

SEQUENCE LISTING

<110> Baylor College of Medicine
 <120> ONCOLYTIC VIROTHERAPY AND IMMUNOTHERAPY
 <130> BAYM.P0227W0
 <160> 64
 <170> PatentIn version 3.5
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<220>
 <223> HER2(C5)-CD28TM,ICD-CD3Z CAR

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			20					25					30		

Gly	Leu	Val	Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser
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Gly	Gly	Ser	Ile	Ser	Ser	Ser	Ser	Tyr	Tyr	Trp	Gly	Trp	Ile	Arg	Gln
	50					55					60				

Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	Gly	Ser	Ile	Tyr	Tyr	Ser	Gly
65					70					75				80	

Ser	Thr	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Val
				85					90					95	

Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala
			100					105					110		

Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Ala	Pro	Asp	Ser	Ser
		115					120					125			

Gly Tyr Leu Val Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
130 135 140

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
145 150 155 160

Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro
165 170 175

Gly Gly Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser
180 185 190

Thr Gly Tyr Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro
195 200 205

Arg Thr Leu Ile Tyr Ser Thr Asn Ser Arg Ser Ser Gly Val Pro Asp
210 215 220

Arg Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr
225 230 235 240

Gly Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Val Leu Tyr Met
245 250 255

Gly Ser Gly Ile Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
260 265 270

Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Thr Arg
275 280 285

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
290 295 300

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
305 310 315 320

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
325 330 335

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
 340 345 350

Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 355 360 365

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 370 375 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 385 390 395 400

Met Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
 405 410 415

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
 420 425 430

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
 435 440 445

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
 450 455 460

Ala Leu Pro Pro Arg
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<210> 2
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<220>
 <223> HER2(E4)-CD28TM,ICD-CD3Z CAR

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Met Thr Arg Ala Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly
 1 5 10 15

Ala Ala Thr Gly Ala His Ser Gln Val Gln Leu Gln Gln Trp Gly Ala
 20 25 30

Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr
35 40 45

Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro
50 55 60

Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr
65 70 75 80

Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr
85 90 95

Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Thr Ala Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Met Gly Ile Asn Ser Gly Gly Tyr
115 120 125

Leu Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
145 150 155 160

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
165 170 175

Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Ser
180 185 190

Tyr Tyr Pro Ser Trp Tyr Gln Gln Ile Pro Gly Gln Ala Pro Arg Thr
195 200 205

Leu Ile Tyr Thr Thr Asn Ile Arg Ser Ser Gly Val Pro Asp Arg Phe
210 215 220

Gly Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
225 230 235 240

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Met Leu Tyr Met Gly Ser
245 250 255

Gly Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
260 265 270

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Thr Arg Phe Trp
275 280 285

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
290 295 300

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
305 310 315 320

Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr
325 330 335

Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr
340 345 350

Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
355 360 365

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
370 375 380

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
385 390 395 400

Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
405 410 415

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
420 425 430

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
435 440 445

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu

450

455

460

Pro Pro Arg
465

<210> 3
<211> 468
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<223> HER2(F1)-CD28TM,ICD-CD3Z CAR

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Ala Ala Thr Gly Ala His Ser Gln Val Gln Leu Val Glu Ser Gly Pro
20 25 30

Gly Leu Val Lys Pro Ser Gly Thr Leu Ser Leu Thr Cys Ala Val Ser
35 40 45

Gly Gly Ser Ile Ser Ser Ser Asn Trp Trp Ser Trp Val Arg Gln Pro
50 55 60

Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Tyr His Ser Gly Ser
65 70 75 80

Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp
85 90 95

Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala
100 105 110

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Met Gly Ala Asn Ser Gly Gly
115 120 125

Tyr Leu Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
130 135 140

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly
165 170 175

Gly Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr
180 185 190

Ser Tyr Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg
195 200 205

Thr Leu Ile Tyr Ser Thr Asn Thr Arg Ser Ser Gly Val Pro Asp Arg
210 215 220

Phe Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly
225 230 235 240

Ala Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Val Leu Tyr Met Gly
245 250 255

Ser Gly Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
260 265 270

Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Thr Arg Phe
275 280 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
290 295 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305 310 315 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
325 330 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
340 345 350

Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr

355 360 365
 Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 370 375 380
 Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 385 390 395 400
 Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 405 410 415
 Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 420 425 430
 Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 435 440 445
 Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 450 455 460
 Leu Pro Pro Arg
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<210> 4
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 <223> CD28 TMD

<400> 4

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
 1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
 20 25

<210> 5
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<223> CD28 ICD

<400> 5

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 6

<211> 113

<212> PRT

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<223> CD3Z ICD

<400> 6

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
50 55 60

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65 70 75 80

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
85 90 95

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro

100

105

110

Arg

<210> 7
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Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
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<210> 8
 <211> 19
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<220>
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<400> 8

Met	Asp	Trp	Ile	Trp	Arg	Ile	Leu	Phe	Leu	Val	Gly	Ala	Ala	Thr	Gly
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Ala His Ser

<210> 9
 <211> 14
 <212> PRT
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<220>
 <223> Hinge

<400> 9

Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Thr	Arg
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<210> 10
<211> 14
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<223> HER2(C5) LC-CDR1

<400> 10

Gly Leu Ser Ser Gly Ser Val Ser Thr Gly Tyr Tyr Pro Ser
1 5 10

<210> 11
<211> 7
<212> PRT
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<220>
<223> HER2(C5) LC-CDR2

<400> 11

Ser Thr Asn Ser Arg Ser Ser
1 5

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(C5) LC-CDR3

<400> 12

Val Leu Tyr Met Gly Ser Gly Ile Ser Val
1 5 10

<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(C5) HC-CDR1

<400> 13

Ser Ser Ser Tyr Tyr Trp Gly

1

5

<210> 14
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(C5) HC-CDR2

<400> 14

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

<210> 15
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(C5) HC-CDR3

<400> 15

Tyr Ala Pro Asp Ser Ser Gly Tyr Leu Val Ala Phe Asp Ile
1 5 10

<210> 16
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(C5) VL

<400> 16

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Gly
20 25 30

Tyr Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Thr
35 40 45

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

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Gly Ile Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

<210> 17
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(C5) VH

<400> 17

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Tyr Ala Pro Asp Ser Ser Gly Tyr Leu Val Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 18
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(E4) LC-CDR1

<400> 18

Gly Leu Ser Ser Gly Ser Val Ser Thr Ser Tyr Tyr Pro Ser
1 5 10

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(E4) LC-CDR2

<400> 19

Thr Thr Asn Ile Arg Ser Ser
1 5

<210> 20
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(E4) LC-CDR3

<400> 20

Met Leu Tyr Met Gly Ser Gly Ile Trp Val
1 5 10

<210> 21
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> HER2(E4) HC-CDR1

<400> 21

Ser Gly Tyr Tyr Trp Ser
1 5

<210> 22

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HER2(E4) HC-CDR2

<400> 22

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

<210> 23

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> HER2(E4) HC-CDR3

<400> 23

Met Gly Ile Asn Ser Gly Gly Tyr Leu Tyr Gly Met Asp Val
1 5 10

<210> 24

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> HER2(E4) VL

<400> 24

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Ser
20 25 30

Tyr Tyr Pro Ser Trp Tyr Gln Gln Ile Pro Gly Gln Ala Pro Arg Thr
35 40 45

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

Gly Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Gly Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

<210> 25
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(E4) VH

<400> 25

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

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

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

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

Lys Leu Ser Ser Val Thr Thr Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Met Gly Ile Asn Ser Gly Gly Tyr Leu Tyr Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(F1) LC-CDR1

<400> 26

Gly Leu Ser Ser Gly Ser Val Ser Thr Ser Tyr Tyr Pro Ser
1 5 10

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(F1) LC-CDR2

<400> 27

Ser Thr Asn Thr Arg Ser Ser
1 5

<210> 28
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(F1) LC-CDR3

<400> 28

Val Leu Tyr Met Gly Ser Gly Ile Trp Val
1 5 10

<210> 29

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

<220>
<223> HER2(F1) HC-CDR1

<400> 29

Ser Ser Asn Trp Trp Ser
1 5

<210> 30
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(F1) HC-CDR2

<400> 30

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

<210> 31
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(F1) HC-CDR3

<400> 31

Met Gly Ala Asn Ser Gly Gly Tyr Leu Tyr Gly Met Asp Val
1 5 10

<210> 32
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(F1) VL

<400> 32

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Ser
20 25 30

Tyr Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Thr
35 40 45

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

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Gly Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ser
100 105 110

<210> 33
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> HER2(F1) VH

<400> 33

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

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser

65					70						75				80
Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Met	Gly	Ala	Asn	Ser	Gly	Gly	Tyr	Leu	Tyr	Gly	Met	Asp	Val
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser					
		115					120								
<210> 34															
<211> 281															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Ad2 E1Delta24															
<400> 34															
Met	Arg	His	Ile	Ile	Cys	His	Gly	Gly	Val	Ile	Thr	Glu	Glu	Met	Ala
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Ala	Ser	Leu	Leu	Asp	Gln	Leu	Ile	Glu	Glu	Val	Leu	Ala	Asp	Asn	Leu
			20					25					30		
Pro	Pro	Pro	Ser	His	Phe	Glu	Pro	Pro	Thr	Leu	His	Glu	Leu	Tyr	Asp
			35				40					45			
Leu	Asp	Val	Thr	Ala	Pro	Glu	Asp	Pro	Asn	Glu	Glu	Ala	Val	Ser	Gln
	50					55				60					
Ile	Phe	Pro	Glu	Ser	Val	Met	Leu	Ala	Val	Gln	Glu	Gly	Ile	Asp	Leu
65					70					75				80	
Phe	Thr	Phe	Pro	Pro	Ala	Pro	Gly	Ser	Pro	Glu	Pro	Pro	His	Leu	Ser
				85					90					95	
Arg	Gln	Pro	Glu	Gln	Pro	Glu	Gln	Arg	Ala	Leu	Gly	Pro	Val	Ser	Met
			100				105						110		

Pro Asn Leu Val Pro Glu Val Ile Asp Pro Pro Ser Asp Asp Glu Asp
115 120 125

Glu Glu Gly Glu Glu Phe Val Leu Asp Tyr Val Glu His Pro Gly His
130 135 140

Gly Cys Arg Ser Cys His Tyr His Arg Arg Asn Thr Gly Asp Pro Asp
145 150 155 160

Ile Met Cys Ser Leu Cys Tyr Met Arg Thr Cys Gly Met Phe Val Tyr
165 170 175

Ser Pro Val Ser Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
180 185 190

Ala Arg Pro Thr Arg Arg Pro Lys Leu Val Pro Ala Ile Leu Arg Arg
195 200 205

Pro Thr Ser Pro Val Ser Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys
210 215 220

Asp Ser Gly Pro Ser Asn Thr Pro Pro Glu Ile His Pro Val Val Pro
225 230 235 240

Leu Cys Pro Ile Lys Pro Val Ala Val Arg Val Gly Gly Arg Arg Gln
245 250 255

Ala Val Glu Cys Ile Glu Asp Leu Leu Asn Glu Ser Gly Gln Pro Leu
260 265 270

Asp Leu Ser Cys Lys Arg Pro Arg Pro
275 280

<210> 35
<211> 536
<212> PRT
<213> Artificial Sequence

<220>
<223> huIL-12p70

<400> 35

Met	Gly	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu				
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Ala	Ser	Pro	Leu	Val	Ala	Ile	Trp	Glu	Leu	Lys	Lys	Asp	Val	Tyr	Val				
			20					25					30						
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu				
		35					40					45							
Thr	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Leu	Asp	Gln				
	50					55					60								
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys				
65					70					75					80				
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val				
				85					90					95					
Leu	Ser	His	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp				
			100					105					110						
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Thr	Phe				
		115					120					125							
Leu	Arg	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp				
	130					135					140								
Leu	Thr	Thr	Ile	Ser	Thr	Asp	Leu	Thr	Phe	Ser	Val	Lys	Ser	Ser	Arg				
145					150					155					160				
Gly	Ser	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser				
				165					170					175					
Ala	Glu	Arg	Val	Arg	Gly	Asp	Asn	Lys	Glu	Tyr	Glu	Tyr	Ser	Val	Glu				
			180					185					190						
Cys	Gln	Glu	Asp	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile				
		195					200					205							

Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
 210 215 220

Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
 225 230 235 240

Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
 245 250 255

Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
 260 265 270

Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
 275 280 285

Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
 290 295 300

Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
 305 310 315 320

Glu Trp Ala Ser Val Pro Cys Ser Val Pro Gly Val Gly Val Pro Gly
 325 330 335

Val Gly Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe
 340 345 350

Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met
 355 360 365

Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu
 370 375 380

Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu
 385 390 395 400

Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser
 405 410 415

Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys

420				425				430							
Thr	Ser	Phe	Met	Met	Ala	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu
		435					440					445			
Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys	Leu	Leu	Met
		450					455					460			
Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Ala	Val	Ile
465					470					475					480
Asp	Glu	Leu	Met	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Glu	Thr	Val	Pro	Gln
				485					490					495	
Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu
				500					505					510	
Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asp	Arg
				515					520					525	
Val	Met	Ser	Tyr	Leu	Asn	Ala	Ser								
				530			535								

Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr
50 55 60

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

Val Pro Glu Pro Met Thr Tyr Trp Arg Val Leu Gly Ala Ser Glu Thr
85 90 95

Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile
100 105 110

Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met
115 120 125

Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Ile Gly
130 135 140

Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile
145 150 155 160

Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg
165 170 175

Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala
180 185 190

Leu Ile Pro Pro Thr Leu Pro Gly Thr Asn Ile Val Leu Gly Ala Leu
195 200 205

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

Glu Arg Leu Asp Leu Ala Met Leu Ala Ala Ile Arg Arg Val Tyr Gly
225 230 235 240

Leu Leu Ala Asn Thr Val Arg Tyr Leu Gln Gly Gly Gly Ser Trp Arg
245 250 255

Glu Asp Trp Gly Gln Leu Ser Gly Thr Ala Val Pro Pro Gln Gly Ala

260						265						270					
Glu	Pro	Gln	Ser	Asn	Ala	Gly	Pro	Arg	Pro	His	Ile	Gly	Asp	Thr	Leu		
		275					280					285					
Phe	Thr	Leu	Phe	Arg	Ala	Pro	Glu	Leu	Leu	Ala	Pro	Asn	Gly	Asp	Leu		
290						295					300						
Tyr	Asn	Val	Phe	Ala	Trp	Ala	Leu	Asp	Val	Leu	Ala	Lys	Arg	Leu	Arg		
305					310					315					320		
Pro	Met	His	Val	Phe	Ile	Leu	Asp	Tyr	Asp	Gln	Ser	Pro	Ala	Gly	Cys		
				325					330					335			
Arg	Asp	Ala	Leu	Leu	Gln	Leu	Thr	Ser	Gly	Met	Ile	Gln	Thr	His	Val		
		340						345					350				
Thr	Thr	Pro	Gly	Ser	Ile	Pro	Thr	Ile	Cys	Asp	Leu	Ala	Arg	Thr	Phe		
		355					360					365					
Ala	Arg	Glu	Met	Gly	Glu	Ala	Asn										
370						375											

<400> 38

Met Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly
1 5 10 15

Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35 40 45

Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Arg Ser Gly His Gly Tyr Ser Tyr Gly Ala Phe Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr
145 150 155 160

Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser
165 170 175

Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp
180 185 190

Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn
195 200 205

Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
 210 215 220

Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu
 225 230 235 240

Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Tyr
 245 250 255

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Ala Lys Ser
 260 265 270

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 275 280 285

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495

Ser Pro Gly Lys Gly Gly Gly Gly Ser Tyr Pro Tyr Asp Val Pro Asp
500 505 510

Tyr Ala Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Tyr Pro Tyr
515 520 525

Asp Val Pro Asp Tyr Ala
530

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1(H12_g1) LC-CDR1

<400> 39

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His
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<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1(H12_g1) LC-CDR2

<400> 40

Gly Asn Ser Asn Arg Pro Ser
1 5

<210> 41

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> PD-L1(H12_g1) LC-CDR3

<400> 41

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Ser Tyr Val Val
1 5 10

<210> 42

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> PD-L1(H12_g1) HC-CDR1

<400> 42

Ser Tyr Ala Ile Ser
1 5

<210> 43

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PD-L1(H12_g1) HC-CDR2

<400> 43

Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 44
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PD-L1(H12_g1) HC-CDR3

<400> 44

Ser Gly His Gly Tyr Ser Tyr Gly Ala Phe Asp Tyr
 1 5 10

<210> 45
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PD-L1(H12_g1) VL

<400> 45

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
 20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
 35 40 45

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
 85 90 95

Leu Ser Gly Ser Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val
 100 105 110

Leu

<210> 46
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> PD-L1(H12_g1) VH

<400> 46

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

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

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Ser Gly His Gly Tyr Ser Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 47
<211> 3750
<212> DNA
<213> Artificial Sequence

<220>
<223> HER2(C5)-CD28TM,ICD-CD3Z CAR

<400> 47

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ccaaacagga tatctgtggt aagcagttcc tgccccggct caggccaag aacagatggt	180
ccccagatgc ggtccagccc tcagcagttt ctagagaacc atcagatggt tccagggtgc	240
cccaaggacc tgaaatgacc ctgtgcctta tttgaactaa ccaatcagtt cgcttctcgc	300
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cgcgccagtc ctccgattga ctgagtcgcc cgggtacccg tgtatccaat aaaccctctt	420
gcagttgcat ccgacttggt gtctcgctgt tccttgggag ggtctcctct gagtgattga	480
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gatcgtttag gactctttgg tgcaccccc ttagaggagg gatatgtggt tctggtagga	840
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cgagacggca ctttaaccg agacctcatc acccagggtta agatcaaggt cttttcacct	1200
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acagcgagat aggaatgaag ggtgaaaggc gtcgtggaaa gggccacgat gggctttacc	3120
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actgagaata gagaagttca gatcaaggthc aggaacagat ggaacagctg aatatgggthc	3480
aaacaggata thtgttggtaa gcagthtctg ccccggtca gggccaagaa cagatggaa	3540
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aagaacagat ggtccccaga thcggtccag cctcagcag thtctagaga accatcagat	3660
gthtccaggg thccccaagg acctgaaatg acctgtgthc thatttgaac taaccaatca	3720
gthcgthtct cgthtctgtt cgcgcgtht	3750

<210> 48

<211> 3744

<212> DNA

<213> Artificial Sequence

<220>

<223> HER2(E4)-CD28TM,ICD-CD3Z CAR

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ccaaacagga thtctgtggt aagcagthtcc thccccggct cagggccaag aacagatggt	180
ccccagatgc ggtccagccc thcagcagtht ctagagaacc atcagatgth thcagggtgc	240
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thtctgttcgc gcgthtctgc thccccgagct caataaaaga gcccacaacc cthcactcgg	360
cgcgccagth thccgattga thgagthcgc cgggtacccg thtatccaat aaacctctth	420
gcagthtgcath ccgactthgtg thtctcgtgt thcttgggag ggtctctctth gathgattga	480
thacccgtca gcgggggtct thcaththggg ggthcgtccg ggatcgggag acctctgccc	540
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athgtctagth gthtatgact gathththtgc gcctgcgtcg thtactagth gthaactagc	660

tctgtatctg gcggacccgt ggtggaactg acgagttcgg aacacccggc cgcaaccctg	720
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accttaggtc actggaaaga tgtcgagcgg atcgttcaca accagtcggt agatgtcaag	1080
aagagacgtt gggttacctt ctgctctgca gaatggccaa cttttaacgt cggatggccg	1140
cgagacggca cttttaaccg agacctcatc acccaggtta agatcaaggt cttttcacct	1200
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aaaataaaag attttattta gtctccagaa aaagggggga atgaaagacc ccacctgtag	3360
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aatagagaag ttcagatcaa ggtcaggaac agatggaaca gctgaatatg ggccaaacag	3480
gatatctgtg gtaagcagtt cctgccccgg ctcagggccca agaacagatg gaacagctga	3540
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agatgggtccc cagatgcggg ccagccctca gcagtttcta gagaaccatc agatgtttcc	3660
agggtgcccc aaggacctga aatgaccctg tgccttattt gaactaacca atcagttcgc	3720
ttctcgcttc tgttcgcgcg cttc	3744

<211> 3747
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HER2(F1)-CD28TM,ICD-CD3Z CAR

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 ccaaacagga tatctgtggt aagcagttcc tgccccggct cagggccaaag aacagatggg 180
 ccccagatgc ggtccagccc tcagcagttt ctagagaacc atcagatggt tccagggtgc 240
 cccaaggacc tgaaatgacc ctgtgcctta tttgaactaa ccaatcagtt cgcttctcgc 300
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35 40 45

Gly Tyr Thr Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
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Gly Gln Gly Leu Glu Trp Met Ala Ile Ile Asn Pro Gly Asn Gly Asp
65 70 75 80

Thr Asn Tyr Ala Gln Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp
85 90 95

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

Asp Thr Ala Val Tyr Phe Cys Ala Arg Glu Ile Ala Ser Tyr Ser Gly
115 120 125

Ser Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
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Ala Val Val Leu Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly Thr
165 170 175

Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Gly His
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Tyr Ala Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Thr Leu
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Phe Tyr Asn Thr Asn Thr Arg Ser Ser Gly Val Pro Asp Arg Phe Ser
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Gly Ser Ile Val Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln
225 230 235 240

Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Val Leu Tyr Val Gly Asp Gly
245 250 255

Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys
260 265 270

Ser Cys Asp Lys Thr His Thr Cys Pro Thr Arg Phe Trp Val Leu Val
275 280 285

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
290 295 300

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
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Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
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Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
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Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
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Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
370 375 380

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
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Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
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Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
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Ser Gly Ser Ile Val Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala		
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Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Val Leu Tyr Val Gly Asp		
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	85	90 95

Ala Arg Glu Ile Ala Ser Tyr Ser Gly Ser Tyr Tyr Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
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