

PCTAU2016050851-seq1-000001-EN-20160920  
SEQUENCE LISTING

<110> CTM@CRC Ltd.

<120> CHIMERIC ANTIGEN RECEPTOR AND USES THEREOF

<130> 1068243

<150> 2015903719

<151> 2015-09-11

<160> 54

<170> PatentIn version 3.5

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Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys  
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Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val  
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Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro  
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Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu  
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Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu  
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Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser  
130 135 140

Lys Gly Ile Gln Thr Gly Arg Cys Val Val Tyr Glu Gly Asn Gln Lys  
145 150 155 160

Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala  
165 170 175

Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile  
180 185 190

Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile  
195 200 205

Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro  
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Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp  
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Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile  
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Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys  
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Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr  
275 280 285

Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val  
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Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu  
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Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr  
325 330 335

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

Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr  
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Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu  
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Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro  
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Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp  
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Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys  
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Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly  
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Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu  
485 490 495

Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu  
500 505 510

Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu  
515 520 525

Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg  
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Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser  
545 550 555 560

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

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg  
 65 70 75 80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met  
 85 90 95

Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn  
 100 105 110

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met  
 115 120 125

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly  
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Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala  
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Leu Pro Pro Arg

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

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys  
50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp  
65 70 75 80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr  
85 90 95

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

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met  
115 120 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu  
130 135 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys  
145 150 155 160

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

Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe  
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Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp  
 65 70 75 80

Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro  
 85 90 95

Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala  
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Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser Ile Phe Val  
 115 120 125

Leu Ala Val Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly Val Arg Gln  
 130 135 140

Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr  
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Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly  
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Asn Gln Leu Arg  
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Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val  
35 40 45

Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile  
50 55 60

Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys  
65 70 75 80

Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Met Cys Gln Ser Cys  
85 90 95

Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val  
100 105 110

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

Thr Trp Leu Thr Val Leu Lys Lys Glu Gln Glu Phe Leu Gly Val Thr  
50 55 60

Gln Ile Leu Thr Ala Met Ile Cys Leu Cys Phe Gly Thr Val Val Cys  
65 70 75 80

Ser Val Leu Asp Ile Ser His Ile Glu Gly Asp Ile Phe Ser Ser Phe  
85 90 95

Lys Ala Gly Tyr Pro Phe Trp Gly Ala Ile Phe Phe Ser Ile Ser Gly  
100 105 110

Met Leu Ser Ile Ile Ser Glu Arg Arg Asn Ala Thr Tyr Leu Val Arg

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120

125

Gly Ser Leu Gly Ala Asn Thr Ala Ser Ser Ile Ala Gly Gly Thr Gly  
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Ile Thr Ile Leu Ile Ile Asn Leu Lys Lys Ser Leu Ala Tyr Ile His  
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Ile His Ser Cys Gln Lys Phe Phe Glu Thr Lys Cys Phe Met Ala Ser  
 165 170 175

Phe Ser Thr Glu Ile Val Val Met Met Leu Phe Leu Thr Ile Leu Gly  
 180 185 190

Leu Gly Ser Ala Val Ser Leu Thr Ile Cys Gly Ala Gly Glu Glu Leu  
 195 200 205

Lys Gly Asn Lys Val Pro Glu Asp Arg Val Tyr Glu Glu Leu Asn Ile  
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Val Phe Gln Glu Glu Thr Val Thr Leu His Cys Glu Val Leu His Leu  
35 40 45

Pro Gly Ser Ser Ser Thr Gln Trp Phe Leu Asn Gly Thr Ala Thr Gln  
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Thr Ser Thr Pro Ser Tyr Arg Ile Thr Ser Ala Ser Val Asn Asp Ser  
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Gly Glu Tyr Arg Cys Gln Arg Gly Leu Ser Gly Arg Ser Asp Pro Ile  
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Gln Leu Glu Ile His Arg Gly Trp Leu Leu Leu Gln Val Ser Ser Arg  
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Val Phe Thr Glu Gly Glu Pro Leu Ala Leu Arg Cys His Ala Trp Lys  
115 120 125

Asp Lys Leu Val Tyr Asn Val Leu Tyr Tyr Arg Asn Gly Lys Ala Phe  
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Lys Phe Phe His Trp Asn Ser Asn Leu Thr Ile Leu Lys Thr Asn Ile  
145 150 155 160

Ser His Asn Gly Thr Tyr His Cys Ser Gly Met Gly Lys His Arg Tyr  
165 170 175

Thr Ser Ala Gly Ile Ser Val Thr Val Lys Glu Leu Phe Pro Ala Pro  
180 185 190

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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Ser Pro Glu Leu Glu Leu Gln Val Leu Gly Leu Gln Leu Pro Thr Pro  
275 280 285

Val Trp Phe His Val Leu Phe Tyr Leu Ala Val Gly Ile Met Phe Leu  
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Val Asn Thr Val Leu Trp Val Thr Ile Arg Lys Glu Leu Lys Arg Lys  
305 310 315 320

Lys Lys Trp Asp Leu Glu Ile Ser Leu Asp Ser Gly His Glu Lys Lys  
325 330 335

Val Ile Ser Ser Leu Gln Glu Asp Arg His Leu Glu Glu Glu Leu Lys  
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Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
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Ala Glu Pro Lys Pro Met Asp Thr Glu Phe Asp Tyr Trp Ser Pro Gly  
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Thr Leu Val Thr Val Ser Ser  
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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PEP2-2-3 coding sequence

&lt;400&gt; 11

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tcatgtgcag caagcgggtt cacctttagg aaccacgata tgggggtgggt gaggcaggct 120

```
ccgggaaagg gtctggaatg ggtgagtgcc atatcaggga gcggaggctc cacctactac 180
gcagactccg tgaagggtcg gtttacgatt tccagagaca attccaagaa taccctgtac 240
ctgcagatga actccctccg cgccgaagat acagcagtct actactgtgc agaaccacaaa 300
ccaatggata cagaattcga ctattggagt cctggaactc ttgtcactgt atccagt 357
```

```
<210> 12
<211> 21
<212> PRT
<213> Homo sapiens
```

```
<400> 12
```

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1          5          10          15
```

```
His Ala Ala Arg Pro
          20
```

```
<210> 13
<211> 72
<212> DNA
<213> Homo sapiens
```

```
<400> 13
```

```
gagcgcgtca tggctcttcc tgtgaccgca ttgtgtctgc cgctggcctt gctgctgcat 60
gcagctcggc ca 72
```

```
<210> 14
<211> 228
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Long hinge
```

```
<400> 14
```

```
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Pro Val
1          5          10          15
```

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
35 40 45

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu  
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr  
65 70 75 80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser  
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 210 215 220

Ser Leu Gly Lys  
 225

<210> 15  
 <211> 684  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Long hinge

<400> 15  
 gagagtaaat atggacctcc gtgtccgagt tgtcccgcg ctcctgtggc cggccccctct 60  
 gtatttctgt ttccacctaa gccgaaagat acattgatga ttagccgaac accagagggtt 120  
 acttgtgtgg ttgttgacgt gagtcaagag gaccctgagg tgcagtttaa ttggtatgtc 180  
 gacggagttg aggtgcataa cgccaagacg aagccgagagg aggagcagtt taattccacc 240  
 tacagggtcg tatccgttct cactgtcctt caccaggact ggctgaatgg gaaggagtac 300  
 aaatgcaaag tgagcaataa aggctgccg agctccatcg aaaaaacat ttccaaggca 360  
 aaaggccaac cccgagagcc acaggtctat accctgccac caagccagga ggaaatgacc 420  
 aagaatcagg tgagcctcac ctgtctgggtc aagggttctt acccgctccga catcgcggtg 480  
 gagtgggaga gtaacggaca gcctgaaaac aattacaaga caaccccgcc tgttttggac 540  
 tctgacggct ctttttttct gtactctcgg cttaccgtgg ataagagtag atggcaagaa 600  
 ggcaacgtct tcagctgttc cgtgatgcat gaggcgctgc ataaccatta tacacaaaaa 660  
 agtctgtcct tgagcctggg caaa 684

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

<220>

<223> Short hinge

<400> 16

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

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Asp Pro Lys  
20 25 30

<210> 17

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Short hinge

<400> 17

ggcggcggcg gctctggcgg tgggggtagc ggaggcggcg gaagcgaatc caaatatggc 60

cctccttggtc caccgtgccc cgatccaaag 90

<210> 18

<211> 68

<212> PRT

<213> Homo sapiens

<400> 18

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 Arg Ser Lys Arg Ser  
20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly  
35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala

50

55

60

Ala Tyr Arg Ser  
65

<210> 19  
<211> 204  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> CD28 coding sequence

<400> 19  
ttttgggtgc tgggtgggtggt ggggggtgtc ctcgcttgct acagtttggt ggtgacagtt 60  
gcctttatta ttttttgggt gcgcagtaag cggagtcgcc tccttcattc cgactatatg 120  
aacatgacac ctcgccgccc aggcccaacg aggaaacatt atcagccata tgcaccacct 180  
agagactttg ccgcttaccg gtcc 204

<210> 20  
<211> 36  
<212> PRT  
<213> Homo sapiens

<400> 20

Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly  
1 5 10 15

Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr  
20 25 30

Leu Ala Lys Ile  
35

<210> 21  
<211> 108  
<212> DNA  
<213> Artificial Sequence

<220>

<223> OX40 coding sequence

<400> 21

cgagatcaaa ggcttccccc cgatgcacac aaaccacccg gcggtggctc atttcgaaca 60

ccaattcagg aagagcaggc agacgccac agcaccctgg ccaagatc 108

<210> 22

<211> 112

<212> PRT

<213> Homo sapiens

<400> 22

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

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

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

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
100 105 110

<210> 23

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for CD3zeta

<400> 23

```

cgggttaaagt tcagccgaag tgcagatgcg ccggcatacc agcagggcca gaatcaattg      60
tacaatgagc ttaacctcgg ccgcagagag gagtatgatg tactggataa gcggcgcgga      120
cgggatcctg agatgggagg aaagcctcgg agaaaaaatc cccaggaagg actttacaat      180
gagttgcaga aggataagat ggccgaagca tattctgaaa tcgggatgaa aggtgagcgg      240
cggagaggaa aaggccacga cgggctctac caggggctga gcacagctac taaagataca      300
tacgacgcac ttcatatgca agccctgcct ccccg      336

```

<210> 24

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> P2A

<400> 24

```

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1           5           10          15

```

```

Glu Glu Asn Pro Gly Pro
          20

```

<210> 25

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Coding sequence for P2A

<400> 25

```

ggaagcgggtg ccacgaactt ttctctcctc aaacaggctg gggacgtcga ggaaaatcca      60

```

ggtccc

66

<210> 26  
 <211> 611  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> CAR-Long hinge

<400> 26

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu  
 1 5 10 15

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

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe  
 35 40 45

Thr Phe Arg Asn His Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys  
 50 55 60

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

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

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
 100 105 110

Ala Val Tyr Tyr Cys Ala Glu Pro Lys Pro Met Asp Thr Glu Phe Asp  
 115 120 125

Tyr Trp Ser Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Glu  
 130 135 140

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Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Pro Val Ala  
145 150 155 160

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
165 170 175

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
180 185 190

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
195 200 205

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
210 215 220

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
225 230 235 240

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
245 250 255

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
260 265 270

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
275 280 285

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
290 295 300

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
305 310 315 320

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
325 330 335

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
340 345 350

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
355 360 365

Leu Gly Lys Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys  
370 375 380

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser  
385 390 395 400

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg  
405 410 415

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg  
420 425 430

Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp Ala  
435 440 445

His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu  
450 455 460

Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser  
465 470 475 480

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr  
485 490 495

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys  
500 505 510

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn  
515 520 525

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu  
530 535 540

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly  
545 550 555 560

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr  
565 570 575

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Ala Thr  
580 585 590

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly  
595 600 605

Pro Gly Glu  
610

<210> 27  
<211> 408  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CAR-Short hinge

<400> 27

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu  
1 5 10 15

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

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe  
35 40 45

Thr Phe Arg Asn His Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys

50

55

60

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

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

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
 100 105 110

Ala Val Tyr Tyr Cys Ala Glu Pro Lys Pro Met Asp Thr Glu Phe Asp  
 115 120 125

Tyr Trp Ser Pro 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 Glu Ser Lys Tyr Gly  
 145 150 155 160

Pro Pro Cys Pro Pro Cys Pro Asp Pro Lys Phe Trp Val Leu Val Val  
 165 170 175

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe  
 180 185 190

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp  
 195 200 205

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr  
 210 215 220

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp  
 225 230 235 240

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe

245

250

255

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala  
                   260                                  265                                  270

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln  
                   275                                  280                                  285

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu  
                   290                                  295                                  300

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly  
                   305                                  310                                  315                                  320

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu  
                                   325                                  330                                  335

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly  
                   340                                  345                                  350

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser  
                   355                                  360                                  365

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro  
                   370                                  375                                  380

Pro Arg Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly  
                   385                                  390                                  395                                  400

Asp Val Glu Glu Asn Pro Gly Pro  
                                   405

&lt;210&gt; 28

&lt;211&gt; 1875

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Coding CAR-long hinge

&lt;400&gt; 28

|                                                                      |      |
|----------------------------------------------------------------------|------|
| gaccggcgcc tactctagag gagcgcggtca tggctctttcc tgtgaccgca ttgctgctgc  | 60   |
| cgctggcctt gctgctgcat gcagctcggc cagaagttca actgctggag agtggagggg    | 120  |
| gcctcgtgca gccgggaggc agcttgcgcc tgtcatgtgc agcaagcggg ttcaccttta    | 180  |
| ggaaccacga tatgggggtgg gtgaggcagg ctccgggaaa gggctctggaa tgggtgagtg  | 240  |
| ccatatcagg gagcggaggc tccacctact acgcagactc cgtgaagggt cggtttacga    | 300  |
| tttccagaga caattccaag aataacctgt acctgcagat gaactccctc cgcgccgaag    | 360  |
| atacagcagt ctactactgt gcagaaccaa aaccaatgga tacagaattc gactattgga    | 420  |
| gtcctggaac tcttgtcact gtatccagtg gaggaggcga gagtaaatat ggacctccgt    | 480  |
| gtccgagttg tcccgcgcct cctgtggccg gccctctgtg atttctgttt ccacctaagc    | 540  |
| cgaaagatac attgatgatt agccgaacac cagaggttac ttgtgtgggt gttgacgtga    | 600  |
| gtcaagagga ccctgagggtg cagtttaatt ggtatgtcga cggagttgag gtgcataacg   | 660  |
| ccaagacgaa gccgcgagag gagcagttta attccacctc cagggtcgta tccgtttctca   | 720  |
| ctgtccttca ccaggactgg ctgaatggga aggagtacaa atgcaaagtg agcaataaag    | 780  |
| gcctgccgag ctccatcgaa aaaaccatth ccaaggcaaa aggccaaccc cgagagccac    | 840  |
| aggtctatac cctgccacca agccaggagg aaatgaccaa gaatcagggtg agcctcacct   | 900  |
| gtctgggtcaa gggcttctac ccgtccgaca tcgcgggtgga gtgggagagt aacggacagc  | 960  |
| ctgaaaacaa ttacaagaca accccgcctg ttttggactc tgacggctcc ttttttctgt    | 1020 |
| actctcggct taccgtggat aagagtagat ggcaagaagg caacgtcttc agctgttccg    | 1080 |
| tgatgcatga ggcgctgcat aaccattata cacaaaaaag tctgtccttg agcctgggca    | 1140 |
| aatthttgggt gctgggtgggt gtgggggggtg tcctcgcttg ctacagtttg ttggtgacag | 1200 |
| ttgcctttat tatthtttgg gtgcgcagta agcggagtcg cctccttcat tccgactata    | 1260 |
| tgaacatgac acctcgccgc ccaggcccaa cgaggaaaca ttatcagcca tatgcaccac    | 1320 |

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ctagagactt tgccgcttac cgggtcccag atcaaaaggct tccccccgat gcacacaaac  | 1380 |
| cacccggcggtg tggctcattt cgaacaccaa ttcaggaaga gcaggcagac gcccacagca | 1440 |
| ccctggccaa gatccgggta aagttcagcc gaagtgcaga tgcgccggca taccagcagg   | 1500 |
| gccagaatca attgtacaat gagcttaacc tcggccgcag agaggagtat gatgtactgg   | 1560 |
| ataagcggcg cggacgggat cctgagatgg gaggaaagcc tcggagaaaa aatccccagg   | 1620 |
| aaggacttta caatgagttg cagaaggata agatggccga agcatattct gaaatcggga   | 1680 |
| tgaaagggtga gcggcggaga ggaaaaggcc acgacgggct ctaccagggg ctgagcacag  | 1740 |
| ctactaaaga tacatacgac gcacttcata tgcaagccct gcctccccgc ggaagcggtg   | 1800 |
| ccacgaactt ttctctctc aaacaggctg gggacgtcga ggaaaatcca ggtcccggcg    | 1860 |
| aattcgccac catgc                                                    | 1875 |

&lt;210&gt; 29

&lt;211&gt; 1272

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Coding CAR-short hinge

&lt;400&gt; 29

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaccggcgcc tactctagag gagcgcgtca tggccctgcc tgtgacagcc ctgctgctgc  | 60  |
| cactcgtctt tctccttcac gccgaagac ccgaagtga gcttctggag tctggagggtg   | 120 |
| gtttggtgca gcctggcggg tctctcagat tgtcatgcgc cgcacccggg ttcacctttc  | 180 |
| ggaaccatga tatgggttgg gtccgccagg ccccaggcaa gggctttgag tgggtctccg  | 240 |
| ccatcagcgg cagtggcggg tccacatact acgcagactc cgtcaaaggc agatttacaa  | 300 |
| tttcacggga taatagtaag aacactctgt acctccagat gaatagtctc cgggcggagg  | 360 |
| acacagctgt gtactattgc gcggagccaa agccaatgga tactgagttt gattattgga  | 420 |
| gcccgggaac cctgggtgaca gtatccagcg gcggcggcgg ctctggcggg gggggtagcg | 480 |
| gaggcggcgg aagcgaatcc aaatatggcc ctcttgttcc accgtgcccc gatccaaagt  | 540 |

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tctgggtgct ggtggtagtg ggtggcgtcc tggcctgtta ttctctgctt gtgacagtcg  | 600  |
| cgtttatcat cttttgggtc cggtctaaac gctctagggtt gttgcactcc gattacatga | 660  |
| acatgacccc acgccggcct ggccctacgc ggaagcacta ccaaccttac gctcctccca  | 720  |
| gggatttcgc cgcttacagg agccgagatc agagactgcc acccgatgca cacaaaccac  | 780  |
| ccggtggtgg gtctttcagg accccaatcc aggaggagca agctgacgcg cattccaccc  | 840  |
| ttgccaagat aagggtcaaa tttagtaggt cagctgacgc gccggcctat caacaggggac | 900  |
| agaaccagtt gtataatgaa ctcaatctcg gacgacgcga ggagtacgac gtactggata  | 960  |
| agaggcgcgg cagggatcct gaaatgggcg gcaagccccg gcgaaaaaac ccccaggagg  | 1020 |
| gactctacaa tgagctgcag aaggacaaaa tggcagaagc ttactccgaa attggaatga  | 1080 |
| agggcgaaaag aaggagaggg aaagggcacg atggcctgta tcagggcctg agtaccgcca | 1140 |
| ccaaggacac gtatgatgcc ctgcatatgc aggcactgcc ccctagagga agcgggggcta | 1200 |
| cgaatttcag cctcctgaaa caggctggcg acgtggagga aaatccgggg ccaggcgaat  | 1260 |
| tcgccaccat gc                                                      | 1272 |

<210> 30  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Pro | Val | Thr | Ala | Leu | Leu | Leu | Pro | Leu | Ala | Leu | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |
|-----|-----|-----|-----|-----|
| His | Ala | Ala | Arg | Pro |
|     |     |     | 20  |     |

<210> 31  
 <211> 63  
 <212> DNA  
 <213> Homo sapiens

<400> 31

atggctcttc ctgtgaccgc attgctgctg ccgctggcct tgctgctgca tgcagctcgg 60

cca 63

<210> 32

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> PEP2-2-1-1 binding peptide

<400> 32

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn His  
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

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

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

Thr Leu Val Thr Val Ser Ser  
115

<210> 33

<211> 119  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PEP2-472-2 binding peptide

<400> 33

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Pro Met Lys  
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

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

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

Thr Leu Val Thr Val Leu Glu  
 115

<210> 34  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PEP2-2-12 binding peptide

<400> 34

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn His  
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asn Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

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

Ala Glu Pro Lys Pro Met Asp Thr Glu Phe Asp Tyr Pro Ser Pro Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> 35

<211> 1864

<212> DNA

<213> Artificial Sequence

<220>

<223> PEP2-2-1-1 Chimeric Antigen Receptor

<400> 35

cctccataga agattctaga gctagcgaat tctgcagtcg acggtaccgc gggccccggga 60

tccaccgggtg ccgccgccat ggctcttcct gtgaccgcat tgctgctgcc gctggccttg 120

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ctgctgcatg cagctcggcc agaagttcaa ctgctggaga gtggaggggg cctcgtgcag   | 180  |
| ccgggcggca gcttgcgctt gtcattgtgca gcaagcgggt tcaccttttag gaaccacgat | 240  |
| atgggggtggg tgaggcaggc tccgggaaag ggtctggaat gggtagtgat catatcaggg  | 300  |
| agcggagggt ccacctacta cgcagactcc gtgaagggtc gggtttacgat ttccagagac  | 360  |
| aattccaaga ataccttgta cctgcagatg aactccctcc gcgccgaaga tacagcagtc   | 420  |
| tactactgtg cagaacaaaa accaatggat acagaattcg actataggag tcctggaact   | 480  |
| cttgtcactg tatccagtgg aggaggcgag agtaaatatg gacctccgtg tccgagttgt   | 540  |
| cccgcgcctc ctgtggccgg cccctctgta tttctgtttc cacctaagcc gaaagataca   | 600  |
| ttgatgatta gccgaacacc agagggttact tgtgtggttg ttgacgtgag tcaagaggac  | 660  |
| cctgaggtgc agtttaattg gtatgtcgac ggagttgagg tgcataacgc caagacgaag   | 720  |
| ccgcgagagg agcagtttaa ttccacctac agggtcgtat ccgttctcac tgtccttcac   | 780  |
| caggactggc tgaatgggaa ggagtacaaa tgcaaagtga gcaataaagg cctgccgagc   | 840  |
| tccatcgaaa aaaccatttc caaggcaaaa ggccaacccc gagagccaca ggtctatacc   | 900  |
| ctgccaccaa gccaggagga aatgaccaag aatcaggtga gcctcacctg tctggtcaag   | 960  |
| ggcttctacc cgtccgacat cgcggtggag tgggagagta acggacagcc tgaaaacaat   | 1020 |
| tacaagacaa ccccgctgt tttggactct gacggctcct tttttctgta ctctcggtt     | 1080 |
| accgtggata agagtagatg gcaagaaggc aacgtcttca gctgttccgt gatgcatgag   | 1140 |
| gcgctgcata accattatac acaaaaaagt ctgtccttga gcctgggcaa acctttttgg   | 1200 |
| gtgctggtgg tggtaggggg tgctctcgct tgctacagtt tgtaggtgac agttgccttt   | 1260 |
| attatTTTTT gggtagcgag taagcggagt cgcctcctt attccgacta tatgaacatg    | 1320 |
| acacctcgcc gccaggccc aacgaggaaa cattatcagc catatgcacc acctagagac    | 1380 |
| tttgccgctt accggtcccg agatcaaagg cttccccccg atgcacacaa accacccggc   | 1440 |
| ggtggctcat ttccaacacc aattcaggaa gagcaggcag acgcccacag caccctggcc   | 1500 |
| aagatccggg taaagttcag ccgaagtgc gatgcgccgg cataccagca gggccagaat    | 1560 |

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|                                                                     |      |
|---------------------------------------------------------------------|------|
| caattgtaca atgagcttaa cctcggccgc agagaggagt atgatgtact ggataagcgg   | 1620 |
| cgcgggacggg atcctgagat gggaggaaaag cctcggagaa aaaatcccca ggaaggactt | 1680 |
| tacaatgagt tgcagaagga taagatggcc gaagcatatt ctgaaatcgg gatgaaaggt   | 1740 |
| gagcggcgga gagggaaaagg ccacgacggg ctctaccagg ggctgagcac agctactaaa  | 1800 |
| gatacatacg acgcacttca tatgcaagcc ctgcctcccc gcgcgccgc agcatcgata    | 1860 |
| agta                                                                | 1864 |

<210> 36  
 <211> 1863  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PEP2-472-2 Chimeric Antigen Receptor

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| <400> 36                                                           |     |
| cctccataga agattctaga gctagcgaat tctgcagtcg acggtaccgc gggcccggga  | 60  |
| tccaccgggtc cgccgccatg gcattgccag ttacggcgct cctcctgcca ctgcactcc  | 120 |
| tcttgacgc agctcgaccc gaggtccagc ttctcgagtc cggtgggtgga cttgtgcaac  | 180 |
| cgggcggctc cttgcgactt tcctgtgccg cctccgggta cactttcccc atgaaagaca  | 240 |
| tgggatgggt gcgccaggcg ccagggaagg gtcttgagtg ggtcagcgct ataagtggga  | 300 |
| gtgggtggggg aacatattat gcagattcag taaaaggccg cttcactatc agtcgcgata | 360 |
| acagcaaaaa cacactgtat cttcagatga atagcttgag agctgaagat acggcgggtgt | 420 |
| attactgtgc ggagccgaaa ccaatggata ccgagttcga ctaccgctcc cctggcacct  | 480 |
| tggttactgt ccttgaaggc ggcggagaga gcaagtacgg gccgccgtgc ccaagttgcc  | 540 |
| ctgccccgcc tgtggctgggt cttcagttt tcctgtttcc gcctaaacca aaagacactc  | 600 |
| ttatgatttc tcgcacgcct gaagtcactt gtgttgctgt agatgtcagt caggaggacc  | 660 |
| cggaagtcca atttaattgg tacgtggatg gagttgaggt gcataacgcc aagacgaagc  | 720 |
| cgcgagagga gcagtttaat tccacctaca gggtcgtatc cgttctcact gtccttcacc  | 780 |

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| aggactggct gaatgggaag gagtacaaat gcaaagtgag caataaaggc ctgccgagct  | 840  |
| ccatcgaaaa aaccatttcc aaggcaaaaag gccaaccccg agagccacag gtctataccc | 900  |
| tgccaccaag ccaggaggaa atgaccaaga atcaggtgag cctcacctgt ctggtcaagg  | 960  |
| gcttctaccc gtccgacatc gcggtggagt gggagagtaa cggacagcct gaaaacaatt  | 1020 |
| acaagacaac cccgcctgtt ttggactctg acggctcctt ttttctgtac tctcggctta  | 1080 |
| ccgtggataa gagtagatgg caagaaggca acgtcttcag ctgttccgtg atgcatgagg  | 1140 |
| cgctgcataa ccattataca caaaaaagtc tgtccttgag cctgggcaaa cttttttggg  | 1200 |
| tgctggtggt ggtggggggt gtcctcgctt gctacagttt gttggtgaca gttgccttta  | 1260 |
| ttatttttttg ggtgcgcagt aagcggagtc gcctccttca ttccgactat atgaacatga | 1320 |
| cacctcgccg cccaggccca acgaggaaac attatcagcc atatgcacca cctagagact  | 1380 |
| ttgccgctta ccggtcccga gatcaaaggc ttccccccga tgcacacaaa ccacccggcg  | 1440 |
| gtggctcatt tcgaacacca attcaggaag agcaggcaga cggccacagc accctggcca  | 1500 |
| agatccgggt aaagttcagc cgaagtgcag atgcgccggc ataccagcag ggccagaatc  | 1560 |
| aattgtacaa tgagcttaac ctcggccgca gagaggagta tgatgtactg gataagcggc  | 1620 |
| gcggacggga tcctgagatg ggaggaaagc ctcggagaaa aaatccccag gaaggacttt  | 1680 |
| acaatgagtt gcagaaggat aagatggccg aagcatattc tgaaatcggg atgaaagggtg | 1740 |
| agcggcggag aggaaaaggc cacgacgggc tctaccaggg gctgagcaca gctactaaag  | 1800 |
| atacatagca cgcacttcat atgcaagccc tgcctccccg cgcggccgca gcatcgataa  | 1860 |
| gta                                                                | 1863 |

<210> 37

<211> 1863

<212> DNA

<213> Artificial Sequence

<220>

<223> PEP2-2-12 Chimeric Antigen Receptor

<400> 37

|                                                                     |      |
|---------------------------------------------------------------------|------|
| cctccataga agattctaga gctagcgaat tctgcagtcg acggtaccgc gggcccggga   | 60   |
| tccaccgggtc cgccgccatg gctctgcccc taactgctct ctttcttcca cttgcaactgc | 120  |
| ttctccacgc ggctaggccg gaagtccaac ttctggaatc tggagggtggc ctcgtgcagc  | 180  |
| ctggcggatc cctccggctt tcttgcgccg cttcaggatt cacatttcgg aaccacgaca   | 240  |
| tgggggtgggt taggcaagcg ccgggcaagg gcctcgaatg ggtttcagcc atatctgggt  | 300  |
| ccggagggttc tacctactat gctaactcag tcaagggcag atttacgac tcaagagaca   | 360  |
| atagtaagaa cacgctgtac cttcagatga actctcttag agcagaagat acagctgtgt   | 420  |
| actattgtgc tgaaccgaag cctatggata ctgagtttga ctaccctagt ccggggacgc   | 480  |
| tggtaaccgt ctccagtggg ggcggagaaa gcaaatacgg tccccctgc ccctcttgcc    | 540  |
| ctgccccgcc tgtggctggc cttcagttt tcctgtttcc gcctaaacca aaagacactc    | 600  |
| ttatgatttc tcgcacgcct gaagtcactt gtgttgtcgt agatgtcagt caggaggacc   | 660  |
| cggaaagtcca atttaattgg tacgtggatg gagttgaggt gcataacgcc aagacgaagc  | 720  |
| cgcgagagga gcagtttaat tccacctaca gggctgtatc cgttctcact gtccttcacc   | 780  |
| aggactggct gaatgggaag gagtacaaat gcaaagtgag caataaaggc ctgccgagct   | 840  |
| ccatcgaaaa aaccatttcc aaggcaaaaag gccaaacccg agagccacag gtctataccc  | 900  |
| tgccaccaag ccaggaggaa atgaccaaga atcagggtgag cctcacctgt ctggtcaagg  | 960  |
| gcttctaccc gtccgacatc gcggtggagt gggagagtaa cggacagcct gaaaacaatt   | 1020 |
| acaagacaac cccgcctgtt ttggactctg acggctcctt ttttctgtac tctcggctta   | 1080 |
| ccgtggataa gagtagatgg caagaaggca acgtcttcag ctgttccgtg atgcatgagg   | 1140 |
| cgctgcataa ccattataca caaaaaagtc tgtccttgag cctgggcaaa cctttttggg   | 1200 |
| tgctgggtggg ggtggggggg gtcctcgctt gctacagttt gttggtgaca gttgccttta  | 1260 |
| ttatTTTTTtg ggtgcgcagt aagcggagtc gcctccttca ttccgactat atgaacatga  | 1320 |
| cacctcgccg cccaggccca acgaggaaac attatcagcc atatgcacca cctagagact   | 1380 |
| ttgccgctta ccggtccccg gatcaaaggc ttccccccga tgcacacaaa ccacccggcg   | 1440 |

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| gtggctcatt tcgaacacca attcaggaag agcaggcaga cgcccacagc accctggcca | 1500 |
| agatccgggt aaagttcagc cgaagtgcag atgcgccggc ataccagcag ggccagaatc | 1560 |
| aattgtacaa tgagcttaac ctcggccgca gagaggagta tgatgtactg gataagcggc | 1620 |
| gcggacggga tcctgagatg ggaggaaagc ctcggagaaa aaatccccag gaaggacttt | 1680 |
| acaatgagtt gcagaaggat aagatggccg aagcatattc tgaaatcggg atgaaaggtg | 1740 |
| agcggcggag aggaaaaggc cacgacgggc tctaccaggg gctgagcaca gctactaaag | 1800 |
| atacatacga cgcacttcat atgcaagccc tgcctccccg cgcggccgca gcatcgataa | 1860 |
| gta                                                               | 1863 |

<210> 38  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pCHD-CMV-For primer

|                       |    |
|-----------------------|----|
| <400> 38              |    |
| ggtgggaggt ctatataagc | 20 |

<210> 39  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pCHD-coGFP-Rev primer

|                      |    |
|----------------------|----|
| <400> 39             |    |
| tgatgcggca ctcgatctc | 19 |

<210> 40  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 2-2-1-1-Rev primer

<400> 40  
cttcacggag tctgcgtag 19

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 2-2-1-1-For primer

<400> 41  
tcttgtcact gtatccagtg 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 2-472-2-Rev primer

<400> 42  
cgtatcttca gctctcaagc 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 2-472-2-For primer

<400> 43  
tggtccttca gttttcctgt 20

<210> 44  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 2-12-2-Rev primer

<400> 44  
 cagctgtatc ttctgctc 18

<210> 45  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Com-For-1 primer

<400> 45  
 agtgggagag taacggacag 20

<210> 46  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Com-For-2 primer

<400> 46  
 agggccagaa tcaattgtac 20

<210> 47  
 <211> 1117  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EXD2\_K193A fusion gene block

<400> 47  
 ggggacaagt ttgtacaaaa aagcaggcta tggagacaga cacactcctg ctatgggtac 60  
 tgctgctctg gggtccaggt tccactgggtg actatccata tgatgttcca gattatgctg 120  
 gggccagtga caagctgtac cagcggaaag agcctgtcat cagttctgtg cacaccaagg 180  
 tgaaggggat agcagagggtg aaagaggaga tcgtggagaa tggagtgaag aagttgggtgc 240  
 acagtgtctt tgacaccgca gactacacct tccctttgca ggggaactct ttcttcgtga 300

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgacaaactt tctcaaaaca gaaggccaag agcagcggtt gtgtcccag tatcccaccc   | 360  |
| gcaggacgct ctgttcctct gaccgagggtt gtaaaaaggg atggatggac ccgcagagca | 420  |
| aaggaattca gaccggaagg tgtgtagtgt atgaaggga ccagaagacc tgtgaagtct   | 480  |
| ctgcctggtg ccccatcgag gcagtgggaag aggcccccg gcctgctctc ttgaacagtg  | 540  |
| ccgaaaactt cactgtgctc atcgcgaaaca atatcgactt ccccgccac aactacacca  | 600  |
| cgagaaacat cctgccaggt ttaaacaatca cttgtacctt ccacaagact cagaatccac | 660  |
| agtgtcccat tttccgacta ggagacatct tccgagaaac aggcgataat ttttcagatg  | 720  |
| tggcaattca gggcggaata atgggcattg agatctactg ggactgcaac ctagaccgtt  | 780  |
| ggttccatca ctgccgtccc aaatacagtt tccgtcgctt tgacgacaag accaccaacg  | 840  |
| tgtccttgta ccctggctac aacttcagat acgccaagta ctacaaggaa aacaatgttg  | 900  |
| agaaagaaca aaaactcatc tcagaagagg atctgaatgc tgtgggccag gacacgcagg  | 960  |
| aggatcatcgt ggtgccacac tccttgccct ttaagggtgt ggtgatctca gccatcctgg | 1020 |
| ccctgggtgt gctcaccatc atctccctta tcatcctcat catgctttgg cagaagaagc  | 1080 |
| cacgttagac ccagctttct tgtacaaagt ggtcccc                           | 1117 |

<210> 48

<211> 1117

<212> DNA

<213> Artificial Sequence

<220>

<223> EXD2\_WT fusion gene block

<400> 48

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ggggacaagt ttgtacaaaa aagcaggcta tggagacaga cacactcctg ctatgggtac  | 60  |
| tgctgctctg ggttccaggt tccactgggtg actatccata tgatgttcca gattatgctg | 120 |
| gggccagtga caagctgtac cagcggaaag agcctgtcat cagttctgtg cacaccaagg  | 180 |
| tgaaggggat agcagagggt aaagaggaga tcgtggagaa tggagtgaag aagttgggtgc | 240 |
| acagtgtctt tgacaccgca gactacacct tccctttgca ggggaactct ttcttcgtga  | 300 |

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|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgacaaactt tctcaaaaca gaaggccaag agcagcggtt gtgtcccag tatcccaccc   | 360  |
| gcaggacgct ctgttcctct gaccgagggtt gtaaaaaggg atggatggac ccgcagagca | 420  |
| aaggaattca gaccggaagg tgtgtagtgt atgaaggga ccagaagacc tgtgaagtct   | 480  |
| ctgcctggtg ccccatcgag gcagtgggaag aggcccccg gcctgctctc ttgaacagtg  | 540  |
| ccgaaaactt cactgtgctc atcaagaaca atatcgactt ccccgccac aactacacca   | 600  |
| cgagaaacat cctgccaggt ttaaacaatca cttgtacctt ccacaagact cagaatccac | 660  |
| agtgtcccat tttccgacta ggagacatct tccgagaaac aggcgataat ttttcagatg  | 720  |
| tggcaattca gggcgggaata atgggcattg agatctactg ggactgcaac ctagaccgtt | 780  |
| ggttccatca ctgccgtccc aaatacagtt tccgtcgctt tgacgacaag accaccaacg  | 840  |
| tgtccttgta ccctggctac aacttcagat acgccaagta ctacaaggaa aacaatgttg  | 900  |
| agaaagaaca aaaactcatc tcagaagagg atctgaatgc tgtgggccag gacacgcagg  | 960  |
| aggatcatcgt ggtgccacac tccttgccct ttaagggtgt ggtgatctca gccatcctgg | 1020 |
| ccctgggtgt gctcaccatc atctccctta tcatcctcat catgcttttg cagaagaagc  | 1080 |
| cacgttagac ccagctttct tgtacaaagt ggtcccc                           | 1117 |

<210> 49  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EXD-F1 primer

|                     |    |
|---------------------|----|
| <400> 49            |    |
| acaagctgta ccagcgga | 20 |

<210> 50  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> EXD2-R1 primer

<400> 50  
caccaccacc ttaaaggga 20

<210> 51  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> EXD2-F1 primer

<400> 51  
acaagctgta ccagcggaaa 20

<210> 52  
<211> 588  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> PEP2-2-1-1 CAR amino acid sequence

<400> 52

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu  
1 5 10 15

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

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe  
35 40 45

Thr Phe Arg Asn His Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys  
50 55 60

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

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser

85

90

95

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
 100 105 110

Ala Val Tyr Tyr Cys Ala Glu Pro Lys Pro Met Asp Thr Glu Phe Asp  
 115 120 125

Tyr Arg Ser Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Glu  
 130 135 140

Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Pro Val Ala  
 145 150 155 160

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 165 170 175

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
 180 185 190

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 195 200 205

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
 210 215 220

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 225 230 235 240

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
 245 250 255

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 260 265 270

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser

275

280

285

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 290 295 300

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 305 310 315 320

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
 325 330 335

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
 340 345 350

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 355 360 365

Leu Gly Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala  
 370 375 380

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg  
 385 390 395 400

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro  
 405 410 415

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro  
 420 425 430

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp  
 435 440 445

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu  
 450 455 460

Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe

465                      470                      475                      480

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu  
                                 485                      490                      495

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp  
                                 500                      505                      510

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys  
                                 515                      520                      525

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala  
                                 530                      535                      540

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys  
545                      550                      555                      560

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr  
                                 565                      570                      575

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
                                 580                      585

<210> 53

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> PEP2-472-2 CAR amino acid sequence

<400> 53

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu  
1                      5                      10                      15

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

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr  
35 40 45

Thr Phe Pro Met Lys Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys  
50 55 60

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

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

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
100 105 110

Ala Val Tyr Tyr Cys Ala Glu Pro Lys Pro Met Asp Thr Glu Phe Asp  
115 120 125

Tyr Arg Ser Pro Gly Thr Leu Val Thr Val Leu Glu Gly Gly Gly Glu  
130 135 140

Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Pro Val Ala  
145 150 155 160

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
165 170 175

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
180 185 190

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
195 200 205

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
210 215 220

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
225 230 235 240

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
245 250 255

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
260 265 270

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
275 280 285

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
290 295 300

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
305 310 315 320

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
325 330 335

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
340 345 350

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
355 360 365

Leu Gly Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala  
370 375 380

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg  
385 390 395 400

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro  
405 410 415

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro  
420 425 430

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp  
435 440 445

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu  
450 455 460

Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe  
465 470 475 480

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu  
485 490 495

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp  
500 505 510

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys  
515 520 525

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala  
530 535 540

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys  
545 550 555 560

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr  
565 570 575

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
580 585

<210> 54  
<211> 588  
<212> PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PEP2-2-12 CAR amino acid sequence

&lt;400&gt; 54

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu  
 1 5 10 15

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

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe  
 35 40 45

Thr Phe Arg Asn His Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys  
 50 55 60

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

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

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr  
 100 105 110

Ala Val Tyr Tyr Cys Ala Glu Pro Lys Pro Met Asp Thr Glu Phe Asp  
 115 120 125

Tyr Pro Ser Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Glu  
 130 135 140

Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Pro Val Ala  
 145 150 155 160

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

165

170

175

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
 180 185 190

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 195 200 205

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
 210 215 220

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 225 230 235 240

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
 245 250 255

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 260 265 270

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
 275 280 285

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 290 295 300

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 305 310 315 320

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
 325 330 335

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
 340 345 350

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

355

360

365

Leu Gly Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala  
 370 375 380

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg  
 385 390 395 400

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro  
 405 410 415

Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro  
 420 425 430

Arg Asp Phe Ala Ala Tyr Arg Ser Arg Asp Gln Arg Leu Pro Pro Asp  
 435 440 445

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu  
 450 455 460

Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe  
 465 470 475 480

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu  
 485 490 495

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp  
 500 505 510

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys  
 515 520 525

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala  
 530 535 540

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys

545                      550                      555                      560

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
580 585