

SEQUENCE LISTING

<110> DECIPHERA PHARMACEUTICALS, LLC

<120> PHENYLAMINOPYRIMIDINE AMIDE AUTOPHAGY INHIBITORS AND METHODS OF USE THEREOF

<130> DCP-079W0

<140>

<141>

<150> 62/711,730

<151> 2019-10-07

<150> 62/911,728

<151> 2019-10-07

<150> 62/846,258

<151> 2019-05-10

<150> 62/846,251

<151> 2019-05-10

<160> 6

<170> PatentIn version 3.5

<210> 1

<211> 344

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1

Met	Ser	Tyr	Tyr	His	His	His	His	His	His	Asp	Tyr	Asp	Ile	Pro	Thr
1				5					10					15	

Thr	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ala	Met	Asp	Pro	Phe	Phe	Met	Glu
		20						25					30		

Pro	Gly	Arg	Gly	Gly	Thr	Glu	Thr	Val	Gly	Lys	Phe	Glu	Phe	Ser	Arg
		35					40					45			

Lys Asp Leu Ile Gly His Gly Ala Phe Ala Val Val Phe Lys Gly Arg
50 55 60

His Arg Glu Lys His Asp Leu Glu Val Ala Val Lys Cys Ile Asn Lys
65 70 75 80

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

Leu Lys Glu Leu Lys His Glu Asn Ile Val Ala Leu Tyr Asp Phe Gln
100 105 110

Glu Met Ala Asn Ser Val Tyr Leu Val Met Glu Tyr Cys Asn Gly Gly
115 120 125

Asp Leu Ala Asp Tyr Leu His Ala Met Arg Thr Leu Ser Glu Asp Thr
130 135 140

Ile Arg Leu Phe Leu Gln Gln Ile Ala Gly Ala Met Arg Leu Leu His
145 150 155 160

Ser Lys Gly Ile Ile His Arg Asp Leu Lys Pro Gln Asn Ile Leu Leu
165 170 175

Ser Asn Pro Ala Gly Arg Arg Ala Asn Pro Asn Ser Ile Arg Val Lys
180 185 190

Ile Ala Asp Phe Gly Phe Ala Arg Tyr Leu Gln Ser Asn Met Met Ala
195 200 205

Ala Thr Leu Cys Gly Ser Pro Met Tyr Met Ala Pro Glu Val Ile Met
210 215 220

Ser Gln His Tyr Asp Gly Lys Ala Asp Leu Trp Ser Ile Gly Thr Ile
225 230 235 240

Val Tyr Gln Cys Leu Thr Gly Lys Ala Pro Phe Gln Ala Ser Ser Pro

245

250

255

Gln Asp Leu Arg Leu Phe Tyr Glu Lys Asn Lys Thr Leu Val Pro Thr
 260 265 270

Ile Pro Arg Glu Thr Ser Ala Pro Leu Arg Gln Leu Leu Leu Ala Leu
 275 280 285

Leu Gln Arg Asn His Lys Asp Arg Met Asp Phe Asp Glu Phe Phe His
 290 295 300

His Pro Phe Leu Asp Ala Ser Pro Ser Val Arg Lys Ser Pro Pro Val
 305 310 315 320

Pro Val Pro Ser Tyr Pro Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser
 325 330 335

Ser Ser Thr Ser His Leu Ala Ser
 340

<210> 2

<211> 283

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 ULK1 sequence"

<400> 2

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

Ser Arg Lys Asp Leu Ile Gly His Gly Ala Phe Ala Val Val Phe Lys
 20 25 30

Gly Arg His Arg Ala Ala His Asp Leu Glu Val Ala Val Lys Cys Ile
 35 40 45

Asn Lys Lys Asn Leu Ala Lys Ser Gln Thr Leu Leu Gly Lys Glu Ile
50 55 60

Lys Ile Leu Lys Glu Leu Lys His Glu Asn Ile Val Ala Leu Tyr Asp
65 70 75 80

Phe Gln Glu Met Ala Asn Ser Val Tyr Leu Val Met Glu Tyr Cys Asn
85 90 95

Gly Gly Asp Leu Ala Asp Tyr Leu His Ala Met Arg Thr Leu Ser Glu
100 105 110

Asp Thr Ile Arg Leu Phe Leu Gln Gln Ile Ala Gly Ala Met Arg Leu
115 120 125

Leu His Ser Lys Gly Ile Ile His Arg Asp Leu Lys Pro Gln Asn Ile
130 135 140

Leu Leu Ser Asn Pro Ala Gly Arg Arg Ala Asn Pro Asn Ser Ile Arg
145 150 155 160

Val Lys Ile Ala Asp Phe Gly Phe Ala Arg Tyr Leu Gln Ser Asn Met
165 170 175

Met Ala Ala Thr Leu Cys Gly Ser Pro Met Tyr Met Ala Pro Glu Val
180 185 190

Ile Met Ser Gln His Tyr Asp Gly Lys Ala Asp Leu Trp Ser Ile Gly
195 200 205

Thr Ile Val Tyr Gln Cys Leu Thr Gly Lys Ala Pro Phe Gln Ala Ser
210 215 220

Ser Pro Gln Asp Leu Arg Leu Phe Tyr Glu Lys Asn Lys Thr Leu Val
225 230 235 240

Pro Thr Ile Pro Arg Glu Thr Ser Ala Pro Leu Arg Gln Leu Leu Leu
245 250 255

Ala Leu Leu Gln Arg Asn His Lys Asp Arg Met Asp Phe Asp Glu Phe
260 265 270

Phe His His Pro Phe Leu Asp Ala Ser Pro Ser
275 280

<210> 3

<211> 542

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 3

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

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

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

115

120

125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Glu Val Leu
 210 215 220

Phe Gln Gly Pro Glu Phe Met Glu Val Val Gly Asp Phe Glu Tyr Ser
 225 230 235 240

Lys Arg Asp Leu Val Gly His Gly Ala Phe Ala Val Val Phe Arg Gly
 245 250 255

Arg His Arg Gln Lys Thr Asp Trp Glu Val Ala Ile Lys Ser Ile Asn
 260 265 270

Lys Lys Asn Leu Ser Lys Ser Gln Ile Leu Leu Gly Lys Glu Ile Lys
 275 280 285

Ile Leu Lys Glu Leu Gln His Glu Asn Ile Val Ala Leu Tyr Asp Val
 290 295 300

Gln Glu Leu Pro Asn Ser Val Phe Leu Val Met Glu Tyr Cys Asn Gly
 305 310 315 320

Gly Asp Leu Ala Asp Tyr Leu Gln Ala Lys Gly Thr Leu Ser Glu Asp
325 330 335

Thr Ile Arg Val Phe Leu His Gln Ile Ala Ala Ala Met Arg Ile Leu
340 345 350

His Ser Lys Gly Ile Ile His Arg Asp Leu Lys Pro Gln Asn Ile Leu
355 360 365

Leu Ser Tyr Ala Asn Arg Arg Lys Ser Ser Val Ser Gly Ile Arg Ile
370 375 380

Lys Ile Ala Asp Phe Gly Phe Ala Arg Tyr Leu His Ser Asn Met Met
385 390 395 400

Ala Ala Thr Leu Cys Gly Ser Pro Met Tyr Met Ala Pro Glu Val Ile
405 410 415

Met Ser Gln His Tyr Asp Ala Lys Ala Asp Leu Trp Ser Ile Gly Thr
420 425 430

Val Ile Tyr Gln Cys Leu Val Gly Lys Pro Pro Phe Gln Ala Asn Ser
435 440 445

Pro Gln Asp Leu Arg Met Phe Tyr Glu Lys Asn Arg Ser Leu Met Pro
450 455 460

Ser Ile Pro Arg Glu Thr Ser Pro Tyr Leu Ala Asn Leu Leu Leu Gly
465 470 475 480

Leu Leu Gln Arg Asn Gln Lys Asp Arg Met Asp Phe Glu Ala Phe Phe
485 490 495

Ser His Pro Phe Leu Glu Gln Gly Pro Val Lys Lys Ser Cys Pro Val
500 505 510

Pro Val Pro Met Tyr Ser Gly Ser Val Ser Gly Ser Ser Cys Gly Ser

515

520

525

Ser Pro Ser Cys Arg Phe Ala Ser His His His His His His
 530 535 540

<210> 4

<211> 1795

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
 LRRK2 sequence"

<400> 4

Met Ala Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

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

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220

His Asn Gln Thr Ser Leu Tyr Lys Lys Ala Gly Thr Met His Ser Asp
225 230 235 240

Ser Ile Ser Ser Leu Ala Ser Glu Arg Glu Tyr Ile Thr Ser Leu Asp
245 250 255

Leu Ser Ala Asn Glu Leu Arg Asp Ile Asp Ala Leu Ser Gln Lys Cys
260 265 270

Cys Ile Ser Val His Leu Glu His Leu Glu Lys Leu Glu Leu His Gln
275 280 285

Asn Ala Leu Thr Ser Phe Pro Gln Gln Leu Cys Glu Thr Leu Lys Ser
290 295 300

Leu Thr His Leu Asp Leu His Ser Asn Lys Phe Thr Ser Phe Pro Ser
305 310 315 320

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

Asp Ile Gly Pro Ser Val Val Leu Asp Pro Thr Val Lys Cys Pro Thr
340 345 350

Leu Lys Gln Phe Asn Leu Ser Tyr Asn Gln Leu Ser Phe Val Pro Glu
355 360 365

Asn Leu Thr Asp Val Val Glu Lys Leu Glu Gln Leu Ile Leu Glu Gly
370 375 380

Asn Lys Ile Ser Gly Ile Cys Ser Pro Leu Arg Leu Lys Glu Leu Lys
385 390 395 400

Ile Leu Asn Leu Ser Lys Asn His Ile Ser Ser Leu Ser Glu Asn Phe
405 410 415

Leu Glu Ala Cys Pro Lys Val Glu Ser Phe Ser Ala Arg Met Asn Phe
420 425 430

Leu Ala Ala Met Pro Phe Leu Pro Pro Ser Met Thr Ile Leu Lys Leu
435 440 445

Ser Gln Asn Lys Phe Ser Cys Ile Pro Glu Ala Ile Leu Asn Leu Pro
450 455 460

His Leu Arg Ser Leu Asp Met Ser Ser Asn Asp Ile Gln Tyr Leu Pro
465 470 475 480

Gly Pro Ala His Trp Lys Ser Leu Asn Leu Arg Glu Leu Leu Phe Ser
485 490 495

His Asn Gln Ile Ser Ile Leu Asp Leu Ser Glu Lys Ala Tyr Leu Trp
500 505 510

Ser Arg Val Glu Lys Leu His Leu Ser His Asn Lys Leu Lys Glu Ile
515 520 525

Pro Pro Glu Ile Gly Cys Leu Glu Asn Leu Thr Ser Leu Asp Val Ser
530 535 540

Tyr Asn Leu Glu Leu Arg Ser Phe Pro Asn Glu Met Gly Lys Leu Ser
545 550 555 560

Lys Ile Trp Asp Leu Pro Leu Asp Glu Leu His Leu Asn Phe Asp Phe
565 570 575

Lys His Ile Gly Cys Lys Ala Lys Asp Ile Ile Arg Phe Leu Gln Gln
580 585 590

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

Gly Asn Thr Gly Ser Gly Lys Thr Thr Leu Leu Gln Gln Leu Met Lys
610 615 620

Thr Lys Lys Ser Asp Leu Gly Met Gln Ser Ala Thr Val Gly Ile Asp
625 630 635 640

Val Lys Asp Trp Pro Ile Gln Ile Arg Asp Lys Arg Lys Arg Asp Leu
645 650 655

Val Leu Asn Val Trp Asp Phe Ala Gly Arg Glu Glu Phe Tyr Ser Thr
660 665 670

His Pro His Phe Met Thr Gln Arg Ala Leu Tyr Leu Ala Val Tyr Asp
675 680 685

Leu Ser Lys Gly Gln Ala Glu Val Asp Ala Met Lys Pro Trp Leu Phe
690 695 700

Asn Ile Lys Ala Arg Ala Ser Ser Ser Pro Val Ile Leu Val Gly Thr
705 710 715 720

His Leu Asp Val Ser Asp Glu Lys Gln Arg Lys Ala Cys Met Ser Lys
725 730 735

Ile Thr Lys Glu Leu Leu Asn Lys Arg Gly Phe Pro Ala Ile Arg Asp
740 745 750

Tyr His Phe Val Asn Ala Thr Glu Glu Ser Asp Ala Leu Ala Lys Leu
755 760 765

Arg Lys Thr Ile Ile Asn Glu Ser Leu Asn Phe Lys Ile Arg Asp Gln
770 775 780

Leu Val Val Gly Gln Leu Ile Pro Asp Cys Tyr Val Glu Leu Glu Lys
785 790 795 800

Ile Ile Leu Ser Glu Arg Lys Asn Val Pro Ile Glu Phe Pro Val Ile
805 810 815

Asp Arg Lys Arg Leu Leu Gln Leu Val Arg Glu Asn Gln Leu Gln Leu
820 825 830

Asp Glu Asn Glu Leu Pro His Ala Val His Phe Leu Asn Glu Ser Gly
835 840 845

Val Leu Leu His Phe Gln Asp Pro Ala Leu Gln Leu Ser Asp Leu Tyr
850 855 860

Phe Val Glu Pro Lys Trp Leu Cys Lys Ile Met Ala Gln Ile Leu Thr
865 870 875 880

Val Lys Val Glu Gly Cys Pro Lys His Pro Lys Gly Ile Ile Ser Arg
885 890 895

Arg Asp Val Glu Lys Phe Leu Ser Lys Lys Arg Lys Phe Pro Lys Asn
900 905 910

Tyr Met Ser Gln Tyr Phe Lys Leu Leu Glu Lys Phe Gln Ile Ala Leu
915 920 925

Pro Ile Gly Glu Glu Tyr Leu Leu Val Pro Ser Ser Leu Ser Asp His
930 935 940

Arg Pro Val Ile Glu Leu Pro His Cys Glu Asn Ser Glu Ile Ile Ile
945 950 955 960

Arg Leu Tyr Glu Met Pro Tyr Phe Pro Met Gly Phe Trp Ser Arg Leu
965 970 975

Ile Asn Arg Leu Leu Glu Ile Ser Pro Tyr Met Leu Ser Gly Arg Glu
980 985 990

Arg Ala Leu Arg Pro Asn Arg Met Tyr Trp Arg Gln Gly Ile Tyr Leu
995 1000 1005

Asn Trp Ser Pro Glu Ala Tyr Cys Leu Val Gly Ser Glu Val Leu
1010 1015 1020

Asp Asn His Pro Glu Ser Phe Leu Lys Ile Thr Val Pro Ser Cys
1025 1030 1035

Arg Lys Gly Cys Ile Leu Leu Gly Gln Val Val Asp His Ile Asp
1040 1045 1050

Ser Leu Met Glu Glu Trp Phe Pro Gly Leu Leu Glu Ile Asp Ile
1055 1060 1065

Cys Gly Glu Gly Glu Thr Leu Leu Lys Lys Trp Ala Leu Tyr Ser
1070 1075 1080

Phe Asn Asp Gly Glu Glu His Gln Lys Ile Leu Leu Asp Asp Leu
1085 1090 1095

Met Lys Lys Ala Glu Glu Gly Asp Leu Leu Val Asn Pro Asp Gln
1100 1105 1110

Pro Arg Leu Thr Ile Pro Ile Ser Gln Ile Ala Pro Asp Leu Ile
1115 1120 1125

Leu Ala Asp Leu Pro Arg Asn Ile Met Leu Asn Asn Asp Glu Leu
1130 1135 1140

Glu Phe Glu Gln Ala Pro Glu Phe Leu Leu Gly Asp Gly Ser Phe
1145 1150 1155

Gly Ser Val Tyr Arg Ala Ala Tyr Glu Gly Glu Glu Val Ala Val
1160 1165 1170

Lys Ile Phe Asn Lys His Thr Ser Leu Arg Leu Leu Arg Gln Glu
1175 1180 1185

Leu Val Val Leu Cys His Leu His His Pro Ser Leu Ile Ser Leu
1190 1195 1200

Leu Ala Ala Gly Ile Arg Pro Arg Met Leu Val Met Glu Leu Ala
1205 1210 1215

Ser Lys Gly Ser Leu Asp Arg Leu Leu Gln Gln Asp Lys Ala Ser
1220 1225 1230

Leu Thr Arg Thr Leu Gln His Arg Ile Ala Leu His Val Ala Asp
1235 1240 1245

Gly Leu Arg Tyr Leu His Ser Ala Met Ile Ile Tyr Arg Asp Leu
1250 1255 1260

Lys Pro His Asn Val Leu Leu Phe Thr Leu Tyr Pro Asn Ala Ala
1265 1270 1275

Ile Ile Ala Lys Ile Ala Asp Tyr Gly Ile Ala Gln Tyr Cys Cys
1280 1285 1290

Arg Met Gly Ile Lys Thr Ser Glu Gly Thr Pro Gly Phe Arg Ala
1295 1300 1305

Pro Glu Val Ala Arg Gly Asn Val Ile Tyr Asn Gln Gln Ala Asp
1310 1315 1320

Val Tyr Ser Phe Gly Leu Leu Leu Tyr Asp Ile Leu Thr Thr Gly
1325 1330 1335

Gly Arg Ile Val Glu Gly Leu Lys Phe Pro Asn Glu Phe Asp Glu
1340 1345 1350

Leu Glu Ile Gln Gly Lys Leu Pro Asp Pro Val Lys Glu Tyr Gly
1355 1360 1365

Cys Ala Pro Trp Pro Met Val Glu Lys Leu Ile Lys Gln Cys Leu
1370 1375 1380

Lys Glu Asn Pro Gln Glu Arg Pro Thr Ser Ala Gln Val Phe Asp
1385 1390 1395

Ile Leu Asn Ser Ala Glu Leu Val Cys Leu Thr Arg Arg Ile Leu
1400 1405 1410

Leu Pro Lys Asn Val Ile Val Glu Cys Met Val Ala Thr His His
1415 1420 1425

Asn Ser Arg Asn Ala Ser Ile Trp Leu Gly Cys Gly His Thr Asp
1430 1435 1440

Arg Gly Gln Leu Ser Phe Leu Asp Leu Asn Thr Glu Gly Tyr Thr
1445 1450 1455

Ser Glu Glu Val Ala Asp Ser Arg Ile Leu Cys Leu Ala Leu Val
1460 1465 1470

His Leu Pro Val Glu Lys Glu Ser Trp Ile Val Ser Gly Thr Gln
1475 1480 1485

Ser Gly Thr Leu Leu Val Ile Asn Thr Glu Asp Gly Lys Lys Arg
1490 1495 1500

His Thr Leu Glu Lys Met Thr Asp Ser Val Thr Cys Leu Tyr Cys
1505 1510 1515

Asn Ser Phe Ser Lys Gln Ser Lys Gln Lys Asn Phe Leu Leu Val
1520 1525 1530

Gly Thr Ala Asp Gly Lys Leu Ala Ile Phe Glu Asp Lys Thr Val
1535 1540 1545

Lys Leu Lys Gly Ala Ala Pro Leu Lys Ile Leu Asn Ile Gly Asn
1550 1555 1560

Val Ser Thr Pro Leu Met Cys Leu Ser Glu Ser Thr Asn Ser Thr
1565 1570 1575

Glu Arg Asn Val Met Trp Gly Gly Cys Gly Thr Lys Ile Phe Ser
1580 1585 1590

Phe Ser Asn Asp Phe Thr Ile Gln Lys Leu Ile Glu Thr Arg Thr
1595 1600 1605

Ser Gln Leu Phe Ser Tyr Ala Ala Phe Ser Asp Ser Asn Ile Ile
1610 1615 1620

Thr Val Val Val Asp Thr Ala Leu Tyr Ile Ala Lys Gln Asn Ser
1625 1630 1635

Pro Val Val Glu Val Trp Asp Lys Lys Thr Glu Lys Leu Cys Gly
1640 1645 1650

Leu Ile Asp Cys Val His Phe Leu Arg Glu Val Met Val Lys Glu
1655 1660 1665

Asn Lys Glu Ser Lys His Lys Met Ser Tyr Ser Gly Arg Val Lys
1670 1675 1680

Thr Leu Cys Leu Gln Lys Asn Thr Ala Leu Trp Ile Gly Thr Gly
1685 1690 1695

Gly Gly His Ile Leu Leu Leu Asp Leu Ser Thr Arg Arg Leu Ile
1700 1705 1710

Arg Val Ile Tyr Asn Phe Cys Asn Ser Val Arg Val Met Met Thr
1715 1720 1725

Ala Gln Leu Gly Ser Leu Lys Asn Val Met Leu Val Leu Gly Tyr
1730 1735 1740

Asn Arg Lys Asn Thr Glu Gly Thr Gln Lys Gln Lys Glu Ile Gln
1745 1750 1755

Ser Cys Leu Thr Val Trp Asp Ile Asn Leu Pro His Glu Val Gln
1760 1765 1770

Asn Leu Glu Lys His Ile Glu Val Arg Lys Glu Leu Ala Glu Lys
1775 1780 1785

Met Arg Arg Thr Ser Val Glu
1790 1795

<210> 5

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 5

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

<210> 6

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 6

Arg	Leu	Gly	Arg	Asp	Lys	Tyr	Lys	Thr	Leu	Arg	Gln	Ile	Arg	Gln
1				5					10					15