

SEQUENCE LISTING

<110> APPLIED MOLECULAR TRANSPORT INC.

<120> COMPOSITIONS, FORMULATIONS, AND INTERLEUKIN PRODUCTION AND
PURIFICATION

<130> 40566-721.601

<140>

<141>

<150> 63/055,886

<151> 2020-07-23

<150> 63/033,077

<151> 2020-06-01

<150> 63/020,996

<151> 2020-05-06

<150> 63/013,309

<151> 2020-04-21

<150> 62/986,579

<151> 2020-03-06

<150> 62/971,126

<151> 2020-02-06

<150> 62/970,627

<151> 2020-02-05

<150> 62/939,495

<151> 2019-11-22

<150> 62/898,934

<151> 2019-09-11

<150> 62/898,709

<151> 2019-09-11

<150> 62/898,729

<151> 2019-09-11

<150> 62/898,899

<151> 2019-09-11

<150> 62/888,144

<151> 2019-08-16

<150> 62/888,237
<151> 2019-08-16

<150> 62/887,963
<151> 2019-08-16

<150> 62/887,933
<151> 2019-08-16

<160> 156

<170> PatentIn version 3.5

<210> 1
<211> 178
<212> PRT
<213> Homo sapiens

<400> 1

Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
1 5 10 15

Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
20 25 30

Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
35 40 45

Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
50 55 60

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

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
85 90 95

Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
100 105 110

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

Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
 130 135 140

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
 145 150 155 160

Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
 165 170 175

Arg Asn

<210> 2

<211> 160

<212> PRT

<213> Homo sapiens

<400> 2

Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
 1 5 10 15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
 20 25 30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
 35 40 45

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
 50 55 60

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
 65 70 75 80

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

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
 100 105 110

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145 150 155 160

<210> 3

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 3

Val Glu Glu Ala Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 4
<211> 386
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 4
Val Glu Glu Ala Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala
 385

<210> 5

<211> 561

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 5

Met Val Glu Glu Ala Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys
1 5 10 15

Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile
20 25 30

Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr
35 40 45

Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser
50 55 60

Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr
65 70 75 80

Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr
85 90 95

Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe
100 105 110

Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile
115 120 125

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

Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp
145 150 155 160

Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn
165 170 175

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

Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu
195 200 205

Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln
210 215 220

Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val
225 230 235 240

Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys
245 250 255

Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala
260 265 270

Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg
275 280 285

Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln
290 295 300

Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser
305 310 315 320

His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu
325 330 335

Val Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro
340 345 350

Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp
355 360 365

Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly
370 375 380

Ala Gln Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe
405 410 415

Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser
420 425 430

Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu
435 440 445

Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln
450 455 460

Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln
465 470 475 480

Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly
485 490 495

Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe
500 505 510

Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala
515 520 525

Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe
530 535 540

Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg
545 550 555 560

Asn

<210> 6
<211> 14

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 6

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

<210> 7

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (1)..(60)

<223> This sequence may encompass 1-15 "Gly Gly Gly Ser" repeating units

<400> 7

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
20 25 30

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
35 40 45

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
50 55 60

<210> 8

<211> 75

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (1)..(75)

<223> This sequence may encompass 1-15 "Gly Gly Gly Gly Ser" repeating units

<400> 8

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75

<210> 9

<211> 90

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<220>

<221> MISC_FEATURE

<222> (1)..(90)

<223> This sequence may encompass 1-15 "Gly Gly Gly Gly Gly Ser" repeating units

<400> 9

Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly

1	5	10	15
Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly	20	25	30
Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser	35	40	45
Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly	50	55	60
Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly	65	70	75
Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser	85	90	

<210> 10
 <211> 1683
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 10	
atggtagaag aagcgctgaa tatttttgac gagtgtcgta gcccgtagtag cctgactccg	60
gaaccgggca agccgattca gtccaaactg tctatcccga gcgacgttgt gctggatgag	120
ggcgtgttgt attacagcat gacgatcaat gatgagcaaa acgacatcaa agacgaagat	180
aagggtgagt ctattatcac cattggcgag tttgcgacgg tgcgtgcaac gcgccattac	240
gtgaatcaag acgcgccgtt tgggtgtcatt cacctggata tcacgaccga aaatggcacg	300
aaaacctatt cgtataatcg caaagagggc gagttcgcga tcaactggct ggttccgatac	360
ggtgaggata gcccggcgag catcaagatc agcgttgatg aactggatca gcagcgcaac	420
attattgaag tcccgaagtt gtatagcatc gacctggata atcagaccct ggagcagtgg	480
aaaaccagg gtaacgttag cttctccgtg acccgccgg agcacaacat tgccattagc	540

tggccgagcg ttagctacaa agccgcacag aaagagggtt cccgccacaa gcgttgggct	600
cattggcata ccggtttggc gctgtgttgg ctggtgccga tggatgcat ctataactac	660
atcacgcagc aaaattgcac gctgggtgac aattggttcg gtggcagcta cgagactgtg	720
gcgggtaccc ctaaggttat taccgtcaaa cagggtattg agcaaaagcc tgtcgagcag	780
cgtatccact ttagcaaggg taacgccatg tctgctctgg cggctcatag agtttgcggc	840
gttccgctgg agactctggc ccgttcccgc aagccgcgtg acctgaccga tgacctgagc	900
tgcgcgtatc aagcgcaaaa cattgttagc ttattcgttg cgacgcgcac tttgttttcg	960
cacctggata gcgtgttcac gctgaacctg gatgaacagg aaccagaagt ggcagagcgt	1020
ctgtcagatc tgcgtcgtat caacgaaaac aaccggggca tggttaccca ggtccttacg	1080
gttgcacgcc agatttacia tgattacgtg acccatcacc cgggtctgac cccagaacaa	1140
accagcgagc gcgcacaagc ggggtggcggg ggttccgggt gcggtggtag cgggtggcggg	1200
ggtagccctg gtcaaggcac ccaatccgag aatagctgca cgcattttcc aggcaatctg	1260
ccgaatatgc tgcgtgacct ccgcgacgcg ttctctcgtg ttaagacctt ttttcagatg	1320
aaagaccagc tggacaatct gctgctgaaa gaatccctgc tggaagattt caaaggctat	1380
ctgggttgcc aggccctgag cgagatgac caattctact tggaagagggt catgccgcag	1440
gccgaaaatc aagaccggga catcaaggca cacgtgaaca gcttgggcga aaacctgaaa	1500
accctgcgtt tgcgcctgcg tcgttgtcac cgtttctgc cgtgcgagaa taagagcaaa	1560
gccgtcgaac aagtcaaaaa tgcattcaac aagctgcaag agaaaggat ctacaaggct	1620
atgagcgagt ttgacatttt cattaactac attgaagcgt acatgaccat gaagatccgt	1680
aac	1683

<210> 11

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 11

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

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 12
<211> 386
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 12
Leu Glu Glu Ala Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala
385

<210> 13

<211> 561

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 13

Met Leu Glu Glu Ala Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys
1 5 10 15

Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile
20 25 30

Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr
35 40 45

Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser
50 55 60

Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr
65 70 75 80

Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr
85 90 95

Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe
100 105 110

Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile
115 120 125

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

Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp
145 150 155 160

Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn
165 170 175

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

Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu
195 200 205

Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln
210 215 220

Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val
225 230 235 240

Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys
245 250 255

Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala
260 265 270

Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg
275 280 285

Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln
290 295 300

Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser
305 310 315 320

His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu
325 330 335

Val Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro
340 345 350

Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp
355 360 365

Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly
370 375 380

Ala Gln Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
385 390 395 400

Gly Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe
405 410 415

Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser
420 425 430

Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu
435 440 445

Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln
450 455 460

Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln
465 470 475 480

Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly
485 490 495

Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe
500 505 510

Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala
515 520 525

Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe
530 535 540

Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg
545 550 555 560

Asn

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 14
gctcattgct gggacttac aa 22

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 15
ccagacttgg cacaagacag g 21

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 16
cacagcagca catcaacaag 20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 17
gtgctcatgt cctcatcctg 20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 18
tgtgtccgtc gtggatctga 20

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 19
cctgcttcac caccttcttg a

21

<210> 20
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 20
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
 145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
 165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
 195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
 210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Ala Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Leu Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 21
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 21
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Ala Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Val Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Asn Gly Gly Leu Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 22

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 22

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Glu Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Asn Gly Gly Leu Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Asp Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 23

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 23

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Met Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Tyr Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Arg Val
565 570 575

Asp Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Pro Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 24
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 24
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

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

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Ala Val
 325 330 335

Ala Glu Arg Leu Ser Ala Ile Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asp Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 25
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 25
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
 65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
 85 90 95

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

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
 115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
 130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys His
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 26
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 26
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp Arg Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Glu Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
 610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 27

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 27

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Asn Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 28

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 28

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Leu Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 29
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 29
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Lys Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 30
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 30
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
 65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
 85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
 100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
 115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
 130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile Tyr Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 31
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 31
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Ala Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 32

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 32

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile Tyr Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 33

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 33

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Lys Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 34
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 34
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Glu Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Arg Val
565 570 575

Asp Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 35
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 35
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
 65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
 85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
 100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
 115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
 130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Asn Gly Gly Leu Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Asp Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 36
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 36
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile His Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Glu Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
 610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 37

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 37

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Ile Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 38

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 38

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Phe Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 39
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 39
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Asn Ala
 290 295 300

Gln Gln Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Thr His
 305 310 315 320

Ile Asp Ser Ile Phe Thr Leu Asn Leu Asp Gly Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Asp Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Ile Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Gln Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Gln Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Ser Ile Val Asn Arg Ile Ser Pro Val Pro Arg Gly
465 470 475 480

Ser Asp Thr Glu Ser Glu Arg Ala Trp Gly Gly Leu Tyr Val Ser Thr
485 490 495

Asp Ala Ser Val Ala Tyr Gly Tyr Ala Arg Ile Gln Glu Gly Thr Ala
500 505 510

Asp Gly Gly Gly Leu Thr Pro Ala Glu Arg Lys Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Leu Pro Gln Ala Ser Leu Glu Arg Phe Tyr Arg Ile
530 535 540

Asn Ala Asp Leu Glu Lys Glu Arg Asn Leu Val Glu Arg Val Ile Gly
545 550 555 560

His Pro Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Thr Asp Ala Glu
565 570 575

Glu Gly Ser Asp Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 40
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 40
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
 65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
 85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
 100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
 115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
 130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
 610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 41
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 41
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Ala Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asp Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
 610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 42

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 42

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Asn Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 43

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 43

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Ile Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 44
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 44
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 45
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 45
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
 65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
 85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
 100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
 115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
 130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Thr Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 46
 <211> 634
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 46
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 47

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 47

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Thr Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
 515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
 530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
 545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 48

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 48

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Leu
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
 485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
 500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 49
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 49
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Ile Pro Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Thr Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 50
 <211> 633
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 50
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
 65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
 85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
 100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
 115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
 130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
 595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
 610 615 620

Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 51
 <211> 633
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 51
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Gln Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
 515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
 595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
 610 615 620

Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 52

<211> 633

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 52

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
 515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
610 615 620

Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 53

<211> 633

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 53

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
610 615 620

Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 54
<211> 633
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 54
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
 225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
 245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
 260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
 290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
610 615 620

Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 55
<211> 633
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 55
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Ile Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
 595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
 610 615 620

Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 625 630

<210> 56
 <211> 633
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 56
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Ile Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
 515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
 595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
 610 615 620

Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 57

<211> 633

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 57

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Glu Val
195 200 205

Val Leu Cys Phe Phe Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Asn Ala Gln Gln Ile Val Ser Leu
290 295 300

Phe Leu Ala Thr Arg Ile Leu Phe Thr His Ile Asp Ser Ile Phe Thr
305 310 315 320

Leu Asn Leu Asp Gly Gln Glu Pro Glu Val Ala Glu Arg Leu Asp Asp
325 330 335

Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val Ile Gln Val Leu
340 345 350

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Ser
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Gln Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Gln Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
 515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
610 615 620

Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 58

<211> 633

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 58

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys Asp Gly
180 185 190

Ala Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Leu Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Met Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Gly
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Gln Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Thr Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Ile Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr Glu His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Glu Ser
385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Lys His Gln Thr
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Ser Ile Val Asn Arg Ile Thr Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Lys Glu Glu Glu Trp Gly Gly Val Tyr Val Ala Thr
485 490 495

His Ala Glu Leu Ala His Arg Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

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

Leu Arg Val Tyr Leu Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Ile Pro Leu Glu Asn Ala Asp Glu His Val Thr Gln Val Ile Gly
545 550 555 560

His Pro Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu His Asp Glu Leu Lys
625 630

<210> 59
<211> 633
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 59
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys Asp Gly
180 185 190

Ala Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Leu Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Met Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Gly
 275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Gln Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Thr Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Ile Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr Glu His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Glu Ser
 385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Lys His Gln Thr
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Ser Ile Val Asn Arg Ile Thr Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Lys Glu Glu Glu Trp Gly Gly Val Tyr Val Ala Thr
485 490 495

His Ala Glu Val Asn His Arg Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

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

Leu Arg Val Tyr Leu Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Ile Pro Leu Glu Asn Ala Asp Glu His Val Thr Gln Val Ile Gly
545 550 555 560

His Pro Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu His Asp Glu Leu Lys
625 630

<210> 60
<211> 633
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 60
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys Asp Gly
180 185 190

Ala Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Leu Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Met Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Gly
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Gln Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Thr Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Ile Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr Glu His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Glu Ser
385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Lys His Gln Thr
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Ser Ile Val Asn Arg Ile Thr Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Lys Glu Glu Glu Trp Gly Gly Val Tyr Val Ala Thr
485 490 495

His Ala Glu Leu Ala His Arg Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

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

Leu Lys Val Tyr Leu Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Ile Pro Leu Glu Asn Ala Asp Glu His Val Thr Gln Val Ile Gly
 545 550 555 560

His Pro Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
 565 570 575

Gly Gly Glu Asn Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly
 580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro
 595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
 610 615 620

Pro Tyr Lys Glu His Asp Glu Leu Lys
 625 630

<210> 61
 <211> 633
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 61
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
 515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
 595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
 610 615 620

Tyr Lys Glu Gln Lys Asp Glu Leu Lys
 625 630

<210> 62

<211> 633

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 62

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Ile Pro Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
 515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ala Tyr Glu Gly Leu Thr Thr Asp Glu Glu Ala Val
595 600 605

Val Lys Glu Ala Ile Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
610 615 620

Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 63

<211> 633

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 63

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Ile Pro Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys Asp Gly
180 185 190

Ala Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Leu Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Met Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Gly
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Gln Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Thr Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Ile Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr Glu His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Glu Ser
385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Lys His Gln Thr
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Ser Ile Val Asn Arg Ile Thr Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Lys Glu Glu Glu Trp Gly Gly Val Tyr Val Ala Thr
485 490 495

His Ala Glu Leu Ala His Arg Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

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

Leu Arg Val Tyr Leu Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Ile Pro Leu Glu Asn Ala Asp Glu His Val Thr Gln Val Ile Gly
545 550 555 560

His Pro Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu His Asp Glu Leu Lys
625 630

<210> 64
<211> 628
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 64
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
 225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
 245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
 260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
 290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys
610 615 620

Asp Glu Leu Lys
625

<210> 65
<211> 628
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 65
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys
 610 615 620

Asp Glu Leu Lys
 625

<210> 66

<211> 628

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 66

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Asn Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Val Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys
 610 615 620

Asp Glu Leu Lys
 625

<210> 67

<211> 628

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 67

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Lys Val
195 200 205

Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Asn Gly Gly Leu Pro Thr
 500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
610 615 620

Asp Glu Leu Lys
625

<210> 68

<211> 628

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 68

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Arg Val Asp Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys
610 615 620

Asp Glu Leu Lys
625

<210> 69
<211> 628
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 69
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Met Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
 225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
 245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
 260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
 290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Arg Val Asp Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys
610 615 620

Asp Glu Leu Lys
625

<210> 70
<211> 628
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 70
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Lys Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Lys Val
195 200 205

Val Leu Cys Phe Tyr Glu Glu Pro Glu Leu Cys Thr Tyr Gly Glu Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Glu Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Gln Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Ala Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
 610 615 620

Asp Glu Leu Lys
 625

<210> 71
 <211> 628
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 71
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Glu Val
195 200 205

Val Leu Cys Phe Phe Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Asn Ala Gln Gln Ile Val Ser Leu
290 295 300

Phe Leu Ala Thr Arg Ile Leu Phe Thr His Ile Asp Ser Ile Phe Thr
305 310 315 320

Leu Asn Leu Asp Gly Gln Glu Pro Glu Val Ala Glu Arg Leu Asp Asp
325 330 335

Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val Ile Gln Val Leu
340 345 350

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Ser
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Gln Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Gln Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Ser Ile
450 455 460

Val Asn Arg Ile Ser Pro Val Pro Arg Gly Ser Asp Thr Glu Ser Glu
465 470 475 480

Arg Ala Trp Gly Gly Leu Tyr Val Ser Thr Asp Ala Ser Val Ala Tyr
485 490 495

Gly Tyr Ala Arg Ile Gln Glu Gly Thr Ala Asp Gly Gly Gly Leu Thr
500 505 510

Pro Ala Glu Arg Lys Ala Arg Gly Val Met Leu Arg Val Tyr Leu Pro
515 520 525

Gln Ala Ser Leu Glu Arg Phe Tyr Arg Ile Asn Ala Asp Leu Glu Lys
530 535 540

Glu Arg Asn Leu Val Glu Arg Val Ile Gly His Pro Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Thr Asp Ala Glu Glu Gly Ser Asp Glu Thr
565 570 575

Ala Ile Gly Trp Asp Met Ala Ile His Gly Val Ala Ile Pro Ser Thr
580 585 590

Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro Ile Asp Glu Glu Ala Val
595 600 605

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
610 615 620

Asp Glu Leu Lys
625

<210> 72

<211> 628

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 72

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Glu Val
195 200 205

Val Leu Cys Phe Phe Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Asn Ala Gln Gln Ile Val Ser Leu
290 295 300

Phe Leu Ala Thr Arg Ile Leu Phe Thr His Ile Asp Ser Ile Phe Thr
305 310 315 320

Leu Asn Leu Asp Gly Gln Glu Pro Glu Val Ala Glu Arg Leu Asp Asp
325 330 335

Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val Ile Gln Val Leu
340 345 350

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Leu
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Ser
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Gln Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Gln Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Ser Ile
 450 455 460

Val Asn Arg Ile Ser Pro Val Pro Arg Gly Ser Asp Thr Glu Ser Glu
 465 470 475 480

Arg Ala Trp Gly Gly Leu Tyr Val Ser Thr Asp Ala Ser Val Ala Tyr
 485 490 495

Gly Tyr Ala Arg Ile Gln Glu Gly Thr Ala Asp Gly Gly Gly Leu Thr
 500 505 510

Pro Ala Glu Arg Lys Ala Arg Gly Val Met Leu Arg Val Tyr Leu Pro
 515 520 525

Gln Ala Ser Leu Glu Arg Phe Tyr Arg Ile Asn Ala Asp Leu Glu Lys
 530 535 540

Glu Arg Asn Leu Val Glu Arg Val Ile Gly His Pro Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Thr Asp Ala Glu Glu Gly Ser Asp Glu Thr
 565 570 575

Ala Ile Gly Trp Asp Met Ala Ile His Gly Val Ala Ile Pro Ser Thr
 580 585 590

Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro Ile Asp Glu Glu Ala Val
595 600 605

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
610 615 620

Asp Glu Leu Lys
625

<210> 73

<211> 628

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 73

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Glu Val
195 200 205

Val Leu Cys Phe Phe Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Asn Ala Gln Gln Ile Val Ser Leu
290 295 300

Phe Leu Ala Thr Arg Ile Leu Phe Thr His Ile Asp Ser Ile Phe Thr
 305 310 315 320

Leu Asn Leu Asp Gly Gln Glu Pro Glu Val Ala Glu Arg Leu Asp Asp
 325 330 335

Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val Ile Gln Val Leu
 340 345 350

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Ser
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Gln Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Gln Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Ser Ile
 450 455 460

Val Asn Arg Ile Ser Pro Val Pro Arg Gly Ser Asp Thr Glu Ser Glu
 465 470 475 480

Arg Ala Trp Gly Gly Leu Tyr Val Ser Thr Asp Ala Ser Val Ala Tyr
 485 490 495

Gly Tyr Ala Arg Ile Gln Glu Gly Thr Ala Asp Gly Gly Gly Leu Thr
 500 505 510

Pro Ala Glu Arg Lys Ala Arg Gly Val Met Leu Arg Val Tyr Leu Pro
515 520 525

Gln Ala Ser Leu Glu Arg Phe Tyr Arg Ile Asn Ala Asp Leu Glu Lys
530 535 540

Glu Arg Asn Leu Val Glu Arg Val Ile Gly His Pro Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Thr Asp Ala Glu Glu Gly Ser Asp Glu Thr
565 570 575

Ala Ile Gly Trp Asp Met Ala Ile His Gly Val Ala Ile Pro Ser Thr
580 585 590

Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro Ile Asp Glu Glu Ala Val
595 600 605

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
610 615 620

Asp Glu Leu Lys
625

<210> 74
<211> 628
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 74
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Phe Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Lys Val
195 200 205

Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
 225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
 245 250 255

Phe Ser Lys Lys Asn Ala Ile Glu Ala Leu Ala Ala His Arg Val Cys
 260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
 290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Ala Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys
610 615 620

Asp Glu Leu Lys
625

<210> 75
<211> 628
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 75
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro Lys Val
195 200 205

Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly Asp Asp
210 215 220

Trp Tyr Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Thr Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Asp Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys
 610 615 620

Asp Glu Leu Lys
 625

<210> 76
 <211> 628
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 76
 Val Glu Asp Glu Leu Lys Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Lys Val
195 200 205

Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
500 505 510

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
610 615 620

Asp Glu Leu Lys
625

<210> 77

<211> 628

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 77

Val Glu Asp Glu Leu Lys Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Lys Val
195 200 205

Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
305 310 315 320

Leu Asn Leu Asp Glu Gln Ala Pro Glu Val Ala Glu Arg Leu Ser Asp
325 330 335

Leu Arg Arg Ile Asn Glu Asp Asn Pro Gly Met Val Thr Gln Val Leu
340 345 350

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Thr Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Arg Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
 515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
 530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
 545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
 565 570 575

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
 580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
610 615 620

Asp Glu Leu Lys
625

<210> 78

<211> 628

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 78

Val Glu Asp Glu Leu Lys Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Lys Val
195 200 205

Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly Asp Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys Ala Ile
225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Ala Val Glu Gln Arg Ile His
245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
260 265 270

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
 435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
 450 455 460

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
 465 470 475 480

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
 485 490 495

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Asn Gly Gly Leu Pro Thr
 500 505 510

Arg Ala Glu Arg Glu Thr Arg Gly Val Met Leu Arg Val Tyr Ile Pro
515 520 525

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
530 535 540

Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
545 550 555 560

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
565 570 575

Val Ile Gly Trp Asp Met Ala Ile Tyr Ala Val Ala Ile Pro Ser Thr
580 585 590

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

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
610 615 620

Asp Glu Leu Lys
625

<210> 79
<211> 617
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 79
Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro Gly
1 5 10 15

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

Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile Ile
35 40 45

Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val Ser
50 55 60

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

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

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

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

Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys Thr
130 135 140

Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile Ala
145 150 155 160

Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys Glu Gly Ser
165 170 175

Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys Trp
180 185 190

Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn Cys
195 200 205

Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala Gly
210 215 220

Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro Val
 225 230 235 240

Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala
 245 250 255

Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg
 260 265 270

Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Asn Ala Gln
 275 280 285

Gln Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Thr His Ile
 290 295 300

Asp Ser Ile Phe Thr Leu Asn Leu Asp Gly Gln Glu Pro Glu Val Ala
 305 310 315 320

Glu Arg Leu Asp Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met
 325 330 335

Val Ile Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val
 340 345 350

Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln
 355 360 365

Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys
 370 375 380

Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser
 385 390 395 400

Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Gln Gln Gly
 405 410 415

Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu
 420 425 430

Thr Gln Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val
435 440 445

Ala Ala Gln Ser Ile Val Asn Arg Ile Ser Pro Val Pro Arg Gly Ser
450 455 460

Asp Thr Glu Ser Glu Arg Ala Trp Gly Gly Leu Tyr Val Ser Thr Asp
465 470 475 480

Ala Ser Val Ala Tyr Gly Tyr Ala Arg Ile Gln Glu Gly Thr Ala Asp
485 490 495

Gly Gly Gly Leu Thr Pro Ala Glu Arg Lys Ala Arg Gly Val Met Leu
500 505 510

Arg Val Tyr Leu Pro Gln Ala Ser Leu Glu Arg Phe Tyr Arg Ile Asn
515 520 525

Ala Asp Leu Glu Lys Glu Arg Asn Leu Val Glu Arg Val Ile Gly His
530 535 540

Pro Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Thr Asp Ala Glu Glu
545 550 555 560

Gly Ser Asp Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly Val
565 570 575

Ala Ile Pro Ser Thr Ile Pro Gly Asn Ser Tyr Ala Gln Leu Pro Ile
580 585 590

Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro
595 600 605

Tyr Lys Glu Gln Lys Asp Glu Leu Lys
610 615

<210> 80

<211> 605

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 80

Ser Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser
1 5 10 15

Met Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly
20 25 30

Glu Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg
35 40 45

His Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile
50 55 60

Thr Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly
65 70 75 80

Glu Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala
85 90 95

Ser Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile
100 105 110

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

Gln Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu
130 135 140

His Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln
145 150 155 160

Lys Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu
165 170 175

Ala Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr
180 185 190

Gln Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu
195 200 205

Thr Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu
210 215 220

Gln Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met
225 230 235 240

Glu Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu
245 250 255

Ala Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala
260 265 270

Tyr Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu
275 280 285

Phe Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu
290 295 300

Pro Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn
305 310 315 320

Asn Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr
325 330 335

Asn Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser
340 345 350

Ala Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala
355 360 365

Asp Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile
370 375 380

Glu Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile
385 390 395 400

Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr
405 410 415

His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly
420 425 430

Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val
435 440 445

Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr
450 455 460

Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu
465 470 475 480

Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg
485 490 495

Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe
500 505 510

Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln
515 520 525

Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro
530 535 540

Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala
545 550 555 560

Ile His Ala Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu
565 570 575

Glu Leu Ala Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser
580 585 590

Thr Lys Pro Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
595 600 605

<210> 81
<211> 594
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 81
Met Thr Ile Asn Asp Glu Gln Asn Asp Ile Met Asp Glu Gly Lys Gly
1 5 10 15

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

His Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile
35 40 45

Thr Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly
50 55 60

Glu Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala
65 70 75 80

Ser Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile
85 90 95

Glu Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu
100 105 110

Gln Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu
115 120 125

Gln Ser Ile Ala Lys Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser
130 135 140

Tyr Lys Ala Ala Gln Lys Glu Gly Ser Arg His Lys Arg Trp Ala His
145 150 155 160

Trp His Thr Gly Leu Ala Leu Cys Trp Leu Val Pro Ile Asp Ala Ile
165 170 175

Tyr Asn Tyr Ile Thr Gln Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe
180 185 190

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

Lys Gln Gly Ile Glu Gln Lys Pro Val Glu Gln Arg Ile His Phe Ser
210 215 220

Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys Gly Val
225 230 235 240

Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp
245 250 255

Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu Phe Val
260 265 270

Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr Leu Asn
275 280 285

Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala Leu Arg
290 295 300

Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln Val Leu Thr Val
305 310 315 320

Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly Leu Thr
325 330 335

Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu
340 345 350

Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn Asp Gln
355 360 365

Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu
370 375 380

Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln
385 390 395 400

Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe
405 410 415

Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn
420 425 430

Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys
435 440 445

Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr
450 455 460

Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala
465 470 475 480

Glu Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala
485 490 495

Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu
500 505 510

Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu
515 520 525

Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile
530 535 540

Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr Ile Pro
545 550 555 560

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

Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys Asp Glu
580 585 590

Leu Lys

<210> 82

<211> 588

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 82

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

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

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Thr Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Lys Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr
165 170 175

Lys Ala Ala Gln Lys Glu Gly Ser Arg His Lys Arg Trp Ala His Trp
180 185 190

His Thr Gly Leu Ala Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr
195 200 205

Asn Tyr Ile Thr Gln Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly
210 215 220

Gly Ser Tyr Glu Thr Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys
225 230 235 240

Gln Gly Ile Glu Gln Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys
245 250 255

Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys Gly Val Pro
260 265 270

Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp
275 280 285

Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala
290 295 300

Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu
305 310 315 320

Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Asp Leu Arg Arg
325 330 335

Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln Val Leu Thr Val Ala
340 345 350

Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly Leu Thr Pro
355 360 365

Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe
370 375 380

Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala
385 390 395 400

Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn
405 410 415

Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu
420 425 430

Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val
435 440 445

Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg
450 455 460

Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp
 465 470 475 480

Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala
 485 490 495

Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu
 500 505 510

Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser
 515 520 525

Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu
 530 535 540

His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala
 545 550 555 560

Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Ile Ile Gly
 565 570 575

Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser
 580 585

<210> 83

<211> 588

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 83

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

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

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Lys Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr
165 170 175

Lys Ala Ala Gln Lys Glu Gly Ser Arg His Lys Arg Trp Ala His Trp
180 185 190

His Thr Gly Leu Ala Leu Cys Trp Leu Val Pro Met Asp Ala Ile Tyr
195 200 205

Asn Tyr Ile Thr Gln Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly
210 215 220

Gly Ser Tyr Glu Thr Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys
225 230 235 240

Gln Gly Ile Glu Gln Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys
245 250 255

Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys Gly Val Pro
260 265 270

Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp
275 280 285

Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala
290 295 300

Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu
305 310 315 320

Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln
325 330 335

Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln Val Leu Thr Val Ala
340 345 350

Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly Leu Thr Pro
355 360 365

Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe
370 375 380

Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala
385 390 395 400

Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn
405 410 415

Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu
420 425 430

Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val
435 440 445

Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg
450 455 460

Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp
465 470 475 480

Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala
485 490 495

Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu
500 505 510

Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser
515 520 525

Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu
530 535 540

His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala
545 550 555 560

Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly
565 570 575

Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser
580 585

<210> 84

<211> 588

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 84

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

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

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
 100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
 115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
 130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
 145 150 155 160

Ser Ile Ala Lys Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr
 165 170 175

Lys Ala Ala Gln Lys Glu Gly Ser Arg His Lys Arg Trp Ala His Trp
 180 185 190

His Thr Gly Leu Ala Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr
 195 200 205

Asn Tyr Ile Thr Gln Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly
 210 215 220

Gly Ser Tyr Glu Thr Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys
 225 230 235 240

Gln Gly Ile Glu Gln Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys
 245 250 255

Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys Gly Val Pro
 260 265 270

Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp
 275 280 285

Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala
 290 295 300

Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu
 305 310 315 320

Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln
 325 330 335

Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln Val Leu Thr Val Ala
 340 345 350

Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly Leu Thr Pro
 355 360 365

Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe
 370 375 380

Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala
 385 390 395 400

Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn
405 410 415

Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu
420 425 430

Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val
435 440 445

Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg
450 455 460

Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp
465 470 475 480

Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala
485 490 495

Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu
500 505 510

Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser
515 520 525

Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu
530 535 540

His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala
545 550 555 560

Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly
565 570 575

Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser
580 585

<210> 85
<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 85

Met Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly
1 5 10 15

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

His Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile
35 40 45

Thr Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly
50 55 60

Glu Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala
65 70 75 80

Ser Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile
85 90 95

Glu Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu
100 105 110

Gln Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu
115 120 125

Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His
130 135 140

Lys Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu
145 150 155 160

Pro Lys Val Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr
165 170 175

Gly Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro
180 185 190

Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Ala Val Glu Gln
195 200 205

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

Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro
225 230 235 240

Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile
245 250 255

Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser
260 265 270

Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg
275 280 285

Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr
290 295 300

Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His
305 310 315 320

His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala
325 330 335

Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala
340 345 350

Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg
355 360 365

Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr
 370 375 380

Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg
 385 390 395 400

Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala
 405 410 415

Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr
 420 425 430

Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu
 435 440 445

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

Leu Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly Val Met Leu Arg Val
 465 470 475 480

Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro
 485 490 495

Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu
 500 505 510

Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu
 515 520 525

Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile Tyr Ala Val Ala Ile
 530 535 540

Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala Ile Asp Glu
 545 550 555 560

Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys
 565 570 575

Glu Gln Lys Asp Glu Leu Lys
580

<210> 86
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 86
Met Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly
1 5 10 15

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

His Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile
35 40 45

Thr Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly
50 55 60

Glu Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala
65 70 75 80

Ser Ile Lys Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile
85 90 95

Glu Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu
100 105 110

Gln Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu
115 120 125

Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His
130 135 140

Lys Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser
145 150 155 160

Pro Lys Val Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr
165 170 175

Gly Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro
180 185 190

Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln
195 200 205

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

Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro
225 230 235 240

Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile
245 250 255

Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser
260 265 270

Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg
275 280 285

Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr
290 295 300

Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His
305 310 315 320

His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala
325 330 335

Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala
340 345 350

Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg
355 360 365

Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr
370 375 380

Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg
385 390 395 400

Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala
405 410 415

Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr
420 425 430

Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu
435 440 445

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

Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met Leu Arg Val
465 470 475 480

Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro
485 490 495

Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu
500 505 510

Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Arg Val Asp Gly Glu
515 520 525

Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile
530 535 540

Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala Ile Asp Glu
 545 550 555 560

Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro Pro Tyr Lys
 565 570 575

Glu Arg Lys Asp Glu Leu Lys
 580

<210> 87

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 87

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Gln Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
 35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
 100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Thr Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Glu Glu Gln Glu Pro
 305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
 325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Arg Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 88
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 88
Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr
 275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
 290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
 325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 89
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 89
Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
 580

<210> 90

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 90

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
 210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
 225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
 245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
 260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
 275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
 290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
 325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Ile Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Pro Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 91

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 91

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Thr Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Glu Glu Gln Glu Pro
305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Asn Gly Gly Leu Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Asp Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 92

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 92

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
 145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
 165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
 180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
 195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
 210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
 225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
 245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
 260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
 275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
 290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

Ala Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
 325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Leu Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
 580

<210> 93

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 93

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
 35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
 100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Met Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Tyr Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Arg Val Asp Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 94
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 94
Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Asp Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
 290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

Ala Val Ala Glu Arg Leu Ser Ala Ile Arg Gln Ile Asn Glu Asn Asn
 325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Ser Asp Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 95

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 95

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Asp Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Ala Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asp Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Leu Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
 580

<210> 96
 <211> 583
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 96
 Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln
 225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser
 245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
 260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr
 275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
 290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

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

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 97

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 97

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

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

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Thr Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 98
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 98
Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

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

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Tyr Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 99
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 99
Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

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

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Asn Gly Gly Leu Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
 580

<210> 100

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 100

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
 35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Lys Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
 290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

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

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 101

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 101

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
 580

<210> 102
 <211> 583
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 102
 Cys Ser Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Ser Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
 225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
 245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
 260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
 275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
 290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
 325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Pro Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 103

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 103

Cys Ser Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 104

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 104

Cys Ser Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Glu Glu Gln Glu Pro
305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 105
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 105
Cys Ser Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Ala Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asp Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
 580

<210> 106
 <211> 583
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 106
 Cys Ser Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
 35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
 305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
 325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
 340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
 355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
 370 375 380

Lys Pro Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Val Glu
 385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
 405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
 420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
 435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
 450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 107
<211> 583
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 107
Cys Ser Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Ala Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
 465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
 485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
 500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
 515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
 530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
 545 550 555 560

Arg Val Asp Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
 565 570 575

His Ala Val Ala Ile Pro Ser
 580

<210> 108

<211> 583

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 108

Cys Ser Leu Thr Pro Glu Leu Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Asp Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Lys Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His
145 150 155 160

Asn Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Gln Lys
165 170 175

Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala
180 185 190

Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln
195 200 205

Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr
210 215 220

Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln
225 230 235 240

Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu
245 250 255

Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala
260 265 270

Arg Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr
275 280 285

Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe
290 295 300

Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro
305 310 315 320

Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn
325 330 335

Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn
340 345 350

Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala
355 360 365

Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp
370 375 380

Lys Pro Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu
385 390 395 400

Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr
405 410 415

Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His
420 425 430

Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr
435 440 445

Asn His Val Ala Ala Gln Asn Ile Val Asn Arg Ile Ala Pro Val Pro
450 455 460

Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val
465 470 475 480

Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly
485 490 495

Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly
500 505 510

Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr
515 520 525

Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val
530 535 540

Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu
545 550 555 560

Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile
565 570 575

His Ala Val Ala Ile Pro Ser
580

<210> 109

<211> 582

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 109

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

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

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
 100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
 115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
 130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
 145 150 155 160

Ser Ile Ala Lys Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr
 165 170 175

Lys Ala Ala His Lys Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp
 180 185 190

Leu Thr Thr Leu Pro Lys Val Val Leu Cys Phe Phe Glu Asp Pro Glu
 195 200 205

Leu Cys Thr Tyr Gly Glu Asp Trp His Gly Gly Ala Tyr Lys Thr Val
 210 215 220

Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys
 225 230 235 240

Thr Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala
 245 250 255

Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg
 260 265 270

Ser Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln
 275 280 285

Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser
 290 295 300

His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu
 305 310 315 320

Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro
 325 330 335

Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp
 340 345 350

Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly
 355 360 365

Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys
 370 375 380

Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser
 385 390 395 400

Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro
405 410 415

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

Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn
435 440 445

His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg
450 455 460

Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala
465 470 475 480

Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr
485 490 495

Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val
500 505 510

Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg
515 520 525

Thr Asn Thr Leu Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile
530 535 540

Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser
545 550 555 560

Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His
565 570 575

Ala Val Ala Ile Pro Ser
580

<210> 110
<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 110

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro
180 185 190

Lys Val Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu
305 310 315 320

Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
 370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
 385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
 405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu
 420 425 430

Asp Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
 435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
 450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
 465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
 485 490 495

Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr
 500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
 515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
 530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
 545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
 565 570 575

Ser

<210> 111

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 111

Cys	Ser	Leu	Thr	Pro	Glu	Pro	Gly	Lys	Pro	Ile	Gln	Ser	Lys	Leu	Ser
1				5				10						15	

Ile	Pro	Ser	Asp	Val	Val	Leu	Asp	Glu	Gly	Val	Leu	Tyr	Tyr	Ser	Met
			20					25					30		

Thr	Ile	Asn	Asp	Glu	Gln	Asn	Asp	Ile	Lys	Asp	Glu	Asp	Lys	Gly	Glu
		35					40					45			

Ser	Ile	Ile	Thr	Ile	Gly	Glu	Phe	Ala	Thr	Val	Arg	Ala	Thr	Arg	His
	50					55					60				

Tyr	Val	Ser	Gln	Asp	Ala	Pro	Phe	Gly	Val	Ile	Asn	Leu	Asp	Ile	Thr
65					70					75				80	

Thr	Glu	Asn	Gly	Thr	Lys	Thr	Tyr	Ser	Phe	Asn	Arg	Lys	Glu	Ser	Glu
				85					90					95	

Phe	Ala	Ile	Asn	Trp	Leu	Val	Pro	Ile	Gly	Glu	Asp	Ser	Pro	Ala	Ser
			100					105					110		

Ile	Lys	Ile	Ser	Val	Asp	Glu	Leu	Asp	Gln	Gln	Arg	Asn	Ile	Ile	Glu
		115					120					125			

Val	Pro	Lys	Leu	Tyr	Ser	Ile	Asp	Leu	Asp	Asn	Gln	Thr	Leu	Glu	Gln
	130					135					140				

Trp Glu Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
 145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
 165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro
 180 185 190

Lys Val Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly
 195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
 210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
 225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
 245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
 260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
 290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu
 305 310 315 320

Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
 325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu
420 425 430

Asp Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Ala Ala Ala Gln
435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
485 490 495

Pro Thr Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr
500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
 545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
 565 570 575

Ser

<210> 112

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 112

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
 35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
 100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Lys Val Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu
 305 310 315 320

Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
 325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
 340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
 355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
 370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
 385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
 405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu
 420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
 435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
 450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
 465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
 485 490 495

Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr
 500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
565 570 575

Ser

<210> 113

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 113

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Lys Val Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Ala Pro Glu Val Ala Glu Arg Leu
305 310 315 320

Ser Asp Leu Arg Arg Ile Asn Glu Asp Asn Pro Gly Met Val Thr Gln
325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
405 410 415

Trp Thr Tyr Gln Glu Leu Glu Thr Thr His Gln Ala Leu Thr Arg Glu
420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
485 490 495

Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly Val Met Leu Arg Val Tyr
500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
565 570 575

Ser

<210> 114

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 114

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Lys Val Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu
305 310 315 320

Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu
420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
 450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
 465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Asn Gly Gly Leu
 485 490 495

Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly Val Met Leu Arg Val Tyr
 500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
 515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
 530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
 545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile Tyr Ala Val Ala Ile Pro
 565 570 575

Ser

<210> 115

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 115

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Ile Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Phe Thr Thr Ser Pro
180 185 190

Lys Val Thr Leu Cys Phe Tyr Glu Asp Pro Ala Gln Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Ile Pro Lys
 210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
 225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
 245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
 260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
 290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu
 305 310 315 320

Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
 325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
 340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
 355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
 370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
 385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
 405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu
420 425 430

Asp Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
485 490 495

Pro Thr Arg Ala Glu Gln Glu Thr Arg Gly Val Met Leu Arg Val Tyr
500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
565 570 575

Ser

<210> 116

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 116

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Lys Val Val Leu Cys Phe Tyr Glu Glu Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Glu Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Gly
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu
305 310 315 320

Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
 385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
 405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu
 420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
 435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
 450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
 465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
 485 490 495

Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr
 500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
 515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
 530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
 545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
 565 570 575

Ser

<210> 117

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 117

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Lys Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Lys Val Val Leu Cys Phe Tyr Glu Glu Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Glu Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Glu
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Ala Val Ala Glu Arg Leu
305 310 315 320

Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn
405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu
420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
485 490 495

Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met Leu Arg Val Tyr
500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
 545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
 565 570 575

Ser

<210> 118

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 118

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
 1 5 10 15

Ile Pro Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
 20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
 35 40 45

Ser Ile Ile Ile Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
 50 55 60

Tyr Val Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
 65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu
 85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
 100 105 110

Ile Lys Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Lys Val Val Leu Cys Phe Tyr Glu Asp Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val
290 295 300

Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu
305 310 315 320

Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln
325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
370 375 380

Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
385 390 395 400

Tyr Leu Pro Glu Asn Arg Val Val Ile Thr Pro Gln Gly Val Thr Asn
405 410 415

Trp Thr Tyr Gln Glu Leu Asp Ala Thr His Gln Ala Leu Thr Arg Glu
420 425 430

Asp Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
435 440 445

Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu
450 455 460

Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val
465 470 475 480

Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu
485 490 495

Pro Thr Arg Ala Glu Arg Glu Thr Arg Gly Val Met Leu Arg Val Tyr
500 505 510

Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu
515 520 525

Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp
545 550 555 560

Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro
565 570 575

Ser

<210> 119
<211> 577
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 119
Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Glu Val Val Leu Cys Phe Phe Glu Asp Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Thr His Ile Asp Ser Ile
 290 295 300

Phe Thr Leu Asn Leu Asp Gly Gln Glu Pro Glu Val Ala Glu Arg Leu
 305 310 315 320

Asp Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val Ile Gln
 325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
 340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp
 355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
 370 375 380

Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
 385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Gln Gln Gly Val Thr Asn
 405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Gln Glu
 420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
 435 440 445

Ser Ile Val Asn Arg Ile Ser Pro Val Pro Arg Gly Ser Asp Thr Glu
 450 455 460

Ser Glu Arg Ala Trp Gly Gly Leu Tyr Val Ser Thr Asp Ala Ser Val
 465 470 475 480

Ala Tyr Gly Tyr Ala Arg Ile Gln Glu Gly Thr Ala Asp Gly Gly Gly
485 490 495

Leu Thr Pro Ala Glu Arg Lys Ala Arg Gly Val Met Leu Arg Val Tyr
500 505 510

Leu Pro Gln Ala Ser Leu Glu Arg Phe Tyr Arg Ile Asn Ala Asp Leu
515 520 525

Glu Lys Glu Arg Asn Leu Val Glu Arg Val Ile Gly His Pro Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Thr Asp Ala Glu Glu Gly Ser Asp
545 550 555 560

Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly Val Ala Ile Pro
565 570 575

Ser

<210> 120

<211> 577

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 120

Cys Ser Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser
1 5 10 15

Ile Pro Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met
20 25 30

Thr Ile Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu
35 40 45

Ser Ile Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His
50 55 60

Tyr Val Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr
65 70 75 80

Thr Glu Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu
85 90 95

Phe Ala Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser
100 105 110

Ile Lys Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu
115 120 125

Val Pro Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln
130 135 140

Trp Glu Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln
145 150 155 160

Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys
165 170 175

Asn Gly Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro
180 185 190

Glu Val Val Leu Cys Phe Phe Glu Asp Pro Glu Leu Cys Thr Tyr Gly
195 200 205

Asp Asp Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Lys
210 215 220

Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg
225 230 235 240

Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg
245 250 255

Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys Pro Arg
260 265 270

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

Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Thr His Ile Asp Ser Ile
290 295 300

Phe Thr Leu Asn Leu Asp Gly Gln Glu Pro Glu Val Ala Glu Arg Leu
305 310 315 320

Asp Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val Ile Gln
325 330 335

Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His
340 345 350

Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Ser Ala Gln Ala Ala Asp
355 360 365

Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser
370 375 380

Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser
385 390 395 400

Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Gln Gln Gly Val Thr Asn
405 410 415

Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Gln Glu
420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln
435 440 445

Ser Ile Val Asn Arg Ile Ser Pro Val Pro Arg Gly Ser Asp Thr Glu
450 455 460

Ser Glu Arg Ala Trp Gly Gly Leu Tyr Val Ser Thr Asp Ala Ser Val
465 470 475 480

Ala Tyr Gly Tyr Ala Arg Ile Gln Glu Gly Thr Ala Asp Gly Gly Gly
485 490 495

Leu Thr Pro Ala Glu Arg Lys Ala Arg Gly Val Met Leu Arg Val Tyr
500 505 510

Leu Pro Gln Ala Ser Leu Glu Arg Phe Tyr Arg Ile Asn Ala Asp Leu
515 520 525

Glu Lys Glu Arg Asn Leu Val Glu Arg Val Ile Gly His Pro Leu Pro
530 535 540

Leu Arg Asn Glu Ala Phe Thr Gly Thr Asp Ala Glu Glu Gly Ser Asp
545 550 555 560

Glu Thr Ala Ile Gly Trp Asp Met Ala Ile His Gly Val Ala Ile Pro
565 570 575

Ser

<210> 121

<211> 531

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 121

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Gln Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Lys Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val
530

<210> 122
<211> 491
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 122
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Glu Lys Asp Gly
180 185 190

Ala Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Leu Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Met Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Gly
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Gln Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Thr Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Ile Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr Glu His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Leu Cys Pro Asp Ala Asp Gly Ser
385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Lys His Gln Thr
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Ser Ile Val Asn Arg Ile Thr Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Lys Glu Glu Glu Trp Gly Gly
485 490

<210> 123

<211> 491

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 123

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala Glu Lys Asp Gly
180 185 190

Ala Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Leu Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Met Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Gly
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Gln Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Thr Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Ile Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr Glu His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Glu Ser
 385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
 420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Lys His Gln Thr
 435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
 450 455 460

Val Ala Ala Gln Ser Ile Val Asn Arg Ile Thr Pro Val Pro Arg Gly
 465 470 475 480

Asn Asn Thr Glu Lys Glu Glu Glu Trp Gly Gly
 485 490

<210> 124

<211> 488

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 124

Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys Thr Gln
1 5 10 15

Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile Ala Ile
20 25 30

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

His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys Trp Leu
50 55 60

Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn Cys Thr
65 70 75 80

Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala Gly Thr
85 90 95

Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro Val Glu
100 105 110

Gln Arg Ile His Phe Ser Asn Gly Asn Ala Met Ser Ala Leu Ala Ala
115 120 125

His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser Arg Lys
130 135 140

Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn
145 150 155 160

Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp
165 170 175

Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu
180 185 190

Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly Met Val
195 200 205

Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr
210 215 220

His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala
225 230 235 240

Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val
245 250 255

Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly
260 265 270

Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val
275 280 285

Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr
290 295 300

Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala
305 310 315 320

Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn
325 330 335

Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala
340 345 350

Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr
355 360 365

Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met Leu Arg
 370 375 380

Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr
 385 390 395 400

Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly His Ser
 405 410 415

Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly
 420 425 430

Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala
 435 440 445

Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala Ile Asp
 450 455 460

Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr
 465 470 475 480

Lys Glu Arg Lys Asp Glu Leu Lys
 485

<210> 125

<211> 459

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:

Cholix sequence

<400> 125

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Lys Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala Ala His Lys Asn Gly
180 185 190

Ser Arg His Lys Arg Trp Ala Asn Trp Leu Thr Thr Leu Pro Lys Val
195 200 205

Val Leu Cys Phe Tyr Glu Glu Pro Glu Leu Cys Thr Tyr Gly Glu Asp
210 215 220

Trp His Gly Gly Ala Tyr Lys Thr Val Ala Gly Thr Pro Glu Ala Ile
 225 230 235 240

Thr Val Lys Gln Gly Ile Glu Gln Lys Thr Val Glu Gln Arg Ile His
 245 250 255

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
 260 265 270

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

Gln Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
 290 295 300

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
 305 310 315 320

Leu Asn Leu Asp Glu Gln Glu Pro Ala Val Ala Glu Arg Leu Ser Ala
 325 330 335

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

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
 355 360 365

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
 370 375 380

Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn
 385 390 395 400

Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu
 405 410 415

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
 420 425 430

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
435 440 445

Val Phe Val Gly Tyr His Gly Thr Asn His Val
450 455

<210> 126
<211> 415
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 126
Val Glu Glu Ala Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Gly Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Ser Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Phe Asn Arg Lys Glu Ser Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Ile Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Asn Ala
290 295 300

Gln Gln Ile Val Ser Leu Phe Leu Ala Thr Arg Ile Leu Phe Thr His
305 310 315 320

Ile Asp Ser Ile Phe Thr Leu Asn Leu Asp Gly Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Asp Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Ile Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Ser Asp Gln Ala Asn Ile Asn Ile Glu Ser
405 410 415

<210> 127

<211> 318

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 127

Leu Phe Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu His Glu Gln
1 5 10 15

Glu Pro Ala Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu
20 25 30

Asn Asn Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile
35 40 45

Tyr Asn Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr
50 55 60

Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp
65 70 75 80

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

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

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

Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His
130 135 140

Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro
145 150 155 160

Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu
165 170 175

Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys
180 185 190

Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala
195 200 205

Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg
210 215 220

Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr
225 230 235 240

Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly
245 250 255

Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met
260 265 270

Ala Ile His Ala Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr
 275 280 285

Glu Glu Leu Ala Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile
 290 295 300

Ser Ala Lys Pro Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
 305 310 315

<210> 128

<211> 208

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
 Cholix sequence

<400> 128

Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu
 1 5 10 15

Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly
 20 25 30

Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile
 35 40 45

Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly
 50 55 60

Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg
 65 70 75 80

Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg
 85 90 95

Asp Ala Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu
 100 105 110

Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His
115 120 125

Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe
130 135 140

Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp
145 150 155 160

Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr Ile Pro Gly Asn
165 170 175

Ala Tyr Glu Glu Leu Ala Ile Asp Glu Glu Ala Val Ala Lys Glu Gln
180 185 190

Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
195 200 205

<210> 129

<211> 207

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 129

Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu
1 5 10 15

Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly
20 25 30

Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile
35 40 45

Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly
50 55 60

Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg
65 70 75 80

Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg
85 90 95

Asp Ala Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu
100 105 110

Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His
115 120 125

Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe
130 135 140

Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp
145 150 155 160

Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr Ile Pro Gly Asn
165 170 175

Ala Tyr Glu Glu Leu Ala Ile Asp Glu Glu Ala Val Ala Lys Glu Gln
180 185 190

Ser Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys Asp Glu Leu
195 200 205

<210> 130
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 130
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
 210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
 225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
 245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
 260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
 275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
 290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
 305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
 325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
 340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
 355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
 370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
 385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
 405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 131
<211> 644
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 131
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Lys Gln Ser Ile Ala Lys Gln Ser Ile Ala Ile Ser Trp Pro Ser
180 185 190

Val Ser Tyr Lys Ala Ala Gln Lys Glu Gly Ser Arg His Lys Arg Trp
195 200 205

Ala His Trp His Thr Gly Leu Ala Leu Cys Trp Leu Val Pro Ile Asp
210 215 220

Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn Cys Thr Leu Gly Asp Asn
225 230 235 240

Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala Gly Thr Pro Lys Ala Ile
245 250 255

Thr Val Lys Gln Gly Ile Glu Gln Lys Pro Val Glu Gln Arg Ile His
260 265 270

Phe Ser Lys Lys Asn Ala Met Glu Ala Leu Ala Ala His Arg Val Cys
275 280 285

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

Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu
305 310 315 320

Phe Val Ala Thr Arg Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr
325 330 335

Leu Asn Leu Asp Glu Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala
340 345 350

Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly Met Val Thr Gln Val Leu
355 360 365

Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly
370 375 380

Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu
385 390 395 400

Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro Cys Val Ala Ser Asn Asn
405 410 415

Asp Gln Ala Asn Ile Asn Val Glu Ser Arg Ser Gly Arg Ser Tyr Leu
420 425 430

Pro Glu Asn Arg Ala Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr
435 440 445

Tyr Gln Glu Leu Glu Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr
450 455 460

Val Phe Val Gly Tyr His Gly Thr Asn His Val Ala Ala Gln Thr Ile
465 470 475 480

Val Asn Arg Ile Ala Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu
485 490 495

Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr His Ala Glu Val Ala His
500 505 510

Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr
515 520 525

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

Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn
545 550 555 560

Ala Glu Arg His Ile Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg
565 570 575

Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr
580 585 590

Val Ile Gly Trp Asp Met Ala Ile His Ala Val Ala Ile Pro Ser Thr
595 600 605

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

Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys
625 630 635 640

Asp Glu Leu Lys

<210> 132

<211> 639

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 132

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Met Asp Glu Gly Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ala Val Thr Arg Pro Glu Gln Ser Ile
165 170 175

Ala Lys Gln Ser Ile Ala Ile Ser Trp Pro Ser Val Ser Tyr Lys Ala
180 185 190

Ala Gln Lys Glu Gly Ser Arg His Lys Arg Trp Ala His Trp His Thr
195 200 205

Gly Leu Ala Leu Cys Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr
210 215 220

Ile Thr Gln Gln Asn Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser
225 230 235 240

Tyr Glu Thr Val Ala Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly
245 250 255

Ile Glu Gln Lys Pro Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn
260 265 270

Ala Met Glu Ala Leu Ala Ala His Arg Val Cys Gly Val Pro Leu Glu
275 280 285

Thr Leu Ala Arg Ser Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser
290 295 300

Cys Ala Tyr Gln Ala Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg
305 310 315 320

Ile Leu Phe Ser His Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu
325 330 335

Gln Glu Pro Glu Val Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn
340 345 350

Glu Asn Asn Pro Gly Met Val Thr Gln Val Leu Thr Val Ala Arg Gln
355 360 365

Ile Tyr Asn Asp Tyr Val Thr His His Pro Gly Leu Thr Pro Glu Gln
370 375 380

Thr Ser Ala Gly Ala Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro
385 390 395 400

Asp Ala Asp Lys Ser Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile
405 410 415

Asn Ile Glu Ser Arg Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala
420 425 430

Val Ile Thr Pro Gln Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu
435 440 445

Ala Thr His Gln Ala Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr
450 455 460

His Gly Thr Asn His Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala
465 470 475 480

Pro Val Pro Arg Gly Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly
485 490 495

Leu Tyr Val Ala Thr His Ala Glu Val Ala His Gly Tyr Ala Arg Ile
500 505 510

Lys Glu Gly Thr Gly Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp
515 520 525

Ala Arg Gly Val Met Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu
530 535 540

Arg Phe Tyr Arg Thr Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile
545 550 555 560

Thr Gln Val Ile Gly His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr
565 570 575

Gly Pro Glu Ser Ala Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp
580 585 590

Met Ala Ile His Ala Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala
595 600 605

Tyr Glu Glu Leu Ala Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser
610 615 620

Ile Ser Thr Lys Pro Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630 635

<210> 133
 <211> 639
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown:
 Cholix sequence

<400> 133
 Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
 1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
 20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
 35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
 50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
 65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
 85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
 100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
 115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
 130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
 145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

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

Pro Ala Glu Glu Ala Val Val Lys Glu Ala Ile Ala Lys Glu Gln Ser
610 615 620

Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630 635

<210> 134
<211> 639
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 134
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile His Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

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

Pro Ala Glu Glu Ala Val Val Lys Glu Ala Ile Ala Lys Glu Gln Ser
610 615 620

Ile Ser Ala Lys Pro Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630 635

<210> 135

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 135

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Gln Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Lys Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 136
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 136
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 137

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 137

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Met Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Val Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Gly Asn Ala Met Ser Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Asp Leu Arg Arg Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ser Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 138
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 138
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Thr Asp Asp Leu Ser Cys Val Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Lys Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 139
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 139
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile His Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 140

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 140

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Ala Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asp Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 141
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 141
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Ile Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 142

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 142

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Ile Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 143

<211> 634

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown:
Cholix sequence

<400> 143

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Met Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Ile Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Glu Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Arg His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Gln Lys Asp Glu Leu Lys
625 630

<210> 144
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 144
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Leu Lys Lys Gly Thr Gly
500 505 510

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

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr His Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Arg Val
565 570 575

Asp Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Val Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Glu Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 145
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 145

Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Lys
145 150 155 160

Thr Gln Gly Asn Val Phe Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Glu Val
325 330 335

Thr Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Pro
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile His Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Thr Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 146
<211> 634
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cholix sequence

<400> 146
Val Glu Asp Glu Leu Asn Ile Phe Asp Glu Cys Arg Ser Pro Cys Ser
1 5 10 15

Leu Thr Pro Glu Pro Gly Lys Pro Ile Gln Ser Lys Leu Ser Ile Pro
20 25 30

Ser Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Lys Asp Glu Asp Lys Gly Glu Ser Ile
50 55 60

Ile Thr Ile Gly Glu Phe Ala Thr Val Arg Ala Thr Arg His Tyr Val
65 70 75 80

Asn Gln Asp Ala Pro Phe Gly Val Ile Asn Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Thr Tyr Ser Tyr Asn Arg Lys Glu Gly Glu Phe Ala
100 105 110

Ile Asn Trp Leu Val Pro Ile Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Val Asp Glu Leu Asp Gln Gln Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Glu
145 150 155 160

Asn Gln Gly Asn Val Ser Phe Ser Val Thr Arg Pro Glu His Asn Ile
165 170 175

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

Ser Arg His Lys Arg Trp Ala His Trp His Thr Gly Leu Ala Leu Cys
195 200 205

Trp Leu Val Pro Ile Asp Ala Ile Tyr Asn Tyr Ile Thr Gln Gln Asn
210 215 220

Cys Thr Leu Gly Asp Asn Trp Phe Gly Gly Ser Tyr Glu Thr Val Ala
225 230 235 240

Gly Thr Pro Lys Ala Ile Thr Val Lys Gln Gly Ile Glu Gln Lys Pro
245 250 255

Val Glu Gln Arg Ile His Phe Ser Lys Lys Asn Ala Met Glu Ala Leu
260 265 270

Ala Ala His Arg Val Cys Gly Val Pro Leu Glu Thr Leu Ala Arg Ser
275 280 285

Arg Lys Pro Arg Asp Leu Pro Asp Asp Leu Ser Cys Ala Tyr Gln Ala
290 295 300

Gln Asn Ile Val Ser Leu Phe Val Ala Thr Arg Ile Leu Phe Ser His
305 310 315 320

Leu Asp Ser Val Phe Thr Leu Asn Leu Asp Glu Gln Glu Pro Ala Val
325 330 335

Ala Glu Arg Leu Ser Ala Leu Arg Gln Ile Asn Glu Asn Asn Pro Gly
340 345 350

Met Val Thr Gln Val Leu Thr Val Ala Arg Gln Ile Tyr Asn Asp Tyr
355 360 365

Val Thr His His Pro Gly Leu Thr Pro Glu Gln Thr Ser Ala Gly Ala
370 375 380

Gln Ala Ala Asp Ile Leu Ser Leu Phe Cys Pro Asp Ala Asp Lys Ser
385 390 395 400

Cys Val Ala Ser Asn Asn Asp Gln Ala Asn Ile Asn Ile Glu Ser Arg
405 410 415

Ser Gly Arg Ser Tyr Leu Pro Glu Asn Arg Ala Val Ile Thr Pro Gln
420 425 430

Gly Val Thr Asn Trp Thr Tyr Gln Glu Leu Glu Ala Thr His Gln Ala
435 440 445

Leu Thr Arg Glu Gly Tyr Val Phe Val Gly Tyr His Gly Thr Asn His
450 455 460

Val Ala Ala Gln Thr Ile Val Asn Arg Ile Ala Pro Val Pro Arg Gly
465 470 475 480

Asn Asn Thr Glu Asn Glu Glu Lys Trp Gly Gly Leu Tyr Val Ala Thr
485 490 495

His Ala Glu Val Ala His Gly Tyr Ala Arg Ile Lys Glu Gly Thr Gly
500 505 510

Glu Tyr Gly Leu Pro Thr Arg Ala Glu Arg Asp Ala Arg Gly Val Met
515 520 525

Leu Arg Val Tyr Ile Pro Arg Ala Ser Leu Glu Arg Phe Tyr Arg Thr
530 535 540

Asn Thr Pro Leu Glu Asn Ala Glu Glu His Ile Thr Gln Val Ile Gly
545 550 555 560

His Ser Leu Pro Leu Arg Asn Glu Ala Phe Thr Gly Pro Glu Ser Ala
565 570 575

Gly Gly Glu Asp Glu Thr Val Ile Gly Trp Asp Met Ala Ile His Ala
580 585 590

Val Ala Ile Pro Ser Thr Ile Pro Gly Asn Ala Tyr Glu Glu Leu Ala
595 600 605

Ile Asp Glu Glu Ala Val Ala Lys Glu Gln Ser Ile Ser Ala Lys Pro
610 615 620

Pro Tyr Lys Glu Arg Lys Asp Glu Leu Lys
625 630

<210> 147

<211> 649

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<221> MOD_RES

<222> (1)..(1)

<223> V or L

<220>

<221> MOD_RES

<222> (3)..(3)

<223> E or D

<220>

<221> MOD_RES

<222> (4)..(4)

<223> A or E

<220>

<221> MOD_RES

<222> (6)..(6)

<223> N or K

<220>

<221> MOD_RES

<222> (16)..(16)

<223> S or L

<220>

<221> MOD_RES

<222> (21)..(21)

<223> P or L

<220>

<221> MOD_RES

<222> (24)..(24)

<223> P or Q

<220>

<221> MOD_RES

<222> (30)..(30)

<223> S or F

<220>

<221> MOD_RES

<222> (33)..(33)

<223> S or G

<220>

<221> MOD_RES

<222> (56)..(56)

<223> K or M

<220>

<221> MOD_RES

<222> (59)..(59)

<223> D or G

<220>

<221> MOD_RES

<222> (67)..(67)

<223> I or F

<220>

<221> MOD_RES

<222> (73)..(73)

<223> V or I

<220>

<221> MOD_RES

<222> (81)..(81)

<223> N or S

<220>

<221> MOD_RES

<222> (90)..(90)

<223> H or N

<220>

<221> MOD_RES

<222> (101)..(101)

<223> T or M

<220>

<221> MOD_RES

<222> (104)..(104)

<223> Y or F

<220>

<221> MOD_RES

<222> (108)..(108)

<223> E or D

<220>

<221> MOD_RES

<222> (109)..(109)

<223> G or S

<220>

<221> MOD_RES

<222> (112)..(112)

<223> A or T

<220>

<221> MOD_RES

<222> (114)..(114)

<223> N or H

<220>

<221> MOD_RES

<222> (118)..(118)

<223> P or I

<220>

<221> MOD_RES

<222> (119)..(119)

<223> I or P

<220>

<221> MOD_RES

<222> (131)..(131)

<223> V or I

<220>

<221> MOD_RES

<222> (134)..(134)

<223> L or I

<220>

<221> MOD_RES

<222> (137)..(137)

<223> Q or K

<220>

<221> MOD_RES

<222> (160)..(160)

<223> K or E

<220>

<221> MOD_RES

<222> (161)..(161)

<223> T or N

<220>

<221> MOD_RES

<222> (166)..(166)

<223> S or F

<220>

<221> MOD_RES

<222> (168)..(168)

<223> S or A

<220>

<221> MOD_RES

<222> (174)..(174)

<223> H or Q

<220>

<221> MISC_FEATURE

<222> (175)..(185)

<223> This region may encompass "N", "S", "SIAKQS", or "SIAKQSIKQS"

<220>

<221> MOD_RES

<222> (196)..(196)

<223> K or N

<220>

<221> MOD_RES

<222> (199)..(199)

<223> Q, E, or H

<220>

<221> MOD_RES

<222> (201)..(201)

<223> E, N, or D

<220>

<221> MOD_RES

<222> (203)..(203)

<223> S or A

<220>

<221> MOD_RES

<222> (210)..(210)

<223> H or N

<220>

<221> MOD_RES

<222> (212)..(212)

<223> H, L, F, or R

<220>

<221> MOD_RES

<222> (214)..(214)

<223> G or T

<220>

<221> MOD_RES

<222> (215)..(215)

<223> L or S

<220>

<221> MOD_RES

<222> (216)..(216)

<223> A or P

<220>

<221> MOD_RES

<222> (217)..(217)

<223> L, E, or K

<220>

<221> MOD_RES

<222> (218)..(218)

<223> C or V

<220>

<221> MOD_RES

<222> (219)..(219)

<223> W, V, or T

<220>

<221> MOD_RES

<222> (221)..(221)

<223> V or not present

<220>

<221> MOD_RES

<222> (222)..(222)

<223> P or not present

<220>

<221> MOD_RES

<222> (223)..(223)

<223> M, I, L, or not present

<220>

<221> MOD_RES

<222> (224)..(224)

<223> D or not present

<220>

<221> MOD_RES

<222> (225)..(225)

<223> A or not present

<220>

<221> MOD_RES

<222> (226)..(226)

<223> I or not present

<220>

<221> MOD_RES

<222> (227)..(227)

<223> Y or C

<220>

<221> MOD_RES

<222> (228)..(228)

<223> N or F

<220>

<221> MOD_RES

<222> (229)..(229)

<223> Y or F

<220>

<221> MOD_RES

<222> (230)..(230)

<223> I or E

<220>

<221> MOD_RES

<222> (231)..(231)

<223> T or D

<220>

<221> MOD_RES

<222> (232)..(232)

<223> Q or P

<220>

<221> MOD_RES

<222> (233)..(233)

<223> Q, E, or A

<220>

<221> MOD_RES

<222> (234)..(234)

<223> N, L, or Q

<220>

<221> MOD_RES

<222> (237)..(237)

<223> L or Y

<220>

<221> MOD_RES

<222> (239)..(239)

<223> D or E

<220>

<221> MOD_RES

<222> (240)..(240)

<223> N or D

<220>

<221> MOD_RES

<222> (242)..(242)

<223> F, H, or Y

<220>

<221> MOD_RES

<222> (245)..(245)

<223> S or A

<220>

<221> MOD_RES

<222> (247)..(247)

<223> E or K

<220>

<221> MOD_RES

<222> (252)..(252)

<223> T or I

<220>

<221> MOD_RES

<222> (254)..(254)

<223> K, E, or G

<220>

<221> MOD_RES

<222> (255)..(255)

<223> V or A

<220>

<221> MOD_RES

<222> (257)..(257)

<223> T or M

<220>

<221> MOD_RES

<222> (262)..(262)

<223> I or M

<220>

<221> MOD_RES

<222> (266)..(266)

<223> P, T, or A

<220>

<221> MOD_RES

<222> (275)..(275)

<223> K, Q, or N

<220>

<221> MOD_RES

<222> (276)..(276)

<223> G or K

<220>

<221> MOD_RES

<222> (279)..(279)

<223> M or I

<220>

<221> MOD_RES

<222> (280)..(280)

<223> S or E

<220>

<221> MOD_RES

<222> (281)..(281)

<223> A or T

<220>

<221> MOD_RES

<222> (298)..(298)

<223> S or G

<220>

<221> MOD_RES

<222> (303)..(303)

<223> D or Y

<220>

<221> MOD_RES

<222> (305)..(305)

<223> T, P, or Q

<220>

<221> MOD_RES

<222> (309)..(309)

<223> S or Q

<220>

<221> MOD_RES

<222> (311)..(311)

<223> A or V

<220>

<221> MOD_RES

<222> (313)..(313)

<223> Q or N

<220>

<221> MOD_RES

<222> (316)..(316)

<223> N or Q

<220>

<221> MOD_RES

<222> (322)..(322)

<223> V or L

<220>

<221> MOD_RES

<222> (326)..(326)

<223> I or M

<220>

<221> MOD_RES

<222> (329)..(329)

<223> S or T

<220>

<221> MOD_RES

<222> (331)..(331)

<223> L or I

<220>

<221> MOD_RES

<222> (334)..(334)

<223> V or I

<220>

<221> MOD_RES

<222> (340)..(340)

<223> D, E, or H

<220>

<221> MOD_RES

<222> (341)..(341)

<223> E or G

<220>

<221> MOD_RES

<222> (343)..(343)

<223> E or A

<220>

<221> MOD_RES

<222> (345)..(345)

<223> E or A

<220>

<221> MOD_RES

<222> (347)..(347)

<223> A or T

<220>

<221> MOD_RES

<222> (351)..(351)

<223> S, D, or T

<220>

<221> MOD_RES

<222> (352)..(352)

<223> D or A

<220>

<221> MOD_RES

<222> (353)..(353)

<223> L or I

<220>

<221> MOD_RES

<222> (355)..(355)

<223> R or Q

<220>

<221> MOD_RES

<222> (359)..(359)

<223> N or D

<220>

<221> MOD_RES

<222> (363)..(363)

<223> M or V

<220>

<221> MOD_RES

<222> (365)..(365)

<223> T or I

<220>

<221> MOD_RES

<222> (370)..(370)

<223> V or I

<220>

<221> MOD_RES

<222> (381)..(381)

<223> H or E

<220>

<221> MOD_RES

<222> (384)..(384)

<223> G or L

<220>

<221> MOD_RES

<222> (386)..(386)

<223> T or I

<220>

<221> MOD_RES

<222> (393)..(393)

<223> G or S

<220>

<221> MOD_RES

<222> (403)..(403)

<223> F or L

<220>

<221> MOD_RES

<222> (404)..(404)

<223> C or Y

<220>

<221> MOD_RES

<222> (407)..(407)

<223> A or T

<220>

<221> MOD_RES

<222> (409)..(409)

<223> K, E, or G

<220>

<221> MOD_RES

<222> (410)..(410)

<223> S, P, or H

<220>

<221> MOD_RES

<222> (414)..(414)

<223> S or L

<220>

<221> MOD_RES

<222> (415)..(415)

<223> N or D

<220>

<221> MOD_RES

<222> (416)..(416)

<223> N or S

<220>

<221> MOD_RES

<222> (423)..(423)

<223> I or V

<220>

<221> MOD_RES

<222> (433)..(433)

<223> P or L

<220>

<221> MOD_RES

<222> (441)..(441)

<223> P or Q

<220>

<221> MOD_RES

<222> (453)..(453)

<223> E or D

<220>

<221> MOD_RES

<222> (454)..(454)

<223> A or T

<220>

<221> MOD_RES

<222> (455)..(455)

<223> T or K

<220>

<221> MOD_RES

<222> (458)..(458)

<223> A or T

<220>

<221> MOD_RES

<222> (461)..(461)

<223> R or Q

<220>

<221> MOD_RES

<222> (463)..(463)

<223> G or D

<220>

<221> MOD_RES

<222> (475)..(475)

<223> V or A

<220>

<221> MOD_RES

<222> (479)..(479)

<223> T, S, or N

<220>

<221> MOD_RES

<222> (485)..(485)

<223> A, S, or T

<220>

<221> MOD_RES

<222> (491)..(491)

<223> N or S

<220>

<221> MOD_RES

<222> (492)..(492)

<223> N or D

<220>

<221> MOD_RES

<222> (495)..(495)

<223> N, S, or K

<220>

<221> MOD_RES

<222> (497)..(497)

<223> E, R, or K

<220>

<221> MOD_RES

<222> (498)..(498)

<223> K, A, or E

<220>

<221> MOD_RES

<222> (502)..(502)

<223> L or V

<220>

<221> MOD_RES

<222> (505)..(505)

<223> A or S

<220>

<221> MOD_RES

<222> (507)..(507)

<223> H or D

<220>

<221> MOD_RES

<222> (509)..(509)

<223> E or S

<220>

<221> MOD_RES

<222> (510)..(510)

<223> V or L

<220>

<221> MOD_RES

<222> (511)..(511)

<223> A or N

<220>

<221> MOD_RES

<222> (512)..(512)

<223> H or Y

<220>

<221> MOD_RES

<222> (513)..(513)

<223> G or R

<220>

<221> MOD_RES

<222> (515)..(515)

<223> A or T

<220>

<221> MOD_RES

<222> (517)..(517)

<223> I or L

<220>

<221> MOD_RES

<222> (518)..(518)

<223> K or Q

<220>

<221> MOD_RES

<222> (519)..(519)

<223> E or K

<220>

<221> MOD_RES

<222> (522)..(522)

<223> G or A

<220>

<221> MOD_RES

<222> (523)..(523)

<223> E, D, or N

<220>

<221> MOD_RES

<222> (524)..(524)

<223> Y, G, A, or N

<220>

<221> MOD_RES

<222> (525)..(525)

<223> G or E

<220>

<221> MOD_RES

<222> (526)..(526)

<223> L or G

<220>

<221> MOD_RES

<222> (527)..(527)

<223> P or L

<220>

<221> MOD_RES

<222> (529)..(529)

<223> R, P, or T

<220>

<221> MOD_RES

<222> (530)..(530)

<223> A or E

<220>

<221> MOD_RES

<222> (531)..(531)

<223> E or K

<220>

<221> MOD_RES

<222> (532)..(532)

<223> R, Q, or K

<220>

<221> MOD_RES

<222> (533)..(533)

<223> D, K, or E

<220>

<221> MOD_RES

<222> (534)..(534)

<223> A, T, or S

<220>

<221> MOD_RES

<222> (540)..(540)

<223> R or K

<220>

<221> MOD_RES

<222> (543)..(543)

<223> I or L

<220>

<221> MOD_RES

<222> (544)..(544)

<223> P or H

<220>

<221> MOD_RES

<222> (545)..(545)

<223> R or Q

<220>

<221> MOD_RES

<222> (554)..(554)

<223> T or I

<220>

<221> MOD_RES

<222> (556)..(556)

<223> T, A, or I

<220>

<221> MOD_RES

<222> (557)..(557)

<223> P or D

<220>

<221> MOD_RES

<222> (560)..(560)

<223> N or K

<220>

<221> MOD_RES

<222> (561)..(561)

<223> A or E

<220>

<221> MOD_RES

<222> (562)..(562)

<223> E, R, or D

<220>

<221> MOD_RES

<222> (563)..(563)

<223> E, N, or R

<220>

<221> MOD_RES

<222> (564)..(564)

<223> H or L

<220>

<221> MOD_RES

<222> (565)..(565)

<223> I or V

<220>

<221> MOD_RES

<222> (566)..(566)

<223> T or E

<220>

<221> MOD_RES

<222> (567)..(567)

<223> Q, R, H, or D

<220>

<221> MOD_RES

<222> (572)..(572)

<223> S or P

<220>

<221> MOD_RES

<222> (583)..(583)

<223> P or T

<220>

<221> MOD_RES

<222> (584)..(584)

<223> E or D

<220>

<221> MOD_RES

<222> (585)..(585)

<223> S, A, or R

<220>

<221> MOD_RES

<222> (586)..(586)

<223> A, E, or V

<220>

<221> MOD_RES

<222> (587)..(587)

<223> G, E, or D

<220>

<221> MOD_RES

<222> (589)..(589)

<223> E or S

<220>

<221> MOD_RES

<222> (590)..(590)

<223> D or N

<220>

<221> MOD_RES

<222> (593)..(593)

<223> V or A

<220>

<221> MOD_RES

<222> (598)..(598)

<223> M or I

<220>

<221> MOD_RES

<222> (601)..(601)

<223> H or Y

<220>

<221> MOD_RES

<222> (602)..(602)

<223> A or G

<220>

<221> MOD_RES

<222> (613)..(613)

<223> A or S

<220>

<221> MOD_RES

<222> (615)..(615)

<223> E or A

<220>

<221> MOD_RES

<222> (616)..(616)

<223> E, A, Q, G, V, or R

<220>

<221> MOD_RES

<222> (618)..(618)

<223> A, P, or T

<220>

<221> MOD_RES

<222> (619)..(619)

<223> I, T, or P

<220>

<221> MOD_RES

<222> (620)..(620)

<223> D or A

<220>

<221> MISC_FEATURE

<222> (624)..(629)

<223> This region may encompass "V" or "VVKEAI"

<220>

<221> MOD_RES

<222> (631)..(631)

<223> K or E

<220>

<221> MOD_RES

<222> (637)..(637)

<223> T, A, or P

<220>

<221> MOD_RES

<222> (644)..(644)

<223> R, Q, or H

<220>

<221> MOD_RES

<222> (645)..(645)

<223> K or not present

<400> 147

Xaa Glu Xaa Xaa Leu Xaa Ile Phe Asp Glu Cys Arg Ser Pro Cys Xaa

1

5

10

15

Leu Thr Pro Glu Xaa Gly Lys Xaa Ile Gln Ser Lys Leu Xaa Ile Pro
20 25 30

Xaa Asp Val Val Leu Asp Glu Gly Val Leu Tyr Tyr Ser Met Thr Ile
35 40 45

Asn Asp Glu Gln Asn Asp Ile Xaa Asp Glu Xaa Lys Gly Glu Ser Ile
50 55 60

Ile Thr Xaa Gly Glu Phe Ala Thr Xaa Arg Ala Thr Arg His Tyr Val
65 70 75 80

Xaa Gln Asp Ala Pro Phe Gly Val Ile Xaa Leu Asp Ile Thr Thr Glu
85 90 95

Asn Gly Thr Lys Xaa Tyr Ser Xaa Asn Arg Lys Xaa Xaa Glu Phe Xaa
100 105 110

Ile Xaa Trp Leu Val Xaa Xaa Gly Glu Asp Ser Pro Ala Ser Ile Lys
115 120 125

Ile Ser Xaa Asp Glu Xaa Asp Gln Xaa Arg Asn Ile Ile Glu Val Pro
130 135 140

Lys Leu Tyr Ser Ile Asp Leu Asp Asn Gln Thr Leu Glu Gln Trp Xaa
145 150 155 160

Xaa Gln Gly Asn Val Xaa Phe Xaa Val Thr Arg Pro Glu Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Ala Ile Ser Trp Pro Ser
180 185 190

Val Ser Tyr Xaa Ala Ala Xaa Lys Xaa Gly Xaa Arg His Lys Arg Trp
195 200 205

Ala Xaa Trp Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa
 210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Thr Xaa Gly Xaa Xaa
 225 230 235 240

Trp Xaa Gly Gly Xaa Tyr Xaa Thr Val Ala Gly Xaa Pro Xaa Xaa Ile
 245 250 255

Xaa Val Lys Gln Gly Xaa Glu Gln Lys Xaa Val Glu Gln Arg Ile His
 260 265 270

Phe Ser Xaa Xaa Asn Ala Xaa Xaa Xaa Leu Ala Ala His Arg Val Cys
 275 280 285

Gly Val Pro Leu Glu Thr Leu Ala Arg Xaa Arg Lys Pro Arg Xaa Leu
 290 295 300

Xaa Asp Asp Leu Xaa Cys Xaa Tyr Xaa Ala Gln Xaa Ile Val Ser Leu
 305 310 315 320

Phe Xaa Ala Thr Arg Xaa Leu Phe Xaa His Xaa Asp Ser Xaa Phe Thr
 325 330 335

Leu Asn Leu Xaa Xaa Gln Xaa Pro Xaa Val Xaa Glu Arg Leu Xaa Xaa
 340 345 350

Xaa Arg Xaa Ile Asn Glu Xaa Asn Pro Gly Xaa Val Xaa Gln Val Leu
 355 360 365

Thr Xaa Ala Arg Gln Ile Tyr Asn Asp Tyr Val Thr Xaa His Pro Xaa
 370 375 380

Leu Xaa Pro Glu Gln Thr Ser Ala Xaa Ala Gln Ala Ala Asp Ile Leu
 385 390 395 400

Ser Leu Xaa Xaa Pro Asp Xaa Asp Xaa Xaa Cys Val Ala Xaa Xaa Xaa
 405 410 415

Asp Gln Ala Asn Ile Asn Xaa Glu Ser Arg Ser Gly Arg Ser Tyr Leu
420 425 430

Xaa Glu Asn Arg Ala Val Ile Thr Xaa Gln Gly Val Thr Asn Trp Thr
435 440 445

Tyr Gln Glu Leu Xaa Xaa Xaa His Gln Xaa Leu Thr Xaa Glu Xaa Tyr
450 455 460

Val Phe Val Gly Tyr His Gly Thr Asn His Xaa Ala Ala Gln Xaa Ile
465 470 475 480

Val Asn Arg Ile Xaa Pro Val Pro Arg Gly Xaa Xaa Thr Glu Xaa Glu
485 490 495

Xaa Xaa Trp Gly Gly Xaa Tyr Val Xaa Thr Xaa Ala Xaa Xaa Xaa Xaa
500 505 510

Xaa Tyr Xaa Arg Xaa Xaa Xaa Gly Thr Xaa Xaa Xaa Xaa Xaa Xaa Thr
515 520 525

Xaa Xaa Xaa Xaa Xaa Xaa Arg Gly Val Met Leu Xaa Val Tyr Xaa Xaa
530 535 540

Xaa Ala Ser Leu Glu Arg Phe Tyr Arg Xaa Asn Xaa Xaa Leu Glu Xaa
545 550 555 560

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Ile Gly His Xaa Leu Pro Leu Arg
565 570 575

Asn Glu Ala Phe Thr Gly Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Glu Thr
580 585 590

Xaa Ile Gly Trp Asp Xaa Ala Ile Xaa Xaa Val Ala Ile Pro Ser Thr
595 600 605

Ile Pro Gly Asn Xaa Tyr Xaa Xaa Leu Xaa Xaa Xaa Glu Glu Ala Xaa
610 615 620

Xaa Xaa Xaa Xaa Xaa Ala Xaa Glu Gln Ser Ile Ser Xaa Lys Pro Pro
625 630 635 640

Tyr Lys Glu Xaa Xaa Asp Glu Leu Lys
645

<210> 148
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 148
Ser Ile Ala Lys Gln Ser
1 5

<210> 149
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 149
Ser Ile Ala Lys Gln Ser Ile Ala Lys Gln Ser
1 5 10

<210> 150
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 150

Val Val Lys Glu Ala Ile
1 5

<210> 151
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MISC_FEATURE
<222> (1)..(30)
<223> This sequence may encompass 1-15 "Gly Ser"
repeating units

<400> 151
Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10 15

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
20 25 30

<210> 152
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MISC_FEATURE
<222> (1)..(45)
<223> This sequence may encompass 1-15 "Gly Gly Ser"
repeating units

<400> 152
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
35 40 45

<210> 153

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 153

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 154

<211> 224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 154

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

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

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

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

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

<210> 155

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 155

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 156

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 156

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

Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
20 25 30

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

Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
65 70 75 80

Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
85 90 95

Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr
 225