

sequence listing PCT_CA2013_050666
SEQUENCE LISTING

<110> MEDICAGO INC.

<120> PICORNA VIRUS-LIKE PARTICLE PRODUCTION IN PLANTS

<130> V84804WO

<150> US 61/697,266

<151> 2012-09-05

<160> 10

<170> PatentIn version 3.5

<210> 1

<211> 645

<212> PRT

<213> Enterovirus A71

<400> 1

Gly Pro Ser Leu Asp Phe Ala Leu Ser Leu Leu Arg Arg Asn Val Arg
1 5 10 15

Gln Val Gln Thr Asp Gln Gly His Phe Thr Met Leu Gly Val Arg Asp
20 25 30

Arg Leu Ala Val Leu Pro Arg His Ser Gln Pro Gly Lys Thr Ile Trp
35 40 45

Ile Glu His Lys Leu Val Asn Val Leu Asp Ala Val Glu Leu Val Asp
50 55 60

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

Glu Lys Phe Arg Asp Ile Thr Lys Phe Ile Pro Glu Asn Ile Ser Ala
85 90 95

Ala Ser Asp Ala Thr Leu Val Ile Asn Thr Glu His Met Pro Ser Met
100 105 110

Phe Val Pro Val Gly Asp Val Val Gln Tyr Gly Phe Leu Asn Leu Ser
115 120 125

Gly Lys Pro Thr His Arg Thr Met Met Tyr Asn Phe Pro Thr Lys Ala
130 135 140

Gly Gln Cys Gly Gly Val Val Thr Ser Val Gly Lys Ile Ile Gly Ile
145 150 155 160

His Ile Gly Gly Asn Gly Arg Gln Gly Phe Cys Ala Gly Leu Lys Arg
165 170 175

Ser Tyr Phe Ala Ser Glu Gln Gly Glu Ile Gln Trp Val Lys Pro Asn
180 185 190

sequence listing PCT_CA2013_050666

Lys Glu Thr Gly Arg Leu Asn Ile Asn Gly Pro Thr Arg Thr Lys Leu
195 200 205

Glu Pro Ser Val Phe His Asp Ile Phe Glu Gly Asn Lys Glu Pro Ala
210 215 220

Val Leu His Ser Lys Asp Pro Arg Leu Glu Val Asp Phe Glu Gln Ala
225 230 235 240

Leu Phe Ser Lys Tyr Val Gly Asn Thr Leu Tyr Glu Pro Asp Glu Tyr
245 250 255

Ile Lys Glu Ala Ala Leu His Tyr Ala Asn Gln Leu Lys Gln Leu Glu
260 265 270

Ile Asn Thr Ser Gln Met Ser Met Glu Glu Ala Cys Tyr Gly Thr Glu
275 280 285

Asn Leu Glu Ala Ile Asp Leu His Thr Ser Ala Gly Tyr Pro Tyr Ser
290 295 300

Ala Leu Gly Ile Lys Lys Arg Asp Ile Leu Asp Pro Thr Thr Arg Asp
305 310 315 320

Val Ser Lys Met Lys Phe Tyr Met Asp Lys Tyr Gly Leu Asp Leu Pro
325 330 335

Tyr Ser Thr Tyr Val Lys Asp Glu Leu Arg Ser Ile Asp Lys Ile Lys
340 345 350

Lys Gly Lys Ser Arg Leu Ile Glu Ala Ser Ser Leu Asn Asp Ser Val
355 360 365

Tyr Leu Arg Met Ala Phe Gly His Leu Tyr Glu Ala Phe His Ala Asn
370 375 380

Pro Gly Thr Ile Thr Gly Ser Ala Val Gly Cys Asn Pro Asp Thr Phe
385 390 395 400

Trp Ser Lys Leu Pro Ile Leu Leu Pro Gly Ser Leu Phe Ala Phe Asp
405 410 415

Tyr Ser Gly Tyr Asp Ala Ser Leu Ser Pro Val Trp Phe Arg Ala Leu
420 425 430

Glu Leu Val Leu Arg Glu Ile Gly Tyr Ser Glu Gly Ala Val Ser Leu
435 440 445

Ile Glu Gly Ile Asn His Thr His His Val Tyr Arg Asn Lys Thr Tyr
450 455 460

sequence listing PCT_CA2013_050666

Cys Val Leu Gly Gly Met Pro Ser Gly Cys Ser Gly Thr Ser Ile Phe
465 470 475 480

Asn Ser Met Ile Asn Asn Ile Ile Ile Arg Ala Leu Leu Ile Lys Thr
485 490 495

Phe Lys Gly Ile Asp Leu Asp Glu Leu Asn Met Val Ala Tyr Gly Asp
500 505 510

Asp Val Leu Ala Ser Tyr Pro Phe Pro Ile Asp Cys Leu Glu Leu Ala
515 520 525

Lys Thr Gly Lys Glu Tyr Gly Leu Thr Met Thr Pro Ala Asp Lys Ser
530 535 540

Pro Cys Phe Asn Glu Val Asn Trp Gly Asn Ala Thr Phe Leu Lys Arg
545 550 555 560

Gly Phe Leu Pro Asp Glu Gln Phe Pro Phe Leu Ile His Pro Thr Met
565 570 575

Pro Met Arg Glu Ile His Glu Ser Ile Arg Trp Thr Lys Asp Ala Arg
580 585 590

Asn Thr Gln Asp His Val Arg Ser Leu Cys Leu Leu Ala Trp His Asn
595 600 605

Gly Lys Gln Glu Tyr Glu Lys Phe Val Ser Thr Ile Arg Ser Val Pro
610 615 620

Val Gly Arg Ala Leu Ala Ile Pro Asn Tyr Glu Asn Leu Arg Arg Asn
625 630 635 640

Trp Leu Glu Leu Phe
645

<210> 2
<211> 1935
<212> DNA
<213> Enterovirus A71

<400> 2
ggccccgagcc ttgattttgc cctctcccta ctgaggagga acgtcaggca agtccaaaca 60
gaccaggggc atttcacat gttgggtgtt agggatcgct tagcagtcct cccacgccac 120
tcacaacccg gcaaaactat ttggattgag cacaaactcg tgaacgtcct tgatgcagtt 180
gaattggtgg atgagcaagg agtcaacctg gagttaacct tcatcactct tgacactaac 240
gaaaagttaa gggatatcac caaattcatc ccagaaaata ttagtgctgc cagtgatgcc 300
accctagtga tcaacacgga gcacatgccc tcaatgtttg tcccgggtgg tgacgttgtg 360

sequence listing PCT_CA2013_050666

```

cagtattggct tcttgaacct cagtggcaag cctacccatc gcaccatgat gtacaacttt      420
cctactaaag caggacagtg tgggggagtg gtgacatctg ttgggaagat tatcgggtatt      480
cacattgggtg gcaatggcag acaagggtttt tgcgcaggcc tcaaaaggag ttactttgct      540
agtgaacaag gagagatcca gtgggttaag cccaataaag aaactggaag actcaacatc      600
aatggaccaa cccgcaccaa gctagaaccc agtgtattcc atgatatctt tgaggggaaat      660
aaggagccag ctgtcttgca cagtaaagac ccccgacttg aggtagattt tgaacaggcc      720
ctgttctcta agtatgtggg gaatacacta tatgagcctg acgagtacat caaagaggca      780
gctcttcatt atgcaaacca attaaagcag ctagaaatca acacctctca aatgagcatg      840
gaggaggcct gctacggtac tgagaatctt gaggctattg atcttcatac tagtgaggt      900
taccctata gtgccctggg gataaagaaa agagacatct tagaccctac caccagggac      960
gtgagtaaaa tgaagttcta catggacaaa tatggctctg atctccctta ctccacttat     1020
gtcaaggacg agctgcgctc aattgataaa attaagaaa ggaagtcccg tctgattgag     1080
gccagtagtt taaatgattc agtgtacctt agaatggcct tcggtcattt gtatgaggct     1140
ttccacgcaa atcctgggac tataactgga tcagccgtgg ggtgtaaccc tgacacattc     1200
tgagcaagc tgccaatttt gctccctggg tcaactcttg cctttgacta ctcaggttat     1260
gatgctagcc ttagccctgt ctggttcaga gcattagaat tggtccttag ggagataggg     1320
tatagtgaag gggcagtcct actcattgag ggaatcaacc acacacacca tgtgtatcgt     1380
aataagacct attgtgtgct tgggtgggatg ccctcaggct gctcgggaac atccattttc     1440
aactcaatga tcaacaacat tattatcaga gcaactgctc taaaaacatt taagggcatt     1500
gatttgatg aactcaacat ggtcgcttat ggagatgatg tgctcgctag ctacccttc     1560
ccaattgatt gcttgagatt agcgaagact ggcaaggagt atgggtctaac catgaccct     1620
gcgataagt ctccttgctt taatgaagtt aattggggta atgcgacctt tctcaagagg     1680
ggctttttac ccgatgaaca gtttccattt ttgatccacc ccactatgcc aatgaggggag     1740
atccatgagt ccattcgatg gaccaaggat gcacgaaaca ctcaagatca tgtgcggtcc     1800
ttgtgcctcc tagcatggca taatggtaag caagaatatg agaaatttgt gagtacaatt     1860
aggtctgtcc cagtgggaag agcgttggct atcccaaatt atgaaaacct tagacgtaat     1920
tggtcagagt tttt                                     1935

```

<210> 3
 <211> 645
 <212> PRT
 <213> Enterovirus A71
 <400> 3

Gly Pro Ser Leu Asp Phe Ala Leu Ser Leu Leu Arg Arg Asn Ile Arg
 1 5 10 15

Gln Val Gln Thr Asp Gln Gly His Phe Thr Met Leu Gly Val Arg Asp
 20 25 30

sequence listing PCT_CA2013_050666

Arg Leu Ala Val Leu Pro Arg His Ser Gln Pro Gly Lys Thr Ile Trp
35 40 45

Ile Glu His Lys Leu Val Asn Ile Leu Asp Ala Val Glu Leu Val Asp
50 55 60

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

Glu Lys Phe Arg Asp Ile Thr Lys Phe Ile Pro Glu Ser Ile Ser Thr
85 90 95

Ala Ser Asp Ala Thr Leu Val Ile Asn Thr Glu His Met Pro Ser Met
100 105 110

Phe Val Pro Val Gly Asp Val Val Gln Tyr Gly Phe Leu Asn Leu Ser
115 120 125

Gly Lys Pro Thr His Arg Thr Met Met Tyr Asn Phe Pro Thr Lys Ala
130 135 140

Gly Gln Cys Gly Gly Val Val Thr Ser Val Gly Lys Val Ile Gly Ile
145 150 155 160

His Ile Gly Gly Asn Gly Arg Gln Gly Phe Cys Ala Gly Leu Lys Arg
165 170 175

Ser Tyr Phe Ala Ser Glu Gln Gly Glu Ile Gln Trp Val Lys Pro Asn
180 185 190

Lys Glu Thr Gly Arg Leu Asn Ile Asn Gly Pro Thr Arg Thr Lys Leu
195 200 205

Glu Pro Ser Val Phe His Asp Val Phe Glu Gly Asn Lys Glu Pro Ala
210 215 220

Val Leu His Gly Lys Asp Pro Arg Leu Glu Val Asp Phe Glu Gln Ala
225 230 235 240

Leu Phe Ser Lys Tyr Val Gly Asn Thr Leu Tyr Glu Pro Asp Glu Tyr
245 250 255

Ile Lys Glu Ala Ala Leu His Tyr Ala Asn Gln Leu Lys Gln Leu Glu
260 265 270

Ile Asn Thr Ser Gln Met Ser Met Glu Glu Ala Cys Tyr Gly Thr Glu
275 280 285

Asn Leu Glu Ala Ile Asp Leu His Thr Ser Ala Gly Tyr Pro Tyr Ser
290 295 300

sequence listing PCT_CA2013_050666

Ala Leu Gly Ile Lys Lys Arg Asp Ile Leu Asp Pro Thr Thr Arg Asp
305 310 315 320

Val Ser Lys Met Lys Ser Tyr Met Asp Lys Tyr Gly Leu Asp Leu Pro
325 330 335

Tyr Ser Thr Tyr Val Lys Asp Glu Leu Arg Ser Ile Asp Lys Ile Lys
340 345 350

Lys Gly Lys Ser Arg Leu Ile Glu Ala Ser Ser Leu Asn Asp Ser Val
355 360 365

Tyr Leu Arg Met Thr Phe Gly His Leu Tyr Glu Ala Phe His Ala Asn
370 375 380

Pro Gly Thr Ile Thr Gly Ser Ala Val Gly Cys Asn Pro Asp Thr Phe
385 390 395 400

Trp Ser Lys Leu Pro Ile Leu Leu Pro Gly Ser Leu Phe Ala Phe Asp
405 410 415

Tyr Ser Gly Tyr Asp Ala Ser Leu Ser Pro Val Trp Phe Arg Ala Leu
420 425 430

Glu Met Val Leu Arg Glu Ile Gly Tyr Ser Glu Glu Ala Val Ser Leu
435 440 445

Ile Glu Gly Ile Asn His Thr His His Val Tyr Arg Asn Lys Thr Tyr
450 455 460

Cys Val Leu Gly Gly Met Pro Ser Gly Cys Ser Gly Thr Ser Ile Phe
465 470 475 480

Asn Ser Met Ile Asn Asn Ile Ile Ile Arg Ala Leu Leu Ile Lys Thr
485 490 495

Phe Lys Gly Ile Asp Leu Asp Glu Leu Asn Met Val Ala Tyr Gly Asp
500 505 510

Asp Val Leu Ala Ser Tyr Pro Phe Pro Ile Asp Cys Leu Glu Leu Ala
515 520 525

Lys Thr Gly Lys Glu Tyr Gly Leu Thr Met Thr Pro Ala Asp Lys Ser
530 535 540

Pro Cys Phe Asn Glu Val Asn Trp Gly Asn Ala Thr Phe Leu Lys Arg
545 550 555 560

Gly Phe Leu Pro Asp Glu Gln Phe Pro Phe Leu Ile His Pro Thr Met
565 570 575

sequence listing PCT_CA2013_050666

Pro Met Arg Glu Ile His Glu Ser Ile Arg Trp Thr Lys Asp Ala Arg
580 585 590

Asn Thr Gln Asp His Val Arg Ser Leu Cys Leu Leu Ala Trp His Asn
595 600 605

Gly Lys Gln Glu Tyr Glu Lys Phe Val Ser Thr Ile Arg Ser Val Pro
610 615 620

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

Trp Leu Glu Leu Phe
645

<210> 4
<211> 1935
<212> DNA
<213> Enterovirus A71

<400> 4
ggccccgagtc ttgattttgc tctctccctg ttaaggagga acatcaggca agtccaaaca 60
gaccagggggc atttcacccat gttgggtgtt agggatcgtt tagcagtcct cccacgtcac 120
tcacaacccg gcaaaaactat ttggatcgaa caaaaactcg tgaacattct tgatgcagtt 180
gaattggtgg atgagcaagg agtcaacctg gaattgacct tcatcactct tgacactaac 240
gaaaagttta gggatatcac caaatccatc ccagaaagta ttagcactgc cagtgatgcc 300
accctagtga tcaacacgga gcacatgccc tcaatgtttg tcccgggtggg tgacgtcgtg 360
cagtatggct ttttgaatct tagtggcaag cccacccatc gcacccatgat gtacaacttt 420
cctactaaag cgggacagtg tggaggagta gtgacatctg ttgggaaagt catcggtatt 480
cacattggtg gcaatggtag acaagggtttt tgcgcaggcc tcaaaaggag ttactttgct 540
agtgaacaag gggagatcca gtgggttaag cccaataaag aaactggaag actcaacatc 600
aatggaccaaa cccgcaccaa gttggaacct agtgtattcc atgatgtctt cgaggggaaat 660
aaggaaccag ctgtcttgca cggcaaagat ccccgactcg aggtagattt tgagcaggcc 720
ctgttctcta agtatgtggg aaacacgcta tatgagcctg acgagtacat caaagaggca 780
gctcttcatt atgcaaatca attaaagcaa ctagaaatta atacctcca gatgagcatg 840
gaggaagcct gctatggtac tgagaatctt gaggctatcg atcttcatac tagtgcaggt 900
taccctata gtgccctggg aataaagaaa agagacatct tagaccctac caccagggac 960
gtgagtaaaa tgaaatccta tatggacaaa tatggtctcg atctccctta ctccacttat 1020
gtcaaggatg agctgcgctc aattgataaa attaagaaag ggaagtcccg tctgatcgag 1080
gccagcagtt taaatgattc agtgtacctc agaatgactt tcggtcattt gtatgaggct 1140
ttccacgcaa atcctgggac gataactgga tcagccgtgg ggtgtaacct tgacacattc 1200

sequence listing PCT_CA2013_050666

tgagcaagc tgccaatctt gcttcctggt tcactctttg cctttgacta ctcaggttat	1260
gatgctagcc ttagccctgt ctggttcaga gcattagaaa tggtccttag ggagataggg	1320
tatagtgaag aggcggtctc actcattgag ggaatcaacc acacacacca cgtgtatcgt	1380
aacaagacct atttgtgtgct tgggtgggatg ccctcaggct gttcgggaac atccatcttc	1440
aactcaatga tcaacaacat tattatcaga gcactgctca taaaaacatt taagggcatt	1500
gatttgatg aactcaacat ggtcgcttat ggggatgatg tgcttgctag ctacccttc	1560
ccaatcgatt gcttggagtt agcaaagact ggcaaggagt atggtctgac catgactcct	1620
gcagataagt ccccttgctt taatgaagt aattggggta atgcgacctt cctcaagagg	1680
ggctttttac ctgatgagca gtttccattt ttgatccacc ctactatgcc aatgcgggag	1740
atccatgaat ccattcgatg gactaaggac gcacgaaaca ctcaagatca tgtacggtcc	1800
ttgtgcctcc tagcatggca taatggtaag caagaatatg aaaaatttgt gagcacaatt	1860
aggctctgtcc caataggaag agctttggct atcccaaatt atgaaaatct tagacgcaat	1920
tggtctgagt ttttt	1935

<210> 5
 <211> 862
 <212> PRT
 <213> Enterovirus A71

<400> 5

Met Gly Ser Gln Val Ser Thr Gln Arg Ser Gly Ser His Glu Asn Ser	
1 5 10 15	

Asn Ser Ala Thr Glu Gly Ser Thr Ile Asn Tyr Thr Thr Ile Asn Tyr	
20 25 30	

Tyr Lys Asp Ser Tyr Ala Ala Thr Ala Gly Lys Gln Ser Leu Lys Gln	
35 40 45	

Asp Pro Asp Lys Phe Ala Asn Pro Val Lys Asp Ile Phe Thr Glu Met	
50 55 60	

Ala Ala Pro Leu Lys Ser Pro Ser Ala Glu Ala Cys Gly Tyr Ser Asp	
65 70 75 80	

Arg Val Ala Gln Leu Thr Ile Gly Asn Ser Thr Ile Thr Thr Gln Glu	
85 90 95	

Ala Ala Asn Ile Ile Val Gly Tyr Gly Glu Trp Pro Ser Tyr Cys Ser	
100 105 110	

Asp Ser Asp Ala Thr Ala Val Asp Lys Pro Thr Arg Pro Asp Val Ser	
115 120 125	

Val Asn Arg Phe Tyr Thr Leu Asp Thr Lys Leu Trp Glu Lys Ser Ser	
130 135 140	

sequence listing PCT_CA2013_050666

Lys Gly Trp Tyr Trp Lys Phe Pro Asp Val Leu Thr Glu Thr Gly Val
 145 150 155 160
 Phe Gly Gln Asn Ala Gln Phe His Tyr Leu Tyr Arg Ser Gly Phe Cys
 165 170 175
 Ile His Val Gln Cys Asn Ala Ser Lys Phe His Gln Gly Ala Leu Leu
 180 185 190
 Val Ala Val Leu Pro Glu Tyr Val Ile Gly Thr Val Ala Gly Gly Thr
 195 200 205
 Gly Thr Glu Asp Ser His Pro Pro Tyr Lys Gln Thr Gln Pro Gly Ala
 210 215 220
 Asp Gly Phe Glu Leu Gln His Pro Tyr Val Leu Asp Ala Gly Ile Pro
 225 230 235 240
 Ile Ser Gln Leu Thr Val Cys Pro His Gln Trp Ile Asn Leu Arg Thr
 245 250 255
 Asn Asn Cys Ala Thr Ile Ile Val Pro Tyr Ile Asn Ala Leu Pro Phe
 260 265 270
 Asp Ser Ala Leu Asn His Cys Asn Phe Gly Leu Leu Val Val Pro Ile
 275 280 285
 Ser Pro Leu Asp Tyr Asp Gln Gly Ala Thr Pro Val Ile Pro Ile Thr
 290 295 300
 Ile Thr Leu Ala Pro Met Cys Ser Glu Phe Ala Gly Leu Arg Gln Ala
 305 310 315 320
 Val Thr Gln Gly Phe Pro Thr Glu Leu Lys Pro Gly Thr Asn Gln Phe
 325 330 335
 Leu Thr Thr Asp Asp Gly Val Ser Ala Pro Ile Leu Pro Asn Phe His
 340 345 350
 Pro Thr Pro Cys Ile His Ile Pro Gly Glu Val Arg Asn Leu Leu Glu
 355 360 365
 Leu Cys Gln Val Glu Thr Ile Leu Glu Val Asn Asn Val Pro Thr Asn
 370 375 380
 Ala Thr Ser Leu Met Glu Arg Leu Arg Phe Pro Val Ser Ala Gln Ala
 385 390 395 400
 Gly Lys Gly Glu Leu Cys Ala Val Phe Arg Ala Asp Pro Gly Arg Asn
 405 410 415

sequence listing PCT_CA2013_050666

Gly Pro Trp Gln Ser Thr Leu Leu Gly Gln Leu Cys Gly Tyr Tyr Thr
420 425 430

Gln Trp Ser Gly Ser Leu Glu Val Thr Phe Met Phe Thr Gly Ser Phe
435 440 445

Met Ala Thr Gly Lys Met Leu Ile Ala Tyr Thr Pro Pro Gly Gly Pro
450 455 460

Leu Pro Lys Asp Arg Ala Thr Ala Met Leu Gly Thr His Val Ile Trp
465 470 475 480

Asp Phe Gly Leu Gln Ser Ser Val Thr Leu Val Ile Pro Trp Ile Ser
485 490 495

Asn Thr His Tyr Arg Ala His Ala Arg Asp Gly Val Phe Asp Tyr Tyr
500 505 510

Thr Thr Gly Leu Val Ser Ile Trp Tyr Gln Thr Asn Tyr Val Val Pro
515 520 525

Ile Gly Ala Pro Asn Thr Ala Tyr Ile Ile Ala Leu Ala Ala Ala Gln
530 535 540

Lys Asn Phe Thr Met Lys Leu Cys Lys Asp Ala Ser Asp Ile Leu Gln
545 550 555 560

Thr Gly Thr Ile Gln Gly Asp Arg Val Ala Asp Val Ile Glu Ser Ser
565 570 575

Ile Gly Asp Ser Val Ser Arg Ala Leu Thr Gln Ala Leu Pro Ala Pro
580 585 590

Thr Gly Gln Asn Thr Gln Val Ser Ser His Arg Leu Asp Thr Gly Lys
595 600 605

Val Pro Ala Leu Gln Ala Ala Glu Ile Gly Ala Ser Ser Asn Ala Ser
610 615 620

Asp Glu Ser Met Ile Glu Thr Arg Cys Val Leu Asn Ser His Ser Thr
625 630 635 640

Ala Glu Thr Thr Leu Asp Ser Phe Phe Ser Arg Ala Gly Leu Val Gly
645 650 655

Glu Ile Asp Leu Pro Leu Glu Gly Thr Thr Asn Pro Asn Gly Tyr Ala
660 665 670

Asn Trp Asp Ile Asp Ile Thr Gly Tyr Ala Gln Met Arg Arg Lys Val
675 680 685

sequence listing PCT_CA2013_050666

Glu Leu Phe Thr Tyr Met Arg Phe Asp Ala Glu Phe Thr Phe Val Ala
690 695 700

Cys Thr Pro Thr Gly Glu Val Val Pro Gln Leu Leu Gln Tyr Met Phe
705 710 715 720

Val Pro Pro Gly Ala Pro Lys Pro Asp Ser Arg Glu Ser Leu Ala Trp
725 730 735

Gln Thr Ala Thr Asn Pro Ser Val Phe Val Lys Leu Ser Asp Pro Pro
740 745 750

Ala Gln Val Ser Val Pro Phe Met Ser Pro Ala Ser Ala Tyr Gln Trp
755 760 765

Phe Tyr Asp Gly Tyr Pro Thr Phe Gly Glu His Lys Gln Glu Lys Asp
770 775 780

Leu Glu Tyr Gly Ala Cys Pro Asn Asn Met Met Gly Thr Phe Ser Val
785 790 795 800

Arg Thr Val Gly Thr Ser Lys Ser Lys Tyr Pro Leu Val Val Arg Ile
805 810 815

Tyr Met Arg Met Lys His Val Arg Ala Trp Ile Pro Arg Pro Met Arg
820 825 830

Asn Gln Asn Tyr Leu Phe Lys Ala Asn Pro Asn Tyr Ala Gly Asn Ser
835 840 845

Ile Lys Pro Thr Gly Thr Ser Arg Thr Ala Ile Thr Thr Leu
850 855 860

<210> 6
<211> 2586
<212> DNA
<213> Enterovirus A71

<400> 6
atgggttcgc aggtgtccac gcagcgctcc ggttctcatg aaaattcaaa ctgagccacc 60
gagggttcca ccataaacta caccaccatt aattattaca aagactccta tgctgccaca 120
gcaggcaaac agagtctcaa gcaggatcca gacaagtttg caaatcctgt taaagacatc 180
ttcactgaaa tggcagcgcc actgaagtcc ccatccgctg aggcatgtgg atacagtgat 240
cgagtagcgc aattaactat tggtaactcc accatcacca cgcaagaagc ggctaacatc 300
atagttggtt atggtgagtg gccttcctac tgctcggatt ctgacgtac agcagtggat 360
aagccaacgc gcccggatgt ttcagtgaac aggttttata cattggacac taaattgtgg 420
gagaaatcgt ccaagggatg gtactggaaa ttcccggatg tgtaactga aactgggggtt 480

540 ttgggcaaa atgcacaatt ccactaccct tacggatcag ggttcctgtat ccacgtgcag

600 tgcattgtcta gtaattcca ccaaggagca ctcttagtcg ctgttctacc agagtacgtc

660 attggacag tggcaggcgg cacaggagcg gaagatagtc accccctta caagcagact

720 caacccggcg ccgattgctt cgaattgcaa caccgtagc tgccttgatgc tggcatccca

780 atatacagt taacagtgtg cccacatcag tggatttaatt tgaagaccaa caattgtgct

840 acaataatag tgcatacat taacgcactg ccttttgatt ccgacctgaa ccactgcaat

900 ttggccctat tagttgtcc tatagccca ctagattacg accaaggagc gacgccagta

960 atccctataa ctatcacatt agcccgaatg tgttctgaaat tcgcaggctc taggcaggca

1020 gtacgcgaag gatttccac cgaattgaaa cctggcaca aaataatttt aaccactgat

1080 gatggcgttt cagcacctat tctaccaaac ttccaccca cccgctgtat ccataacct

1140 ggtgaagtta ggaacttgct agattatgc caggtgaaaa ccatcctaga ggttaacaat

1200 gtgccccaag atgccactag ttaattgag agactgcgt ttccagttc agcacaagca

1260 gggaaagtgt agctgtgtgc ggtgttcaga gctgattcctg ggcgaatgg gccgtggcag

1320 tccaccttgc tgggtcagtt gttgtgggtat tacacccaat ggtcaggtac attggaagtc

1380 accttcagt ttacttgatc ctttatgct accggcaaga tgcctcatagc ctatacacgg

1440 ccaggaggcc cttggcccaa ggaacgggcg accgcatgt tgggcacgca cgtcatcttg

1500 gattttgggc tgcattcgtc cgttaacctt gtaataccat ggtacagcaa cactcactac

1560 agagcgcgatg cccgagatgg agttttgac tactacacca cagggttagt cagtatatgg

1620 tatagacaa attacgttgt tccaattggg gcgcctaata cagcctatat aatagcacta

1680 gcggcagccc aaaaagaatt cactatgaag ttgtgcaagg atgctagtga taccctacaa

1740 accggcca ca tccagggaga taggttagca gatgtaattg aaagttccat aggggtagc

1800 gtgagcagag cctcatca agcttacca gcaaccacag gccagaacac acaggttagc

1860 agtcatcgac tggatatag caagttcca gcactccaag ctgctgaaat tggagcatca

1920 tcaatgtcta gtgacggagag catgatcgag acacgctgtg ttcttaact gcacagcaca

1980 gctgagacca ctcttgatag ttcttcagc agagcgggat tagttgaga gatagatctt

2040 cctcttgaag gcacaactaa cccaatgtgt tatgccaaat gggaacataga tataacaggt

2100 tacgcacaaa tgcgcagaaa gttgaggtta ttcaacctaca tgcgctttga tgcagagttc

2160 actttcgttg cgtgcacacc tacggggaaa gttgtccca aattgctcca atatatgttt

2220 gtaccacctg gagccctaa gccagactcc agggagctcc tgcattgca aaccgccacc

2280 aacccctcag tttttgtcaa gttgtcagac cctccagcac aggtttcagt accattcatg

2340 tcaaccgcga gtgttacca atgtttctat gacggatatc ccacattcgg ggaacacaaa

2400 caggagaag atcttgagta tggggcgtgc cctaataaca tgaatggtaac gttctcagtg

2460 cggactgtag ggacttccaa atccaagtat ccttagtggt ttaggattta catgaggatg

2520 aagcacgtca gggcgtggat acctcgcccg atgcgtaac aaactacct attcaaggcc

sequence listing PCT_CA2013_050666
 2580 aacccaatt atgctggca ctcattaa ccaactggta ctatcgcac agcgatcact
 2586 actctt

<210> 7
 <211> 1932
 <212> DNA
 <213> Enterovirus C
 <400> 7

ggaccagggt tcgattacgc agtggctatg gctaagaaga acattgttac agcaactact
 60
 agcaaggag agttcactat gttaggagtc cagacaacg tggctattt accaaccac
 120
 gcttcacctg gtgaagcat tgtgatcgat ggcaagaag tggagatctt ggatgccaaa
 180
 gcgctcgag atcaagcagg aaccaatct gaaatcata taatcactct aaagagaat
 240
 gaaagttca gagacattag accacatata cctactcaaa tcactgagac aatgatgga
 300
 gtcttgatcg tgaacattag caagtacccc aatatgtatg ttccgtgcgg tgcgtgact
 360
 gaacagggat atctaactc cgttgggcgc caaactgctc gtaacttaat gtacaacttt
 420
 ccaaccagag caggacagt tggtagagtc atcacatgta ctgggaagt catcgggatg
 480
 catgttgggt ggaacggttc acacgggttt gcagcgggcc tgaagcgatc atacttact
 540
 cagagtcaag gtgaatcca gtgtagtga ccttcgaag aagtgggata tccaatcata
 600
 aatgcccggt ccaaaacca gcttgaacc agtgccttcc actatgtgtt tgaagggtg
 660
 aaggaaaccag cagtccctac taaaaacgat ccaggtcta agacagactt tgaaggagca
 720
 attttctcca agtacgttgg taacaaaat actgaagtg atgagtacat gaaagagca
 780
 gtagaccact atgttgcca gctcatgtca ctagacatca acacagaaca aatgtgcctg
 840
 gaggatgcca tgtatggcac tgatgtcta gaagcactg attgttccac cagtgcctggc
 900
 tacccttatg tagcaatggg aaagaagag agagacatct tgaacaaaac aaccagagac
 960
 actaaggaaa tgcaaaaact gctgcacaca tatggaatca acctccact ggtgacttat
 1020
 gtaaggatg aacttagtc caaaacaag gttagagcag ggaatccag attaattgaa
 1080
 gcttctagt tgaatgactc agtggcaatg agaattgctt ttgggaacct atatgctgct
 1140
 ttccaacaaa acccaggagt gataacaggt tcagcagtgg ggtgcgattc agatttgttt
 1200
 tggagcaaaa ttccggtatt gatggaagag aagctgtttg ctittgacta cacagggtat
 1260
 gatgcatctc tcagccctgc ttggttcgag gcactaaaga tgggtcttga gaaatcggg
 1320
 ttccggagca gatttgacta catcgactac ctaaaccaact cacaccaact gtaacaagaat
 1380
 aaaaacatact gtgtcaaggg cgttatgcc tctggctgct cagycacttc aatttttaac
 1440
 tcaatgatta acaacttgat tatcaggaca ctcttactga aaacctacaa gggcatagat
 1500
 ttgagccacc taaaaatgat tgccatggt gatgagttaa ttgcttccca ccccatgaa
 1560
 gttgacgcta gtctcctagc ccaatcagga aaagactatg gactaacat gactccagct
 1620
 gacaatcag ctacattga aacagtccaca tgggagaatg taacattctt gaagagattc
 1680
 ttcaaggcag acgagaata cccatttctt attcatccag taatgccaat gaaggaattt
 1740

sequence listing PCT_CA2013_050666

catgaatcaa ttagatggac taaagatcct aggaacactc aggatcacgt tcgctctctg 1800
 tgccttttag cttggcaca tggcgaagaa gaatataaca aattcctagc taaaatcagg 1860
 agtgtgccaa ttggaagagc tttattgctc ccagagtact caacattgta ccgccgttgg 1920
 cttgactcat tt 1932

<210> 8
 <211> 644
 <212> PRT
 <213> Enterovirus C

<400> 8

Gly Pro Gly Phe Asp Tyr Ala Val Ala Met Ala Lys Arg Asn Ile Val
 1 5 10 15

Thr Ala Thr Thr Ser Lys Gly Glu Phe Thr Met Leu Gly Val His Asp
 20 25 30

Asn Val Ala Ile Leu Pro Thr His Ala Ser Pro Gly Glu Ser Ile Val
 35 40 45

Ile Asp Gly Lys Glu Val Glu Ile Leu Asp Ala Lys Ala Leu Glu Asp
 50 55 60

Gln Ala Gly Thr Asn Leu Glu Ile Thr Ile Ile Thr Leu Lys Arg Asn
 65 70 75 80

Glu Lys Phe Arg Asp Ile Arg Pro His Ile Pro Thr Gln Ile Thr Glu
 85 90 95

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

Tyr Val Pro Val Gly Ala Val Thr Glu Gln Gly Tyr Leu Asn Leu Gly
 115 120 125

Gly Arg Gln Thr Ala Arg Thr Leu Met Tyr Asn Phe Pro Thr Arg Ala
 130 135 140

Gly Gln Cys Gly Gly Val Ile Thr Cys Thr Gly Lys Val Ile Gly Met
 145 150 155 160

His Val Gly Gly Asn Gly Ser His Gly Phe Ala Ala Ala Leu Lys Arg
 165 170 175

Ser Tyr Phe Thr Gln Ser Gln Gly Glu Ile Gln Trp Met Arg Pro Ser
 180 185 190

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

sequence listing PCT_CA2013_050666

Glu Pro Ser Ala Phe His Tyr Val Phe Glu Gly Val Lys Glu Pro Ala
 210 215 220
 Val Leu Thr Lys Asn Asp Pro Arg Leu Lys Thr Asp Phe Glu Glu Ala
 225 230 235 240
 Ile Phe Ser Lys Tyr Val Gly Asn Lys Ile Thr Glu Val Asp Glu Tyr
 245 250 255
 Met Lys Glu Ala Val Asp His Tyr Ala Gly Gln Leu Met Ser Leu Asp
 260 265 270
 Ile Asn Thr Glu Gln Met Cys Leu Glu Asp Ala Met Tyr Gly Thr Asp
 275 280 285
 Gly Leu Glu Ala Leu Asp Leu Ser Thr Ser Ala Gly Tyr Pro Tyr Val
 290 295 300
 Ala Met Gly Lys Lys Lys Arg Asp Ile Leu Asn Lys Gln Thr Arg Asp
 305 310 315 320
 Thr Lys Glu Met Gln Lys Leu Leu Asp Thr Tyr Gly Ile Asn Leu Pro
 325 330 335
 Leu Val Thr Tyr Val Lys Asp Glu Leu Arg Ser Lys Thr Lys Val Glu
 340 345 350
 Gln Gly Lys Ser Arg Leu Ile Glu Ala Ser Ser Leu Asn Asp Ser Val
 355 360 365
 Ala Met Arg Met Ala Phe Gly Asn Leu Tyr Ala Ala Phe His Lys Asn
 370 375 380
 Pro Gly Val Ile Thr Gly Ser Ala Val Gly Cys Asp Pro Asp Leu Phe
 385 390 395 400
 Trp Ser Lys Ile Pro Val Leu Met Glu Glu Lys Leu Phe Ala Phe Asp
 405 410 415
 Tyr Thr Gly Tyr Asp Ala Ser Leu Ser Pro Ala Trp Phe Glu Ala Leu
 420 425 430
 Lys Met Val Leu Glu Lys Ile Gly Phe Gly Asp Arg Val Asp Tyr Ile
 435 440 445
 Asp Tyr Leu Asn His Ser His His Leu Tyr Lys Asn Lys Thr Tyr Cys
 450 455 460
 Val Lys Gly Gly Met Pro Ser Gly Cys Ser Gly Thr Ser Ile Phe Asn
 465 470 475 480

sequence listing PCT_CA2013_050666

Ser Met Ile Asn Asn Leu Ile Ile Arg Thr Leu Leu Leu Lys Thr Tyr
485 490 495

Lys Gly Ile Asp Leu Asp His Leu Lys Met Ile Ala Tyr Gly Asp Asp
500 505 510

Val Ile Ala Ser Tyr Pro His Glu Val Asp Ala Ser Leu Leu Ala Gln
515 520 525

Ser Gly Lys Asp Tyr Gly Leu Thr Met Thr Pro Ala Asp Lys Ser Ala
530 535 540

Thr Phe Glu Thr Val Thr Trp Glu Asn Val Thr Phe Leu Lys Arg Phe
545 550 555 560

Phe Arg Ala Asp Glu Lys Tyr Pro Phe Leu Ile His Pro Val Met Pro
565 570 575

Met Lys Glu Ile His Glu Ser Ile Arg Trp Thr Lys Asp Pro Arg Asn
580 585 590

Thr Gln Asp His Val Arg Ser Leu Cys Leu Leu Ala Trp His Asn Gly
595 600 605

Glu Glu Glu Tyr Asn Lys Phe Leu Ala Lys Ile Arg Ser Val Pro Ile
610 615 620

Gly Arg Ala Leu Leu Leu Pro Glu Tyr Ser Thr Leu Tyr Arg Arg Trp
625 630 635 640

Leu Asp Ser Phe

<210> 9
<211> 2643
<212> DNA
<213> Enterovirus C

<400> 9
atgggtgctc aggtttcatc acagaaagtg ggcgcacatg aaaactcaaa tagagcgtat 60
ggtggttcta ccattaatta caccaccatt aattattata gagattcagc tagtaacgcg 120
gcttcgaaac aggacttctc tcaagaccct tccaagttca ccgagcccat caaggatgtc 180
ctgataaaaa cagccccaat gctaaactcg ccaaacatag aggcttgcg gtagatcgat 240
agagtactgc aattaacact gggaaactcc actataacca cacaggaggc ggctaattca 300
gtagtcgctt atgggcggtt gcctgaatat ctgagggaca gcgaagccaa tccagtggac 360
cagccgacag aaccagacgt cgctgcatgc aggttttata cgctagacac cgtgtcttgg 420
acgaaagagt cgcgaggggt gtggtggaag ttgcctgatg cactgagggg catgggactc 480
tttgggcaaa atatgtacta ccactaccta ggtaggtccg ggtacaccgt gcatgtacag 540

sequence listing PCT_CA2013_050666

tgtaacgcct ccaaattcca ccagggggca ctaggggtat tcgccgtacc agagatgtgt	600
ctggccgggg atagcaacac cactaccatg cacaccagct atcaaaatgc caatcctggc	660
gagaaaggag gcactttcac gggtagcttc actcctgaca acaaccagac atcacctgcc	720
cgcaggttct gcccgggtga ttacctcctt ggaaatggca cgttgttggg gaatgccttt	780
gtgttccccg accagataat aaacctacgg accaacaact gtgctacact ggtactccct	840
tacgtgaact ccctctcgat agatagtatg gtaaagcaca ataattgggg aattgcaata	900
ttaccattgg ccccatataa ttttgctagt gagtcctccc cagagattcc aatcaccttg	960
accatagccc ctatgtgctg tgagttcaat ggattaagaa acatcacctt gccacgctta	1020
cagggcctgc cgggtcatgaa caccctgggt agcaatcaat atcttactgc agacaacttc	1080
cagtcaccgt gtgcgctgcc tgaatttgat gtgacccac ctattgacat acccggtgaa	1140
gtaaagaaca tgatggaatt ggcagaaatc gacaccatga ttccctttga cttagtgc	1200
acaaaaaaga acaccatgga aatgtatagg gttcgggttaa gtgacaaacc acatacagac	1260
gatcccatac tctgcctgtc actctctcca gcttcagatc ctaggttgtc acatactatg	1320
cttgagagaaa tcctaaatta ctacacacac tgggcaggat ccctgaagtt cacgtttctg	1380
ttctgtggat tcatgatggc aactggcaaa ctgttggtgt ctagcgcc tcctggagcc	1440
gacccaccaaa agaagcgtaa ggaggcgatg ttgggaacac atgtgatctg ggacatagga	1500
ctgcagtcct catgtactat ggtagtgcca tggattagca acaccacgta tcggcaaacc	1560
atagatgata gtttcaccga aggcgggatac atcagcgtct tctaccaaac tagaatagtc	1620
gtccctcttt cgacaccag agagatggac atccttggtt ttgtgtcagc gtgtaatgac	1680
ttcagcgtgc gcttgttgcg agataccaca catatagagc aaaaagcgct agcacagggg	1740
ttaggtcaga tgcttgaaag catgattgac aacacagtcc gtgaaacggt gggggcggca	1800
acatctagag acgctctccc aaacactgaa gccagtggac caacacactc caaggaaatt	1860
ccggcactca ccgcagtgga aactggggcc acaaaccac tagtcccttc tgatacagtg	1920
caaaccagac atgttgatac acataggtca aggtcagagt ctagcataga gtctttcttc	1980
gcgcgggggtg catgcgtgac cattatgacc gtggataacc cagcttcac cacgaataag	2040
gataagctat ttgcagtgtg gaagatcact tataaagata ctgtccagtt acggaggaaa	2100
ttggagttct tcacctattc tagatttgat atggaactta ctttgtggt tactgcaaat	2160
ttcactgaga ctaacaatgg gcatgcctta aatcaagtgt accaaattat gtacgtacca	2220
ccaggcgctc cagtggccga gaaatgggac gactacacat ggcaaaccct atcaaatcca	2280
tcaatctttt acacctacgg aacagctcca gcccgatct cggtaccgta tgttggtatt	2340
tcgaacgcct attcacactt ttacgacggt ttttcaaag taccactgaa ggaccagtcg	2400
gcagcactag gtgactccct ttatggtgca gcatctctaa atgacttcgg tattttggct	2460
gttagagtag tcaatgatca caaccgacc aaggtcacct ccaaaatcag agtgtatcta	2520
aaacccaaac acatcagagt ctggtgcccg cgtccaccga gggcagtggc gtactacggc	2580

sequence listing PCT_CA2013_050666

cctggagtg attacaagga tggtacgctt acaccctct ccaccaagga tctgaccaca 2640
tat 2643

<210> 10
<211> 881
<212> PRT
<213> Enterovirus C

<400> 10

Met Gly Ala Gln Val Ser Ser Gln Lys Val Gly Ala His Glu Asn Ser
1 5 10 15

Asn Arg Ala Tyr Gly Gly Ser Thr Ile Asn Tyr Thr Thr Ile Asn Tyr
20 25 30

Tyr Arg Asp Ser Ala Ser Asn Ala Ala Ser Lys Gln Asp Phe Ser Gln
35 40 45

Asp Pro Ser Lys Phe Thr Glu Pro Ile Lys Asp Val Leu Ile Lys Thr
50 55 60

Ala Pro Met Leu Asn Ser Pro Asn Ile Glu Ala Cys Gly Tyr Ser Asp
65 70 75 80

Arg Val Leu Gln Leu Thr Leu Gly Asn Ser Thr Ile Thr Thr Gln Glu
85 90 95

Ala Ala Asn Ser Val Val Ala Tyr Gly Arg Trp Pro Glu Tyr Leu Arg
100 105 110

Asp Ser Glu Ala Asn Pro Val Asp Gln Pro Thr Glu Pro Asp Val Ala
115 120 125

Ala Cys Arg Phe Tyr Thr Leu Asp Thr Val Ser Trp Thr Lys Glu Ser
130 135 140

Arg Gly Trp Trp Trp Lys Leu Pro Asp Ala Leu Arg Asp Met Gly Leu
145 150 155 160

Phe Gly Gln Asn Met Tyr Tyr His Tyr Leu Gly Arg Ser Gly Tyr Thr
165 170 175

Val His Val Gln Cys Asn Ala Ser Lys Phe His Gln Gly Ala Leu Gly
180 185 190

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

Thr Met His Thr Ser Tyr Gln Asn Ala Asn Pro Gly Glu Lys Gly Gly
210 215 220

sequence listing PCT_CA2013_050666

Thr Phe Thr Gly Thr Phe Thr Pro Asp Asn Asn Gln Thr Ser Pro Ala
225 230 235 240

Arg Arg Phe Cys Pro Val Asp Tyr Leu Leu Gly Asn Gly Thr Leu Leu
245 250 255

Gly Asn Ala Phe Val Phe Pro His Gln Ile Ile Asn Leu Arg Thr Asn
260 265 270

Asn Cys Ala Thr Leu Val Leu Pro Tyr Val Asn Ser Leu Ser Ile Asp
275 280 285

Ser Met Val Lys His Asn Asn Trp Gly Ile Ala Ile Leu Pro Leu Ala
290 295 300

Pro Leu Asn Phe Ala Ser Glu Ser Ser Pro Glu Ile Pro Ile Thr Leu
305 310 315 320

Thr Ile Ala Pro Met Cys Cys Glu Phe Asn Gly Leu Arg Asn Ile Thr
325 330 335

Leu Pro Arg Leu Gln Gly Leu Pro Val Met Asn Thr Pro Gly Ser Asn
340 345 350

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

Phe Asp Val Thr Pro Pro Ile Asp Ile Pro Gly Glu Val Lys Asn Met
370 375 380

Met Glu Leu Ala Glu Ile Asp Thr Met Ile Pro Phe Asp Leu Ser Ala
385 390 395 400

Thr Lys Lys Asn Thr Met Glu Met Tyr Arg Val Arg Leu Ser Asp Lys
405 410 415

Pro His Thr Asp Asp Pro Ile Leu Cys Leu Ser Leu Ser Pro Ala Ser
420 425 430

Asp Pro Arg Leu Ser His Thr Met Leu Gly Glu Ile Leu Asn Tyr Tyr
435 440 445

Thr His Trp Ala Gly Ser Leu Lys Phe Thr Phe Leu Phe Cys Gly Phe
450 455 460

Met Met Ala Thr Gly Lys Leu Leu Val Ser Tyr Ala Pro Pro Gly Ala
465 470 475 480

Asp Pro Pro Lys Lys Arg Lys Glu Ala Met Leu Gly Thr His Val Ile
485 490 495

sequence listing PCT_CA2013_050666

Trp Asp Ile Gly Leu Gln Ser Ser Cys Thr Met Val Val Pro Trp Ile
500 505 510

Ser Asn Thr Thr Tyr Arg Gln Thr Ile Asp Asp Ser Phe Thr Glu Gly
515 520 525

Gly Tyr Ile Ser Val Phe Tyr Gln Thr Arg Ile Val Val Pro Leu Ser
530 535 540

Thr Pro Arg Glu Met Asp Ile Leu Gly Phe Val Ser Ala Cys Asn Asp
545 550 555 560

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

Leu Ala Gln Gly Leu Gly Gln Met Leu Glu Ser Met Ile Asp Asn Thr
580 585 590

Val Arg Glu Thr Val Gly Ala Ala Thr Ser Arg Asp Ala Leu Pro Asn
595 600 605

Thr Glu Ala Ser Gly Pro Thr His Ser Lys Glu Ile Pro Ala Leu Thr
610 615 620

Ala Val Glu Thr Gly Ala Thr Asn Pro Leu Val Pro Ser Asp Thr Val
625 630 635 640

Gln Thr Arg His Val Val Gln His Arg Ser Arg Ser Glu Ser Ser Ile
645 650 655

Glu Ser Phe Phe Ala Arg Gly Ala Cys Val Thr Ile Met Thr Val Asp
660 665 670

Asn Pro Ala Ser Thr Thr Asn Lys Asp Lys Leu Phe Ala Val Trp Lys
675 680 685

Ile Thr Tyr Lys Asp Thr Val Gln Leu Arg Arg Lys Leu Glu Phe Phe
690 695 700

Thr Tyr Ser Arg Phe Asp Met Glu Leu Thr Phe Val Val Thr Ala Asn
705 710 715 720

Phe Thr Glu Thr Asn Asn Gly His Ala Leu Asn Gln Val Tyr Gln Ile
725 730 735

Met Tyr Val Pro Pro Gly Ala Pro Val Pro Glu Lys Trp Asp Asp Tyr
740 745 750

Thr Trp Gln Thr Ser Ser Asn Pro Ser Ile Phe Tyr Thr Tyr Gly Thr
755 760 765

sequence listing PCT_CA2013_050666

Ala Pro Ala Arg Ile Ser Val Pro Tyr Val Gly Ile Ser Asn Ala Tyr
770 775 780

Ser His Phe Tyr Asp Gly Phe Ser Lys Val Pro Leu Lys Asp Gln Ser
785 790 795 800

Ala Ala Leu Gly Asp Ser Leu Tyr Gly Ala Ala Ser Leu Asn Asp Phe
805 810 815

Gly Ile Leu Ala Val Arg Val Val Asn Asp His Asn Pro Thr Lys Val
820 825 830

Thr Ser Lys Ile Arg Val Tyr Leu Lys Pro Lys His Ile Arg Val Trp
835 840 845

Cys Pro Arg Pro Pro Arg Ala Val Ala Tyr Tyr Gly Pro Gly Val Asp
850 855 860

Tyr Lys Asp Gly Thr Leu Thr Pro Leu Ser Thr Lys Asp Leu Thr Thr
865 870 875 880

Tyr