

9869SG4402-seq1-000001 (2)
SEQUENCE LISTING

<110> AGENCY FOR SCIENCE, TECHNOLOGY AND RESEARCH

<120> ANTI-ERBB-2 ANTIBODIES AND USES THEREOF

<130> 9869SG4402

<160> 12

<170> PatentIn version 3.5

<210> 1

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated peptide sequence

<400> 1

Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Ala	Glu	Leu	Met	Lys	Pro	Gly	Ala
1				5					10					15	

Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr	Phe	Ser	Asn	Tyr
			20					25					30		

Trp	Ile	Glu	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp	Ile
		35					40					45			

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

Lys	Gly	Lys	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Tyr
65					70					75				80	

Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Ala	Arg	Gly	Gly	Ser	Asn	Tyr	Gly	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		

Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
			115				120

<210> 2
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Isolated peptide sequence

<400> 2

Asp Ile Leu Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15

Asp Arg Val Ser Ile Pro Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60

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

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Arg Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 3
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Isolated peptide sequence

<400> 3

Gly Tyr Thr Phe Ser Asn Tyr Trp Ile Glu
 1 5 10

<210> 4
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Isolated peptide sequence

<400> 4

Glu	Ile	Leu	Pro	Gly	Ser	Asp	Ser	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys
1				5					10					15	

Gly

<210> 5
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Isolated peptide sequence

<400> 5

Gly	Gly	Ser	Asn	Tyr	Gly	Tyr	Tyr	Phe	Asp	Tyr
1				5					10	

<210> 6
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Isolated peptide sequence

<400> 6

Lys	Ala	Ser	Gln	Asp	Val	Gly	Thr	Ala	Val	Ala
1				5					10	

<210> 7
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Isolated peptide sequence

<400> 7

Trp Ala Ser Thr Arg His Thr
1 5

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated peptide sequence

<400> 8

Gln Gln Tyr Ser Ser Tyr Arg Thr
1 5

<210> 9

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Isolated nucleotide sequence

<400> 9

caggtgaagc tgcaggagtc tggagctgag ctgatgaagc ctggggcctc agtgaagata	60
tcctgcaagg ctactggcta cacattcagt aactactgga tagagtgggt aaagcagagg	120
cctggacatg gccttgagtg gattggagag attttacctg gaagtgatag tactaactac	180
aatgagaagt tcaagggcaa ggccacattc actgcagata catcctccaa cacagcctac	240
atgcaactca gcagcctgac atctgaggac tctgccgtct attactgtgc aagaggaggg	300
tcgaactacg ggtactactt tgactactgg ggccaaggga ccacggtcac cgtctcctca	360

<210> 10

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Isolated nucleotide sequence

<400> 10

```

gacattctga tgaccagtc tcacaaattc atgtccacat cagtaggaga cagggtcagc      60
atcccctgca aggccagtca ggatgtgggt actgctgtag cctggtatca aaaaaacca      120
gggcaatctc ctaaactact gatttactgg gcatccaccc ggcacactgg agtccttgat      180
cgcttcacag gcagtggatc tgggacagat ttcactctct ccattagcaa tgtgcagtct      240
gaagacttgg cagattatct ctgtcagcaa tatagcagct atcggacgtt cggtggaggc      300
accaagctgg aaatcaaacg g                                     321

```

<210> 11

<211> 1240

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated peptide sequence

<400> 11

```

Met Pro Arg Gly Ser Trp Lys Pro Gln Val Cys Thr Gly Thr Asp Met
1           5           10           15

```

```

Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg
20           25           30

```

```

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

```

```

Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu
50           55           60

```

```

Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro
65           70           75           80

```

```

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

```

```

Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr
100          105          110

```

9869SG4402-seq1-000001 (2)

Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg
115 120 125

Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro
130 135 140

Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys
145 150 155 160

Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala
165 170 175

Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu
180 185 190

Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly
195 200 205

Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln
210 215 220

Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys
225 230 235 240

Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu
245 250 255

Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly
260 265 270

Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr
275 280 285

Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn
290 295 300

Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser
305 310 315 320

9869SG4402-seq1-000001 (2)

Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg
325 330 335

Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys
340 345 350

Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly
355 360 365

Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val
370 375 380

Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp
385 390 395 400

Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile
405 410 415

Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly
420 425 430

Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser
435 440 445

Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr
450 455 460

Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His
465 470 475 480

Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys
485 490 495

His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln
500 505 510

Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu
515 520 525

9869SG4402-seq1-000001 (2)

Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His
530 535 540

Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr
545 550 555 560

Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys
565 570 575

Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp
580 585 590

Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys
595 600 605

Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp
610 615 620

Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile
625 630 635 640

Ser Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe
645 650 655

Gly Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met
660 665 670

Arg Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser
675 680 685

Gly Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu
690 695 700

Leu Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr
705 710 715 720

Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala
725 730 735

9869SG4402-seq1-000001 (2)

Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile
740 745 750

Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser
755 760 765

Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln
770 775 780

Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly
785 790 795 800

Arg Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys
805 810 815

Gly Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala
820 825 830

Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp
835 840 845

Phe Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala
850 855 860

Asp Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu
865 870 875 880

Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
885 890 895

Val Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro
900 905 910

Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln
915 920 925

Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp
930 935 940

9869SG4402-seq1-000001 (2)

Met Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu
945 950 955 960

Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn
965 970 975

Glu Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser
980 985 990

Leu Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
995 1000 1005

Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly
1010 1015 1020

Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
1025 1030 1035

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu
1040 1045 1050

Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser
1055 1060 1065

Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu
1070 1075 1080

Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser
1085 1090 1095

Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val
1100 1105 1110

Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
1115 1120 1125

Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
1130 1135 1140

Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro Lys Thr Leu
1145 1150 1155

Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe Ala Phe Gly
1160 1165 1170

Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln Gly Gly Ala
1175 1180 1185

Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp
1190 1195 1200

Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala Pro
1205 1210 1215

Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
1220 1225 1230

Leu Gly Leu Asp Val Pro Val
1235 1240

<210> 12

<211> 603

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated peptide sequence

<400> 12

Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu
1 5 10 15

Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu
20 25 30

Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln
35 40 45

9869SG4402-seq1-000001 (2)

Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val
50 55 60

Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp
65 70 75 80

Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr
85 90 95

Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu
100 105 110

Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn
115 120 125

Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His
130 135 140

Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg
145 150 155 160

Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly
165 170 175

Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly
180 185 190

Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu
195 200 205

Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala
210 215 220

Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala
225 230 235 240

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

9869SG4402-seq1-000001 (2)

Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn
 260 265 270

Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His
 275 280 285

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

Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu
 305 310 315 320

Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly
 325 330 335

Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp
 340 345 350

Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln
 355 360 365

Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala
 370 375 380

Trp Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val
 385 390 395 400

Ile Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln
 405 410 415

Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly
 420 425 430

Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His
 435 440 445

Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu
 450 455 460

9869SG4402-seq1-000001 (2)

His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala
465 470 475 480

Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr
485 490 495

Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu
500 505 510

Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg
515 520 525

His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val
530 535 540

Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr
545 550 555 560

Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro
565 570 575

Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala
580 585 590

Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser
595 600