JPOXMLDOC01-seql

SEQUENCE LISTING

<110> YAMAGUCHI UNIVERSITY

<120> CAR-expressing vector and CAR-expressing T cells

<130> FH26-030WO

<150> JP 2014-208200
<151> 2014-10-09

<160> 12

<170> PatentIn version 3.1

<210> 1
<211> 8
<212> PRT
<213> artificial

<220>
<223> 2A peptide cleavage region

<220>
<223> Inventor: Tamada, Koji
Inventor: Sakoda, Yukimi
Inventor: Adachi, Keishi

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<223> Val or Ile

<220>
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<223> any amino acid

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<223> 2Apeptide(F2A)

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Gly Asp Val Glu Ser Asn Pro Gly Pro
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<220>
<223> human IL-7

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


Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
    50                  55                  60


Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
65                  70                  75                  80


Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
                85                  90                  95


Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
            100                 105                 110


Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
        115                 120                 125
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Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
    130                 135                 140

Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
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Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
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His
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<220>
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<400> 4

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Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
            20                  25                  30

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
        35                  40                  45

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
    50                  55                  60

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
65                  70                  75                  80

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg
                85                  90                  95
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Ser Ser

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<223> human SHP1DN

<400> 5

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

Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly Asp Gln
        35                  40                  45

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

Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr Tyr Thr
65                  70                  75                  80

Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile His Leu
                85                  90                  95

Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp Tyr His
            100                 105                 110

Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala Lys Gly
        115                 120                 125

Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro Gly Asp
    130                 135                 140

Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro Gly Ser
145                 150                 155                 160
```

```
Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly Arg Tyr
                165                 170                 175

Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu Val Glu
            180                 185                 190

His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe Val Tyr
        195                 200                 205

Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp Ile Glu
    210                 215                 220

Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp Thr Ala
225                 230                 235                 240

Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln Glu Val
                245                 250                 255

Lys Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn Lys Gly
            260                 265                 270

Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg Val Ile
        275                 280                 285

Leu Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile Asn Ala
    290                 295                 300

Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala Lys Thr
305                 310                 315                 320

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

Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr Thr Arg
            340                 345                 350

Glu Val Glu Lys Gly Arg Asn Lys Cys Val Pro Tyr Trp Pro Glu Val
        355                 360                 365
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```
Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys Gly Glu
    370                 375                 380

His Asp Thr Thr Glu Tyr Lys Leu Arg Thr Leu Gln Val Ser Pro Leu
385                 390                 395                 400

Asp Asn Gly Asp Leu Ile Arg Glu Ile Trp His Tyr Gln Tyr Leu Ser
                405                 410                 415

Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu Ser Phe
            420                 425                 430

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

Ile Ile Val His Ser Ser Ala Gly Ile Gly Arg Thr Gly Thr Ile Ile
    450                 455                 460

Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu Asp Cys
465                 470                 475                 480

Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln Arg Ser
                485                 490                 495

Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val Ala Ile
            500                 505                 510

Ala Gln Phe Ile Glu Thr Thr Lys Lys Lys Leu Glu Val Leu Gln Ser
        515                 520                 525

Gln Lys Gly Gln Glu Ser Glu Tyr Gly Asn Ile Thr Tyr Pro Pro Ala
    530                 535                 540

Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys His Lys
545                 550                 555                 560

Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu Glu Lys
                565                 570                 575
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Val Lys Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly Ser Leu
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Lys Arg Lys
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<223> human SHP2DN

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Glu Asn Leu Leu Leu Thr Arg Gly Val Asp Gly Ser Phe Leu Ala Arg
            20                  25                  30


Pro Ser Lys Ser Asn Pro Gly Asp Phe Thr Leu Ser Val Arg Arg Asn
        35                  40                  45


Gly Ala Val Thr His Ile Lys Ile Gln Asn Thr Gly Asp Tyr Tyr Asp
    50                  55                  60


Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Ala Glu Leu Val Gln Tyr
65                  70                  75                  80


Tyr Met Glu His His Gly Gln Leu Lys Glu Lys Asn Gly Asp Val Ile
                85                  90                  95


Glu Leu Lys Tyr Pro Leu Asn Cys Ala Asp Pro Thr Ser Glu Arg Trp
            100                 105                 110


Phe His Gly His Leu Ser Gly Lys Glu Ala Glu Lys Leu Leu Thr Glu
        115                 120                 125
```

```
Lys Gly Lys His Gly Ser Phe Leu Val Arg Glu Ser Gln Ser His Pro
    130                 135                 140

Gly Asp Phe Val Leu Ser Val Arg Thr Gly Asp Asp Lys Gly Glu Ser
145                 150                 155                 160

Asn Asp Gly Lys Ser Lys Val Thr His Val Met Ile Arg Cys Gln Glu
                165                 170                 175

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

Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr
        195                 200                 205

Val Leu Gln Leu Lys Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Ala
    210                 215                 220

Glu Ile Glu Ser Arg Val Arg Glu Leu Ser Lys Leu Ala Glu Thr Thr
225                 230                 235                 240

Asp Lys Val Lys Gln Gly Phe Trp Glu Glu Phe Glu Thr Leu Gln Gln
                245                 250                 255

Gln Glu Cys Lys Leu Leu Tyr Ser Arg Lys Glu Gly Gln Arg Gln Glu
            260                 265                 270

Asn Lys Asn Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Thr
        275                 280                 285

Arg Val Val Leu His Asp Gly Asp Pro Asn Glu Pro Val Ser Asp Tyr
    290                 295                 300

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn
305                 310                 315                 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn
                325                 330                 335
```

```
Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val
            340                 345                 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val
        355                 360                 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg
    370                 375                 380

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu
385                 390                 395                 400

Leu Lys Leu Ser Lys Val Gly Gln Gly Asn Thr Glu Arg Thr Val Trp
                405                 410                 415

Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val Pro Ser Asp Pro
            420                 425                 430

Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His Lys Gln Glu Ser
        435                 440                 445

Ile Met Asp Ala Gly Pro Val Val Val His Ser Ser Ala Gly Ile Gly
    450                 455                 460

Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile Asp Ile Ile Arg
465                 470                 475                 480

Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys Thr Ile Gln Met
                485                 490                 495

Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Arg
            500                 505                 510

Phe Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr Leu Gln Arg Arg
        515                 520                 525

Ile Glu Glu Glu Gln Lys Ser Lys Arg Lys Gly His Glu Tyr Thr Asn
    530                 535                 540
```

Ile Lys Tyr Ser Leu Ala Asp Gln Thr Ser Gly Asp Gln Ser Pro Leu
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Ala Arg Val Tyr Glu Asn Val Gly Leu Met Gln Gln Gln Lys Ser Phe
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tcttgcagat ctagtcagag ccttgtacac agtaatggaa acacctattt acgttggtac 180

ctgcagaagc caggccagtc tccaaaggtc ctgatctaca aagtttccaa ccgattttct 240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc 300

agagtggagg ctgaggatct gggagtttat ttctgctctc aaagtacaca tgttccgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaaagtagtg ctgatgatgc taagaaggat 420

gctgctaaga aggatgatgc taagaaggat gatgctaaga aggatggtga ggtgaagctg 480

gatgagactg gaggaggctt ggtgcaacct gggaggccca tgaaactctc ctgtgttgcc 540

tctggattca cttttagtga ctactggatg aactgggtcc gccagtctcc agagaaagga 600

ctggagtggg tagcacaaat tagaaacaaa ccttataatt atgaaacata ttattcagat 660

tctgtgaaag gcagattcac catctcaaga gatgattcca aaagtagtgt ctacctgcaa 720

atgaacaact taagagttga agacatgggt atctattact gtacgggttc ttactatggt 780

atggactact ggggtcaagg aacctcagtc accgtctccg cggccgcagt cgtgccagtc 840

cttcagaaag tgaactctac tactaccaag ccagtgctgc gaactccctc acctgtgcac 900

cctaccggga catctcagcc ccagagacca gaagattgtc ggccccgtgg ctcagtgaag 960

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agaaggaaca gactccttca aagtgactac atgaacatga ctccccggag gcctgggctc 1140

actcgaaagc cttaccagcc ctacgccccct gccagagact ttgcagcgta ccgccccaaa 1200

tggatcagga aaaaattccc ccacatattc aagcaaccat ttaagaagac cactggagca 1260

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ggctatgagc tgagagcaaa attcagcagg agtgcagaga ctgctgccaa cctgcaggac 1380

cccaaccagc tctacaatga gctcaatcta gggcgaagag aggaatatga cgtcttggag 1440

aagaagcggg ctcgggatcc agagatggga ggcaaacagc agaggaggag gaacccccag 1500

gaaggcgtat acaatgcact gcagaaagac aagatggcag aagcctacag tgagatcggc 1560

acaaaaggcg agaggcggag aggcaagggg cacgatggcc tttaccaggg tctcagcact 1620

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acaaaggcca aaaaggccaa cgtacg 146

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<211> 864
<212> DNA
<213> artificial

<220>

<223> mouseIL-7-F2A-mouseCCL19

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ctgatgatca gcatcgatga attggacaaa atgacaggaa ctgatagtaa ttgcccgaat 180

aatgaaccaa acttttttag aaaacatgta tgtgatgata caaaggaagc tgcttttcta 240

aatcgtgctg ctcgcaagtt gaagcaattt cttaaaatga atatcagtga agaattcaat 300

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gaaaaaaacg taaaggaaca gaaaaagaat gacgcatgtt tcctaaagag actactgaga 420

gaaataaaaa cttgttggaa taaaattttg aagggcagta taggaagcgg agtgaaacag 480

actttgaatt ttgaccttct caagttggcg ggagacgtgg agtccaaccc tggacctatg 540

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cctgctgttg tgttcaccac actaaggggc tatcagctct gtgcacctcc agaccagccc 780

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acctgcagag ccagcagcag cgtgtcctac atccactggt tccagcagaa gcccggcagc 180

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caacctggtg attttgtgct ctctgtgctc aatgaccagc ccaaggctgg cccaggttcc 480

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gagaacgtgg gcctcatgca gcagcagagg agtttcagat ga 1782