

# SEQUENCE LISTING

<110> Icon Genetics GmbH

<120> HER2/NEU CANCER VACCINE

<130> PCT-16413

<160> 22

<170> PatentIn version 3.5

<210> 1

<211> 653

<212> PRT

<213> Homo sapiens

<400> 1

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35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
65 70 75 80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu  
85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr  
100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro  
115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser  
130 135 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln  
145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn  
165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys  
180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser  
 195 200 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys  
 210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys  
 225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu  
 245 250 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val  
 260 265 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg  
 275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu  
 290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln  
 305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys  
 325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu  
 340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys  
 355 360 365

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

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe  
 385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro  
 405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg  
 420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu  
 435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly  
 450 455 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val  
465 470 475 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr  
485 490 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His  
500 505 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys  
515 520 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys  
530 535 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys  
545 550 555 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys  
565 570 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp  
580 585 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu  
595 600 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln  
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<212> PRT  
<213> Homo sapiens

<400> 2

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Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys Pro Cys Ala Arg Val  
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Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu Val Arg Ala Val Thr  
35 40 45

Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser  
 50 55 60

Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr  
 65 70 75 80

Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu  
 85 90 95

Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp  
 100 105 110

Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His  
 115 120 125

Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu  
 130 135 140

Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His  
 145 150 155 160

His Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu  
 165 170 175

Phe Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu  
 180 185 190

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

Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln  
 210 215 220

Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly  
 225 230 235 240

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

Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala  
 260 265 270

Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val  
 275 280 285

Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile  
 290 295 300

Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn  
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Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu  
 325 330 335

Gln Arg Ala Ser Pro Leu Thr Ser  
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 <212> PRT  
 <213> Rattus rattus

<400> 3

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Cys Tyr Gly Leu Gly Met Glu His Leu Arg Gly Ala Arg Ala Ile Thr  
 35 40 45

Ser Asp Asn Val Gln Glu Phe Asp Gly Cys Lys Lys Ile Phe Gly Ser  
 50 55 60

Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ser Ser Gly Ile  
 65 70 75 80

Ala Pro Leu Arg Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu  
 85 90 95

Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Arg Asp  
 100 105 110

Leu Ser Val Phe Gln Asn Leu Arg Ile Ile Arg Gly Arg Ile Leu His  
 115 120 125

Asp Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile His Ser Leu  
 130 135 140

Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His  
 145 150 155 160

Arg Asn Ala His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu  
 165 170 175

Phe Arg Asn Pro His Gln Ala Leu Leu His Ser Gly Asn Arg Pro Glu  
 180 185 190

Glu Asp Cys Gly Leu Glu Gly Leu Val Cys Asn Ser Leu Cys Ala His  
 195 200 205

Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser His  
 210 215 220

Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Trp Lys Gly  
 225 230 235 240

Leu Pro Arg Glu Tyr Val Ser Asp Lys Arg Cys Leu Pro Cys His Pro  
 245 250 255

Glu Cys Gln Pro Gln Asn Ser Ser Glu Thr Cys Phe Gly Ser Glu Ala  
 260 265 270

Asp Gln Cys Ala Ala Cys Ala His Tyr Lys Asp Ser Ser Ser Cys Val  
 275 280 285

Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile  
 290 295 300

Trp Lys Tyr Pro Asp Glu Glu Gly Ile Cys Gln Pro Cys Pro Ile Asn  
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Cys Thr His Ser Cys Val Asp Leu Asp Glu Arg Gly Cys Pro Ala Glu  
 325 330 335

Gln Arg Ala Ser Pro Val Thr Phe  
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 <211> 338  
 <212> PRT  
 <213> homo sapients

<400> 4

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 20 25 30

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 35 40 45

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

Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro  
 65 70 75 80

Leu Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr  
 85 90 95

Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser  
100 105 110

Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly  
115 120 125

Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu  
130 135 140

Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn  
145 150 155 160

Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg  
165 170 175

Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu  
180 185 190

Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His  
195 200 205

Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu  
210 215 220

Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro  
225 230 235 240

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

Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln  
260 265 270

Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg  
275 280 285

Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys  
290 295 300

Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr  
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His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg  
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 <213> homo sapiens

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 35 40 45

Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu  
 50 55 60

Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu  
 65 70 75 80

Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile  
 85 90 95

Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile Ser  
 100 105 110

Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu Ala Leu  
 115 120 125

Ile His His Asn Thr His Leu Cys Phe Val His Thr Val Pro Trp Asp  
 130 135 140

Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr Ala Asn Arg  
 145 150 155 160

Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His Gln Leu Cys  
 165 170 175

Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn Cys  
 180 185 190

Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val Leu  
 195 200 205

Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro Cys  
 210 215 220

His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly Pro  
 225 230 235 240

Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro Phe



245

250

255

Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met  
 260 265 270

Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro  
 275 280 285

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

Ala Glu Gln Arg Ala Ser  
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 <211> 1154  
 <212> DNA  
 <213> Artificial Sequence

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 <223> rat Her2-ED44-His construct

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 agctgaggac ggaacacagc gttgtgagaa atgcagcaag ccctgtgctc gagtgtgcta 180  
 tgggtctgggc atggagcacc ttcgaggggc gagggccatc accagtgaca atgtccagga 240  
 gtttgatggc tgcaagaaga tctttgggag cctggcattt ttgccggaga gctttgatgg 300  
 ggacccctcc tccggcattg ctccgctgag gcctgagcag ctccaagtgt tcgaaaccct 360  
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 ccagctcttc cggaaccac atcaggccct gctccacagt ggggaaccggc cggaagagga 660  
 ttgtggactc gagggcttgg tctgtaactc actgtgtgcc cacgggcact gctgggggcc 720  
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 gtgccgagta tggaaggggc tccccggga gtatgtgagt gacaagcgct gtctgccgtg 840  
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<210> 7  
 <211> 382  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> rat Her2-ED44-His

<400> 7

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 20 25 30

Pro Pro Asn Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys  
 35 40 45

Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met  
 50 55 60

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

Phe Asp Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu  
 85 90 95

Ser Phe Asp Gly Asp Pro Ser Ser Gly Ile Ala Pro Leu Arg Pro Glu  
 100 105 110

Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr  
 115 120 125

Ile Ser Ala Trp Pro Asp Ser Leu Arg Asp Leu Ser Val Phe Gln Asn  
 130 135 140

Leu Arg Ile Ile Arg Gly Arg Ile Leu His Asp Gly Ala Tyr Ser Leu  
 145 150 155 160

Thr Leu Gln Gly Leu Gly Ile His Ser Leu Gly Leu Arg Ser Leu Arg  
 165 170 175

Glu Leu Gly Ser Gly Leu Ala Leu Ile His Arg Asn Ala His Leu Cys  
 180 185 190

Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln  
 195 200 205

Ala Leu Leu His Ser Gly Asn Arg Pro Glu Glu Asp Cys Gly Leu Glu  
 210 215 220

Gly Leu Val Cys Asn Ser Leu Cys Ala His Gly His Cys Trp Gly Pro  
 225 230 235 240

Gly Pro Thr Gln Cys Val Asn Cys Ser His Phe Leu Arg Gly Gln Glu  
 245 250 255

Cys Val Glu Glu Cys Arg Val Trp Lys Gly Leu Pro Arg Glu Tyr Val  
 260 265 270

Ser Asp Lys Arg Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn  
 275 280 285

Ser Ser Glu Thr Cys Phe Gly Ser Glu Ala Asp Gln Cys Ala Ala Cys  
 290 295 300

Ala His Tyr Lys Asp Ser Ser Ser Cys Val Ala Arg Cys Pro Ser Gly  
 305 310 315 320

Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Tyr Pro Asp Glu  
 325 330 335

Glu Gly Ile Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val  
 340 345 350

Asp Leu Asp Glu Arg Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Val  
 355 360 365

Thr Phe Ser Gly Ser Ala Ala Ala His His His His His His  
 370 375 380

<210> 8  
 <211> 1484  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> rat Her2-ED44-kappa construct

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 agctgaggac ggaacacagc gttgtgagaa atgcagcaag ccctgtgctc gagtgtgcta 180  
 tgggtctgggc atggagcacc ttcgaggggc gagggccatc accagtgaca atgtccagga 240  
 gtttgatggc tgcaagaaga tctttgggag cctggcattt ttgccggaga gctttgatgg 300  
 ggacccctcc tccggcattg ctccgctgag gcctgagcag ctccaagtgt tcgaaaccct 360  
 ggaggagatc acagggttacc tgtacatctc agcatggcca gacagtctcc gtgacctcag 420  
 tgtcttccag aaccttcgaa tcattcgggg acggattctc cacgatggcg cgtactcatt 480  
 gacactgcaa ggccctggga tccactcgct ggggctgcgc tcaactgcggg agctgggcag 540

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tggattggct ctgattcacc gcaacgccca tctctgcttt gtacacactg taccttggga      600
ccagctcttc cggaaccac atcaggccct gctccacagt gggaaccggc cggaagagga      660
ttgtggactc gagggcttgg tctgtaactc actgtgtgcc cacgggcact gctggggggc      720
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gtgccgagta tggaaggggc tccccggga gtatgtgagt gacaagcgct gtctgccgtg      840
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tgttactgaa caagactcta aggactctac ttacagtctt tcttcaactc ttaccctatc     1380
aaaggcagat tacgaaaagc ataaggtcta tgcttgtgaa gttacacatc aaggattgag     1440
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<210> 9
<211> 490
<212> PRT
<213> Artificial Sequence

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<220>
<223> rat Her2-ED44-kappa

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<400> 9

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Met Gly Lys Gln Met Ala Ala Leu Cys Gly Phe Leu Leu Val Ala Leu
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Leu Trp Leu Thr Pro Asp Val Ala Ser Gly Ser Cys Thr Leu Val Cys
                20              25              30

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Pro Pro Asn Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys
          35              40              45

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Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met
50              55              60

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

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Phe Asp Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu
          85              90              95

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Ser Phe Asp Gly Asp Pro Ser Ser Gly Ile Ala Pro Leu Arg Pro Glu  
 100 105 110

Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr  
 115 120 125

Ile Ser Ala Trp Pro Asp Ser Leu Arg Asp Leu Ser Val Phe Gln Asn  
 130 135 140

Leu Arg Ile Ile Arg Gly Arg Ile Leu His Asp Gly Ala Tyr Ser Leu  
 145 150 155 160

Thr Leu Gln Gly Leu Gly Ile His Ser Leu Gly Leu Arg Ser Leu Arg  
 165 170 175

Glu Leu Gly Ser Gly Leu Ala Leu Ile His Arg Asn Ala His Leu Cys  
 180 185 190

Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln  
 195 200 205

Ala Leu Leu His Ser Gly Asn Arg Pro Glu Glu Asp Cys Gly Leu Glu  
 210 215 220

Gly Leu Val Cys Asn Ser Leu Cys Ala His Gly His Cys Trp Gly Pro  
 225 230 235 240

Gly Pro Thr Gln Cys Val Asn Cys Ser His Phe Leu Arg Gly Gln Glu  
 245 250 255

Cys Val Glu Glu Cys Arg Val Trp Lys Gly Leu Pro Arg Glu Tyr Val  
 260 265 270

Ser Asp Lys Arg Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn  
 275 280 285

Ser Ser Glu Thr Cys Phe Gly Ser Glu Ala Asp Gln Cys Ala Ala Cys  
 290 295 300

Ala His Tyr Lys Asp Ser Ser Ser Cys Val Ala Arg Cys Pro Ser Gly  
 305 310 315 320

Val Lys Pro Asp Leu Ser Tyr Met Pro Trp Lys Tyr Pro Asp Glu Glu  
 325 330 335

Gly Ile Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp  
 340 345 350

Leu Asp Glu Arg Gly Cys Pro Ala Glu Arg Ala Ser Pro Val Thr Phe  
 355 360 365

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg  
 370 375 380

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr  
 405 410 415

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser  
 420 425 430

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr  
 435 440 445

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
 450 455 460

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro  
 465 470 475 480

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 485 490

<210> 10

<211> 1154

<212> DNA

<213> Artificial Sequence

<220>

<223> human Her2-ED44-His construct

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cgctgaggat ggaactcaga ggtgtgagaa atgtagcaaa ccttgtgcta gagtttgcta	180
tggtttggga atggagcatc ttcgtgaagt tagagccgtt acgtctgccca atatccaaga	240
gtttgcaggc tgtaagaaga tattcggatc tttggcattt ctccctgaat cattcgatgg	300
tgatccagcg tcaaacacag caccattaca acctgagcaa ctccaagtgt ttgagacact	360
agaggagatt acgggggtatc tctacatttc tgcgtggcct gactccttgc cagatctttc	420
agtgtttcag aacttgcaag tgattcgtgg taggatactt cacaacggtg cttatagcct	480
cacattacaa gggttgggca tttcatggct agggttacga agtcttagag aacttggttc	540
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tcagttgttc agaaatcctc atcaagctct gctgcataca gctaatcgtc cagaagatga	660
gtgtgtcgga gaaggtctag catgtcacca gttatgcgct agaggccatt gttggggacc	720

tggaccaact cagtgcgtta attgcagtca gttcctcagg ggtcaggaat gtgtcgaaga 780  
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 gtgcgttgca tgcgcacact acaaggatcc acctttctgt gttgccagat gtccaagcgg 960  
 agtaaaacca gacctttcct atatgccc attgaaattt cccgatgaag agggagcttg 1020  
 ccaaccttgt ccataaaact gcactcatag ttgcgtcgat ttggacgaca aaggttgtcc 1080  
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<210> 11  
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<220>  
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<400> 11

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Leu Trp Leu Thr Pro Asp Val Ala Ser Gly Ser Cys Thr Leu Val Cys  
20 25 30

Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys  
35 40 45

Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met  
50 55 60

Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu  
65 70 75 80

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

Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu  
100 105 110

Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr  
115 120 125

Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn  
130 135 140

Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu  
145 150 155 160

Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg  
165 170 175

Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys  
180 185 190

Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln  
195 200 205

Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu  
210 215 220

Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro  
225 230 235 240

Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu  
245 250 255

Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val  
260 265 270

Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn  
275 280 285

Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys  
290 295 300

Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly  
305 310 315 320

Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu  
325 330 335

Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val  
340 345 350

Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu  
355 360 365

Thr Ser Ser Gly Ser Ala Ala Ala His His His His His His  
370 375 380

<210> 12

<211> 1484

<212> DNA

<213> Artificial Sequence

<220>

<223> human Her2-ED44-kappa construct

<400> 12

aatggggaag caaatggccg ccctgtgtgg ctttctcctc gtggcggtgc tctggctcac

60



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ccccgacgtc gcgtcagggt cttgtactct ggtatgtcca ctacacaatc aggaagtaac      120
cgctgaggat ggaactcaga ggtgtgagaa atgtagcaaa ccttgtgcta gagtttgcta      180
tggtttggga atggagcatc ttcgtgaagt tagagccgtt acgtctgcca atatccaaga      240
gtttgcaggc tgtaagaaga tattcggatc tttggcattt ctccctgaat cattcgatgg      300
tgatccagcg tcaaacacag caccattaca acctgagcaa ctccaagtgt ttgagacact      360
agaggagatt acgggggtatc tctacatttc tgcgtggcct gactccttgc cagatctttc      420
agtgtttcag aacttgcaag tgattcgtgg taggatactt cacaacggtg cttatagcct      480
cacattacaa gggttgggca tttcatggct agggttacga agtcttagag aacttggttc      540
tggtattggc cttatccacc ataacacca tttgtgcttt gtgcacacag taccatggga      600
tcagttgttc agaaatcctc atcaagctct gctgcataca gctaatcgtc cagaagatga      660
gtgtgtcgga gaaggtctag catgtcacca gttatgcgct agaggccatt gttggggacc      720
tggaaccaact cagtgcgtta attgcagtca gttcctcagg ggtcaggaat gtgtcgaaga      780
atgcaggggt ttacaagggc ttcctagaga atacgtgaat gcccgcatt gcctgccttg      840
tcatccagaa tgtcaacccc aaaatgggtc cgttacttgt tttggcccag aggctgatca      900
gtgcgttgca tgcgcacact acaaggatcc acctttctgt gttgccagat gtccaagcgg      960
agtaaaacca gacctttcct atatgcccac ttggaaattt cccgatgaag agggagcttg     1020
ccaaccttgt ccataaaact gcactcatag ttgcgtcgat ttggacgaca aaggttgctc     1080
agctgaacaa agagctttctc cgcttacatc aggaggcgga ggaagtggag gcggtggatc     1140
aggaggcggt ggctcacgaa cagttgctgc tctagtgtt tttatttttc ccccatccga     1200
tgaacaattg aaatctggaa ctgcatccgt agtatgcttg ttgaacaatt tctaccctag     1260
agaagctaag gttcaatgga aagtcgataa tgcactacag tctggtaatt cacaagagtc     1320
tgttactgaa caagactcta aggactctac ttacagtctt tcttcaactc ttaccctatc     1380
aaaggcagat tacgaaaagc ataaggctta tgcttggtgaa gttacacatc aaggattgag     1440
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<210> 13
<211> 492
<212> PRT
<213> Artificial Sequence

<220>
<223> human Her2-ED44-kappa

<400> 13

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Met Gly Lys Gln Met Ala Ala Leu Cys Gly Phe Leu Leu Val Ala Leu
1           5           10          15

Leu Trp Leu Thr Pro Asp Val Ala Ser Gly Ser Cys Thr Leu Val Cys
          20          25          30

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Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys  
 35 40 45

Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met  
 50 55 60

Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu  
 65 70 75 80

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

Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu  
 100 105 110

Gln Leu Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr  
 115 120 125

Ile Ser Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn  
 130 135 140

Leu Gln Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu  
 145 150 155 160

Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg  
 165 170 175

Glu Leu Gly Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys  
 180 185 190

Phe Val His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln  
 195 200 205

Ala Leu Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu  
 210 215 220

Gly Leu Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro  
 225 230 235 240

Gly Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu  
 245 250 255

Cys Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val  
 260 265 270

Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn  
 275 280 285

Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys  
 290 295 300

Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly  
305 310 315 320

Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu  
325 330 335

Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val  
340 345 350

Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu  
355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
370 375 380

Ser Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
385 390 395 400

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
405 410 415

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
420 425 430

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
435 440 445

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
450 455 460

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
465 470 475 480

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
485 490

<210> 14

<211> 1805

<212> DNA

<213> Artificial Sequence

<220>

<223> Tetanus toxin fragment C-kappa construct

<400> 14

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tggtatcctg aaaaagtcta ccattctgaa cttggacatc aacaacgata ttatctccga 180

catctctggt ttcaactcct ctgttatcac atatccagat gctcaattgg tgccggggcat 240

caacggcaaa gctatccacc tggttaacaa cgaatcttct gaagttatcg tgcacaaggc 300

catggacatc gaatacaacg acatgttcaa caacttcacc gttagcttct ggctgcgcgt	360
tccgaaagtt tctgcttccc acctggaaca gtacggcact aacgagtact ccatcatcag	420
ctctatgaag aaacactccc tgtccatcgg ctctggttgg tctgtttccc tgaagggtaa	480
caacctgacg tggactctga aagactccgc gggcgaagtt cgtcagatca ctttcgcgca	540
cctgccggac aagttcaacg cgtacctggc taacaaatgg gttttcatca ctatcactaa	600
cgatcgtctg tcatctgcta acctgtacat caacggcggt ctgatgggct ccgctgaaat	660
cactgggtctg ggcgctatcc gtgaggacaa caacatcact cttaagctgg accggttgca	720
caacaacaac cagtacgtat ccatcgacaa gttccgtatc ttctgcaaag cactgaaccc	780
gaaagagatc gaaaaactgt ataccagcta cctgtctatc accttcctgc gtgacttctg	840
gggtaacccg ctgcgttacg acaccgaata ttacctgacg ccggtagctt ctagctctaa	900
agacgttcag ctgaaaaaca tctactgacta catgtacctg accaacgcgc cgtcctacac	960
taacggtaaa ctgaacatct actaccgacg tctgtacaac ggctgaaat tcatcatcaa	1020
acgctacact ccgaacaacg aaatcgattc tttcgttaaa tctggtgact tcatcaaact	1080
gtacgtttct tacaacaaca acgaacacat cgttggttac ccgaaagacg gtaacgcttt	1140
caacaacctg gacagaattc tgcgtggttg ttacaacgct ccgggtatcc cgctgtacaa	1200
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cccgaaccgt gacatcctga tcgcttctaa ctggtacttc aaccacctga aagacaaaat	1380
cctgggttgc gactggtact tcgttccgac cgatgaaggt tggaccaacg acggaggcgg	1440
aggaagtgga ggcggtggat caggaggcgg tggctcacga acagttgctg ctccatgtgt	1500
ttttattttt ccccatccg atgaacaatt gaaatctgga actgcatccg tagtatgctt	1560
gttgaacaat ttctacccta gagaagctaa ggttcaatgg aaagtcgata atgcactaca	1620
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ttcttcaact cttaccctat caaaggcaga ttacgaaaag cataaggtct atgcttgtga	1740
agttacacat caaggattga gttcaccagt tacaaagagt tttaaccgtg gtgagtgtta	1800
agctt	1805

<210> 15  
 <211> 599  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Tetanus toxin fragment C-kappa

<400> 15

Met	Gly	Lys	Gln	Met	Ala	Ala	Leu	Cys	Gly	Phe	Leu	Leu	Val	Ala	Leu
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Leu Trp Leu Thr Pro Asp Val Ala Ser Gly Lys Asn Leu Asp Cys Trp  
 20 25 30

Val Asp Asn Glu Glu Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile  
 35 40 45

Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe  
 50 55 60

Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile  
 65 70 75 80

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

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

Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu  
 115 120 125

Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys  
 130 135 140

His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn  
 145 150 155 160

Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile  
 165 170 175

Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys  
 180 185 190

Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu  
 195 200 205

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

Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn  
 225 230 235 240

Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys  
 245 250 255

Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser  
 260 265 270

Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr  
 275 280 285

Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser Ser Lys Asp Val Gln Leu  
290 295 300

Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr Asn Ala Pro Ser Tyr Thr  
305 310 315 320

Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg Leu Tyr Asn Gly Leu Lys  
325 330 335

Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn Glu Ile Asp Ser Phe Val  
340 345 350

Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val Ser Tyr Asn Asn Asn Glu  
355 360 365

His Ile Val Gly Tyr Pro Lys Asp Gly Asn Ala Phe Asn Asn Leu Asp  
370 375 380

Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro Gly Ile Pro Leu Tyr Lys  
385 390 395 400

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

Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser Leu Gly Leu Val Gly Thr  
420 425 430

His Asn Gly Gln Ile Gly Asn Asp Pro Asn Arg Asp Ile Leu Ile Ala  
435 440 445

Ser Asn Trp Tyr Phe Asn His Leu Lys Asp Lys Ile Leu Gly Cys Asp  
450 455 460

Trp Tyr Phe Val Pro Thr Asp Glu Gly Trp Thr Asn Asp Gly Gly Gly  
465 470 475 480

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Thr Val Ala  
485 490 495

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser  
500 505 510

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
515 520 525

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
530 535 540

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

545                      550                      555                      560  
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
                          565                      570                      575  
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
                          580                      585                      590  
 Ser Phe Asn Arg Gly Glu Cys  
                          595  
  
 <210> 16  
 <211> 161  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> TMV-CPlys  
  
 <400> 16  
 Met Ala Asp Phe Lys Ser Tyr Asn Ile Thr Asn Pro Asn Gln Tyr Gln  
 1                      5                      10                      15  
 Tyr Phe Ala Ala Val Trp Ala Glu Pro Ile Pro Met Leu Asn Gln Cys  
                          20                      25                      30  
 Met Ser Ala Leu Ser Gln Ser Tyr Gln Thr Gln Ala Ala Arg Asp Thr  
                          35                      40                      45  
 Val Arg Gln Gln Phe Ser Asn Leu Leu Ser Ala Val Val Thr Pro Ser  
                          50                      55                      60  
 Gln Arg Phe Pro Asp Thr Gly Ser Arg Val Tyr Val Asn Ser Ala Val  
 65                      70                      75                      80  
 Ile Lys Pro Leu Tyr Glu Ala Leu Met Lys Ser Phe Asp Thr Arg Asn  
                          85                      90                      95  
 Arg Ile Ile Glu Thr Glu Glu Glu Ser Arg Pro Ser Ala Ser Glu Val  
                          100                      105                      110  
 Ala Asn Ala Thr Gln Arg Val Asp Asp Ala Thr Val Ala Ile Arg Ser  
                          115                      120                      125  
 Gln Ile Gln Leu Leu Leu Ser Glu Leu Ser Asn Gly His Gly Tyr Met  
                          130                      135                      140  
 Asn Arg Ala Glu Phe Glu Ala Leu Leu Pro Trp Thr Thr Ala Pro Ala  
 145                      150                      155                      160  
 Thr

<210> 17  
 <211> 265  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> DOM1 domain of tetanus toxin fragment C

<400> 17

Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly  
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Val His Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile  
 20 25 30

Asp Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn  
 35 40 45

Asp Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr  
 50 55 60

Pro Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu  
 65 70 75 80

Val Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile  
 85 90 95

Glu Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg  
 100 105 110

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

Tyr Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser  
 130 135 140

Gly Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys  
 145 150 155 160

Asp Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp  
 165 170 175

Lys Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr  
 180 185 190

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

Gly Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn  
 210 215 220



Ile Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser  
 225 230 235 240

Ile Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile  
 245 250 255

Glu Lys Leu Tyr Thr Ser Tyr Leu Ser  
 260 265

<210> 18  
 <211> 1255  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu  
 1 5 10 15

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

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
 35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
 50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
 65 70 75 80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu  
 85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr  
 100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro  
 115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser  
 130 135 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln  
 145 150 155 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn  
 165 170 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys  
 180 185 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser  
195 200 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys  
210 215 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys  
225 230 235 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu  
245 250 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val  
260 265 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg  
275 280 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu  
290 295 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln  
305 310 315 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys  
325 330 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu  
340 345 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys  
355 360 365

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

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe  
385 390 395 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro  
405 410 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg  
420 425 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu  
435 440 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly

450		455		460
Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val				
465		470		475 480
Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr				
	485		490	495
Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His				
	500		505	510
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys				
	515		520	525
Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys				
	530		535	540
Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys				
545		550		555 560
Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys				
	565		570	575
Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp				
	580		585	590
Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu				
	595		600	605
Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln				
	610		615	620
Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys				
625		630		635 640
Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Val Ser				
	645		650	655
Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly				
	660		665	670
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg				
	675		680	685
Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly				
	690		695	700
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu				
705		710		715 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys  
                     725                    730                    735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile  
                     740                    745                    750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu  
                     755                    760                    765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg  
                     770                    775                    780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu  
                     785                    790                    795                    800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg  
                     805                    810                    815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly  
                     820                    825                    830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala  
                     835                    840                    845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe  
                     850                    855                    860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp  
                     865                    870                    875                    880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg  
                     885                    890                    895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val  
                     900                    905                    910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala  
                     915                    920                    925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro  
                     930                    935                    940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met  
                     945                    950                    955                    960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe  
                     965                    970                    975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu  
                     980                    985                    990

Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu
		995					1000					1005			
Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	
	1010					1015					1020				
Leu	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	
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