp Thr Asp Glu His Ile
725 730 735

Arg Asp Phe Leu Ile Thr Val Ser Arg Leu Leu Ala Pro Asn Gly Val
740 745 750

Phe Ile Phe Thr Thr Met Asp Gly Glu Ser Ile Val Lys Leu Leu Ala
755 760 765

Asp His Lys Val Arg Pro Gly Glu Ala Trp Thr Ile His Thr Gly Asp
770 775 780

Val Asn Ser Pro Asp Ser Thr Val Pro Lys Tyr Ser Ile Arg Arg Leu
785 790 795 800

Tyr Asp Ser Asp Lys Leu Thr Lys Thr Gly Gln Gln Ile Glu Val Leu
805 810 815

Leu Pro Met Ser Gly Glu Met Lys Ala Glu Pro Leu Cys Asn Ile Lys
820 825 830

Asn Ile Ile Ser Met Ala Arg Lys Met Gly Leu Asp Leu Val Glu Ser
835 840 845

Ala Asn Phe Ser Val Leu Tyr Glu Ala Tyr Ala Arg Asp Tyr Pro Asp
850 855 860

Ile Tyr Ala Arg Met Thr Pro Asp Asp Lys Leu Tyr Asn Asp Leu His
865 870 875 880

Thr Tyr Ala Val Phe Lys Arg Lys Lys Gly Ala Ser Thr Ala Ser Thr
885 890 895

Asn Thr Ile Asn Ile Ala Lys Asn Asp Phe Ser Asp Ile Glu Leu Ala
900 905 910

Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Glu Arg Leu Ala
915 920 925

Arg Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Met Gly Glu Ala
930 935 940

Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val Ala
945 950 955 960

Asp Asn Ala Ala Ala Lys Pro Leu Ile Thr Thr Leu Leu Pro Lys Met
965 970 975

Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg Gly
980 985 990

Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu Ala
995 1000 1005

Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
1010 1015 1020

Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg
1025 1030 1035

Ala Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu
1040 1045 1050

Ala	Lys	His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg
1055						1060					1065			
Val	Gly	His	Val	Tyr	Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala
1070						1075					1080			
Asp	Met	Leu	Ser	Lys	Gly	Leu	Leu	Gly	Gly	Glu	Ala	Trp	Ser	Ser
1085						1090					1095			
Trp	His	Lys	Glu	Asp	Ser	Ile	His	Val	Gly	Val	Arg	Cys	Ile	Glu
1100						1105					1110			
Met	Leu	Ile	Glu	Ser	Thr	Gly	Met	Val	Ser	Leu	His	Arg	Gln	Asn
1115						1120					1125			
Ala	Gly	Val	Val	Gly	Gln	Asp	Ser	Glu	Thr	Ile	Glu	Leu	Ala	Pro
1130						1135					1140			
Glu	Tyr	Ala	Glu	Ala	Ile	Ala	Thr	Arg	Ala	Gly	Ala	Leu	Ala	Gly
1145						1150					1155			
Ile	Ser	Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp
1160						1165					1170			
Thr	Gly	Ile	Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Arg	Arg	Pro
1175						1180					1185			
Leu	Ala	Leu	Val	Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Met	Arg	Tyr
1190						1195					1200			
Glu	Asp	Val	Tyr	Met	Pro	Glu	Val	Tyr	Lys	Ala	Ile	Asn	Ile	Ala
1205						1210					1215			
Gln	Asn	Thr	Ala	Trp	Lys	Ile	Asn	Lys	Lys	Val	Leu	Ala	Val	Ala
1220						1225					1230			
Asn	Val	Ile	Thr	Lys	Trp	Lys	His	Cys	Pro	Val	Glu	Asp	Ile	Pro
1235						1240					1245			

Ala	Ile	Glu	Arg	Glu	Glu	Leu	Pro	Met	Lys	Pro	Glu	Asp	Ile	Asp
1250						1255					1260			
Met	Asn	Pro	Glu	Ala	Leu	Thr	Ala	Trp	Lys	Arg	Ala	Ala	Ala	Ala
1265						1270					1275			
Val	Tyr	Arg	Lys	Asp	Lys	Ala	Arg	Lys	Ser	Arg	Arg	Ile	Ser	Leu
1280						1285					1290			
Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala	Asn	His	Lys	Ala
1295						1300					1305			
Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg	Val	Tyr	Ala
1310						1315					1320			
Val	Ser	Met	Phe	Asn	Pro	Gln	Gly	Asn	Asp	Met	Thr	Lys	Gly	Leu
1325						1330					1335			
Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Lys	Glu	Gly	Tyr	Tyr
1340						1345					1350			
Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	Val
1355						1360					1365			
Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	His	Glu	Asn
1370						1375					1380			
Ile	Met	Ala	Cys	Ala	Lys	Ser	Pro	Leu	Glu	Asn	Thr	Trp	Trp	Ala
1385						1390					1395			
Glu	Gln	Asp	Ser	Pro	Phe	Cys	Phe	Leu	Ala	Phe	Cys	Phe	Glu	Tyr
1400						1405					1410			
Ala	Gly	Val	Gln	His	His	Gly	Leu	Ser	Tyr	Asn	Cys	Ser	Leu	Pro
1415						1420					1425			
Leu	Ala	Phe	Asp	Gly	Ser	Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala
1430						1435					1440			
Met	Leu	Arg	Asp	Glu	Val	Gly	Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro
1445						1450					1455			

Ser	Glu	Thr	Val	Gln	Asp	Ile	Tyr	Gly	Ile	Val	Ala	Lys	Lys	Val
1460						1465					1470			
Asn	Glu	Ile	Leu	Gln	Ala	Asp	Ala	Ile	Asn	Gly	Thr	Asp	Asn	Glu
1475						1480					1485			
Val	Val	Thr	Val	Thr	Asp	Glu	Asn	Thr	Gly	Glu	Ile	Ser	Glu	Lys
1490						1495					1500			
Val	Lys	Leu	Gly	Thr	Lys	Ala	Leu	Ala	Gly	Gln	Trp	Leu	Ala	Tyr
1505						1510					1515			
Gly	Val	Thr	Arg	Ser	Val	Thr	Lys	Arg	Ser	Val	Met	Thr	Leu	Ala
1520						1525					1530			
Tyr	Gly	Ser	Lys	Glu	Phe	Gly	Phe	Arg	Gln	Gln	Val	Leu	Glu	Asp
1535						1540					1545			
Thr	Ile	Gln	Pro	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu	Met	Phe	Thr
1550						1555					1560			
Gln	Pro	Asn	Gln	Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile	Trp	Glu
1565						1570					1575			
Ser	Val	Ser	Val	Thr	Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn	Trp
1580						1585					1590			
Leu	Lys	Ser	Ala	Ala	Lys	Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys
1595						1600					1605			
Lys	Thr	Gly	Glu	Ile	Leu	Arg	Lys	Arg	Cys	Ala	Val	His	Trp	Val
1610						1615					1620			
Thr	Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	Glu	Tyr	Lys	Lys	Pro	Ile
1625						1630					1635			
Gln	Thr	Arg	Leu	Asn	Leu	Met	Phe	Leu	Gly	Gln	Phe	Arg	Leu	Gln
1640						1645					1650			

Pro Thr Ile Asn Thr Asn Lys Asp Ser Glu Ile Asp Ala His Lys
 1655 1660 1665

Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly
 1670 1675 1680

Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu Lys Tyr Gly
 1685 1690 1695

Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr Ile Pro
 1700 1705 1710

Ala Asp Ala Ala Asn Leu Phe Lys Ala Val Arg Glu Thr Met Val
 1715 1720 1725

Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
 1730 1735 1740

Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala
 1745 1750 1755

Leu Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu Ser
 1760 1765 1770

Asp Phe Ala Phe Ala
 1775

<210> 21
 <211> 5337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<220>
 <221> misc_feature
 <223> Nucleotide sequence of H3C2:T7 RNA polymerase fusion protein

<400> 21
 atgaagattg aggagcatca tcatcatcat catcatcatg gcgcgagcac cgcaagcgt 60
 ctgcagcgtt gccaggacgt gaaccaagtg tgcgaaatct acaacagcaa gggtggcatt 120

ggcgagctgg aactgcgttt cgataaactg ccgcagaacc tgttcgcggg cgtttttgat	180
aagctgaaac cggacggcga gattcaaacc accatgcgtg ttagcaaccg tgacgggtgtg	240
gcgcgtgaaa tcacctttgg tggcgggtgtt aagaccaacg agatcttcgt gaagaaacag	300
aacatttgcg ttttcgacgt ggttgatata tttagctaca aggtggcggg tagcaccgag	360
gaaaccgtgg ttgaaaagcc gaccatggag accaccgcgg gcgtgcgttt taaaattcgt	420
ctgagcgttg aagacgtggt taaggattgg cgtatcgatc tgaccgcggg gaagaccgcg	480
gagctgggta aaatcgcgca gcacaccgcg agcattgttc aacgtacctt cccggataac	540
ctgctgaagc tgaccggtgc ggaagtggcg aaactggcgg cggacagcta cgagctggaa	600
ctggagtata ccggcaagag cccggcgacc aacgaaaagg tgaacgttgc ggcgaaatac	660
gcggttgagc tgctgagcag cgtgcgtaac gcgaacagca ccgcggcggc gagctttggt	720
gaaagcgta gcgacctgtg ccgtgtggcg aaaatcattc acaccacga gtacgcgaac	780
gtggtttgcc gtaccccag cttcaaaatg ctgctgccgc aggtggtttag cctgaccaag	840
agcagctact atggcggctt gtatccgccg gaaaacctgt ggctggcggg caagaccgat	900
ggcgtgcgtg cgctggttgt gtgcgaagac ggctggcgga aagttatcac cgcggagagc	960
gttgatatta cccacggtgt gtgcagcgcg accaccattc tggattgcga gctgaacgtt	1020
gacgcgaaga tcctgtacgt gtttgacgtt atcattagca acaacacca ggtgtatacc	1080
caaccgttca gcacccgtat caccaccgac attagcgata tcaagatcga tggttacaag	1140
atcgaaatga agccgtttgt taagggtggt aaggcggacg aggcgacctt caagagcgcg	1200
tataaagcgc cgcaaacga aggcctgatc atgattgaag atggtgcggc gtacgcggcg	1260
accaagacct ataagtggaa accgctgagc cacaacacca tcgatttcct gattaaggcg	1320
tgcccgaaac agctgattaa cgtggacccg tacaagccgc gtgcgggtta taaactgtgg	1380
ctgctgttta ccacatcag cctggatcag caacgtgaac tgggcatcga gttcattccg	1440
gcgtggaaaa tcctgttcac cgacattaac atgtttggta gccgtgtgcc gatccagttt	1500
caaccggcga ttaacccgct ggcgtacgtt tgctatctgc cggaagacgt gaacgttaac	1560
gacggcgata ttgttgagat gcgtgcgggtg gacggttacg ataccatccc gaaatgggaa	1620
ctggttcgta gccgtaacga tcgtaagaac gagccgggtt tctacggcaa caactataaa	1680
atcgcgagcg acatttacct gaactatatt gatgttttcc actttgaaga cctgtacaaa	1740

tataacccgg gctacttcga gaagaacaag agcgatatct acgtggcgcc gaacaagtac	1800
cgctcgttatc tgatcaaaag cctgttcggg cgttacctgc gtgatgcgaa gtgggtgatt	1860
gatgcggcgg cgggtcgtgg cgcggacctg cacctgtata aagcggaatg cgttgagcac	1920
ctgctggcga tcgacattga tccgaccgcg atcagcgaac tgggtgcgtcg tcgtaacgag	1980
attaccggct acaacaagag ccaccgtggc ggtcgttaaca tgcacagcca ccgtggtcag	2040
agccactgcg cgaaaagcac cagcctgcac gcgctggttg cggatctgcg tgaaaacccg	2100
gacgttctga ttccgaagat cattcaaagc cgtccgcacg agcgttgcta cgatgcgac	2160
gttattaact ttgcgatcca ctatctgtgc gacaccgatg aacacatccg tgacttcctg	2220
attaccgtga gccgtctgct ggcgccgaac ggtgttttca tctttaccac catggatggt	2280
gaaagcattg tgaagctgct ggcgggaccac aaagttcgtc cgggtgaagc gtggaccatc	2340
cacaccggtg atgtgaacag cccggacagc accgttccga aatacagcat tcgtcgtctg	2400
tatgacagcg ataagctgac caaaaccggc cagcaaatacg aggttctgct gccgatgagc	2460
ggtgaaatga aggcggagcc gctgtgcaac attaaaaaca tcattagcat ggcgcgtaag	2520
atgggtctgg atctgggtga aagcgcgaaac tttagcgttc tgtacgaggc gtatgcgcgt	2580
gactacccgg atatctatgc gcgtatgacc ccggacgata agctgtacaa cgacctgcac	2640
acctatgcgg tgttcaagcg taagaaaggc gcgagcaccg cgagcaccaa caccatcaac	2700
attgcgaaga acgactttag cgatatcgag ctggcggcga ttccgttcaa caccctggcg	2760
gaccactacg gtgaacgtct ggcgcgtagag cagctggcgc tggaacacga gagctatgaa	2820
atgggagagg cgcgtttccg taagatgttt gaacgtcaac tgaaagcggg tgaggttgcg	2880
gataacgcgg cggcgaaacc gctgattacc accctgctgc cgaagatgat cgcgcgatt	2940
aacgactggt tcgaggaagt taaggcgaac cgtggtaaac gtccgaccgc gttccagttt	3000
ctgcaagaaa tcaaaccgga ggcggtggcg tacatcacca ttaaaaccac cctggcgtgc	3060
ctgaccagcg cggacaacac caccgtgcag gcggttgca gcgcgattgg tcgtgcgatt	3120
gaagatgagg cgcgttttgg tcgtatccgt gacctggaag cgaagcactt caagaaaaac	3180
gttgaggaac agctgaacaa acgtgtgggc cacgtttata agaaagcggt catgcaagtg	3240
gttgaggcgg atatgctgag caagggtctg ctgggcggtg aagcgtggag cagctggcac	3300
aaagaggaca gcatccacgt gggcgttcgt tgcatacgaac tgctgattga gagcaccggt	3360

atggttagcc tgcaccgtca gaacgcgggt gtggttgcc aagatagcga aaccatcgag	3420
ctggcgccgg aatacgcgga ggcgattgcg acccgctcgg gtgcgctggc gggatatcagc	3480
ccgatgtttc aaccgtgcgt ggttccgccg aagccgtgga ccggtattac cggcgggtggc	3540
tactgggcga acggtcgtcg tccgctggcg ctggtgcgta cccacagcaa gaaagcgctg	3600
atgcgttacg aagacgttta tatgccgga gtgtataagg cgatcaacat tgcgcaaaac	3660
accgcgtgga aaattaacaa gaaagtgtg gcggttgca acgtgatcac caagtggaaa	3720
cactgcccgg ttgaagatat cccggcgatt gagcgtgagg aactgccgat gaaaccggaa	3780
gacatcgata tgaaccgga agcgtgacc gcgtggaaac gtgcggcggc ggcggtgtac	3840
cgtaaggaca aagcgcgtaa aagccgtcgt attagcctgg aattcatgct ggagcaggcg	3900
aacaagtttg cgaaccacaa agcgatctgg ttcccgtaca acatggattg gcgtggccgt	3960
gtttatgctg tgagcatgtt caaccgcaa ggcaacgaca tgaccaaggg cctgctgacc	4020
ctggcgaagg gtaaaccgat tggcaaggaa ggctactatt ggctgaaaat ccacggtgcg	4080
aactgcgcgg gcgttgataa agtgccgttc ccggaacgta tcaagtttat tgaggaaaac	4140
cacgagaaca tcatggcgtg cgcgaaaagc ccgctggaaa acacctgggtg ggcggagcag	4200
gacagcccgt tctgctttct ggcgttctgc tttgagtacg cgggtgttca acaccacggc	4260
ctgagctata actgcagcct gccgctggcg tttgatggta gctgcagcgg catccagcac	4320
ttcagcgcgga tgctgcgtga cgaagtgggt ggccgtgcgg tgaacctgct gccgagcgag	4380
accgtgcagg atatctacgg tattgttgcg aagaaagtga acgagatcct gcaagcggat	4440
gcgattaacg gcaccgacaa cgaagtgggt accgtgaccg acgagaacac cggtgaaatc	4500
agcgagaagg ttaaaactggg taccaaagcg ctggcgggcc agtggctggc gtacggtgtt	4560
acccgtagcg tgaccaagcg tagcgttatg accctggcgt atggtagcaa agaattcggc	4620
tttcgtcagc aagtgcgtga ggataccatc caaccggcga ttgacagcgg caagggcctg	4680
atgtttaccc agccgaacca agcggcgggt tacatggcga aactgatctg ggaaagcgtg	4740
agcgttaccg tggttgcggc ggttgaggcg atgaactggc tgaagagcgc ggcgaaactg	4800
ctggcggcgg aagtgaaaga taagaaaacc ggcgagattc tgcgtaagcg ttgcgcggtt	4860
cactgggtga ccccgacgg tttcccggtt tggcaggaat ataagaaacc gatccaaacc	4920
cgtctgaacc tgatgttcct gggccagttt cgtctgcaac cgaccatcaa caccaacaaa	4980

gatagcga	aa	ttgacgcg	ca	caagcagg	ag	gcggcatt	gc	cgccgaact	t	tgtgcacag	c	5040
caagacgg	ta	gccacctg	cg	taaaaccg	tg	gtttgggc	gc	acgaaaag	ta	cggcatcg	ag	5100
agcttcgc	gc	tgattcac	ga	tagctttg	gt	accattcc	gg	cggatgcg	gc	gaacctgt	tc	5160
aaggcggt	tc	gtgaaacc	at	ggtggata	cc	tacgagag	ct	gcgacgtg	ct	ggcggact	tc	5220
tatgatcag	t	ttgcggat	ca	actgcacg	ag	agccagct	gg	acaaaatg	cc	ggcgctgc	cg	5280
gcgaaggg	ta	acctgaac	ct	gcgtgac	att	ctggagag	cg	attttgcg	tt	tgcgtaa		5337