SEQUENCE LISTING

<110> Noile-Immune Biotech Inc.
Takeda Pharmaceutical Company Limited

<120> CAR-Expressing T Cell and CAR Expression Vector

<130> PT38-9034WO

<150> JP2018-163310
<151> 2018-08-31

<160> 19

<170> PatentIn version 3.5

<210> 1
<211> 1637
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment comprising anti-human CD20 CAR (DNA segment #1)

<220>
<221> misc_feature
<222> (1)..(6)
<223> restriction site (Nco I)

<220>
<221> CDS
<222> (3)..(1637)
<223> nucleic acid sequence encoding an anti-human CD20 scFv, a 3rd TM domain (mouse CD8) and a CP domain (mouse CD28_4-1BB_CD3zeta)

<220>
<221> misc_feature
<222> (3)..(785)
<223> anti-human CD20 scFv

<220>
<221> misc_feature
<222> (795)..(1040)
<223> transmembrane domain of mouse CD8

<220>
<221> misc_feature
<222> (1041)..(1163)

<223> cytoplasmic domain of mouse CD28

<220>
<221> misc_feature
<222> (1164)..(1298)
<223> cytoplasmic domain of mouse 4-1BB

<220>
<221> misc_feature
<222> (1299)..(1637)
<223> cytoplasmic domain of mouse CD3 zeta

<220>
<221> misc_feature
<222> (1337)..(1344)
<223> restriction site (Sbf I)

<400> 1
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cc atg gac tgg acc tgg cgg atc ctg ttc ctg gtg gct gct gct aca          47
   Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr
   1               5                  10                  15

ggc gcc cac agc cag atc gtg ctg tct cag tct ccc gcc atc ctg tct         95
Gly Ala His Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser
                20                  25                  30

gct agc cct ggc gag aaa gtg acc atg acc tgc aga gcc agc agc agc        143
Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser
            35                  40                  45

gtg tcc tac atc cac tgg ttc cag cag aag ccc ggc agc agc ccc aag        191
Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys
        50                  55                  60

cct tgg atc tac gcc aca agc aac ctg gcc tct ggc gtg cca gtg cgg        239
Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg
    65                  70                  75

ttt agc ggc tct ggc tct ggc acc agc tac agc ctg acc atc agc aga        287
Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
80                  85                  90                  95

gtg gaa gcc gag gac gcc gcc acc tac tac tgt cag cag tgg acc agc        335
Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser
                100                 105                 110

aac ccc ccc aca ttc ggc gga ggc acc aag ctg gaa atc aag ggc gga        383
Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly
            115                 120                 125
```

```
ggc gga tct ggc ggc gga gga tct ggg gga ggc ggc tct cag gtg cag        431
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln
        130                 135                 140

ctg cag cag cct ggc gct gag ctc gtg aaa cct ggc gcc tcc gtg aag        479
Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
    145                 150                 155

atg agc tgc aag gcc agc ggc tac acc ttc aca agc tac aac atg cac        527
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His
160                 165                 170                 175

tgg gtc aag cag acc cct ggc aga ggc ctg gaa tgg atc ggc gct atc        575
Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile
                180                 185                 190

tac ccc ggc aac ggc gac acc tcc tac aac cag aag ttc aag ggc aag        623
Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys
            195                 200                 205

gcc acc ctg acc gcc gac aag agc agc agc aca gcc tac atg cag ctg        671
Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
        210                 215                 220

tcc tcc ctg acc agc gag gac agc gcc gtg tac tac tgc gcc aga tct        719
Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser
    225                 230                 235

acc tac tac ggc ggc gac tgg tac ttc aac gtg tgg ggc gct ggc acc        767
Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly Thr
240                 245                 250                 255

acc gtg acc gtg tct gct gcg gcc gca gtc gtg cca gtc ctt cag aaa        815
Thr Val Thr Val Ser Ala Ala Ala Ala Val Val Pro Val Leu Gln Lys
                260                 265                 270

gtg aac tct act act acc aag cca gtg ctg cga act ccc tca cct gtg        863
Val Asn Ser Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val
            275                 280                 285

cac cct acc ggg aca tct cag ccc cag aga cca gaa gat tgt cgg ccc        911
His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro
        290                 295                 300

cgt ggc tca gtg aag ggg acc gga ttg gac ttc gcc tgt gat att tac        959
Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr
    305                 310                 315
```

```
atc tgg gca ccc ttg gcc gga atc tgc gtg gcc cct ctg ctg tcc ttg       1007
Ile Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Pro Leu Leu Ser Leu
320                 325                 330                 335

atc atc act ctc atc tgc tac cac agg agc cga aat agt aga agg aac       1055
Ile Ile Thr Leu Ile Cys Tyr His Arg Ser Arg Asn Ser Arg Arg Asn
                340                 345                 350

aga ctc ctt caa agt gac tac atg aac atg act ccc cgg agg cct ggg       1103
Arg Leu Leu Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
            355                 360                 365

ctc act cga aag cct tac cag ccc tac gcc cct gcc aga gac ttt gca       1151
Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala
        370                 375                 380

gcg tac cgc ccc aaa tgg atc agg aaa aaa ttc ccc cac ata ttc aag       1199
Ala Tyr Arg Pro Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys
    385                 390                 395

caa cca ttt aag aag acc act gga gca gct caa gag gaa gat gct tgt       1247
Gln Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys
400                 405                 410                 415

agc tgc cga tgt cca cag gaa gaa gaa gga gga gga gga ggc tat gag       1295
Ser Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu
                420                 425                 430

ctg aga gca aaa ttc agc agg agt gca gag act gct gcc aac ctg cag       1343
Leu Arg Ala Lys Phe Ser Arg Ser Ala Glu Thr Ala Ala Asn Leu Gln
            435                 440                 445

gac ccc aac cag ctc tac aat gag ctc aat cta ggg cga aga gag gaa       1391
Asp Pro Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
        450                 455                 460

tat gac gtc ttg gag aag aag cgg gct cgg gat cca gag atg gga ggc       1439
Tyr Asp Val Leu Glu Lys Lys Arg Ala Arg Asp Pro Glu Met Gly Gly
    465                 470                 475

aaa cag cag agg agg agg aac ccc cag gaa ggc gta tac aat gca ctg       1487
Lys Gln Gln Arg Arg Arg Asn Pro Gln Glu Gly Val Tyr Asn Ala Leu
480                 485                 490                 495

cag aaa gac aag atg gca gaa gcc tac agt gag atc ggc aca aaa ggc       1535
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Thr Lys Gly
                500                 505                 510

gag agg cgg aga ggc aag ggg cac gat ggc ctt tac cag ggt ctc agc       1583
```

```
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
            515                 520                 525

act gcc acc aag gac acc tat gat gcc ctg cat atg cag acc ctg gcc       1631
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Thr Leu Ala
        530                 535                 540

cct cgc                                                               1637
Pro Arg
    545
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<210> 2
<211> 545
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

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


Ala His Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala
            20                  25                  30


Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
        35                  40                  45


Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro
    50                  55                  60


Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe
65                  70                  75                  80


Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val
                85                  90                  95


Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
            100                 105                 110
```

```
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    130                 135                 140

Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met
145                 150                 155                 160

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp
                165                 170                 175

Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr
            180                 185                 190

Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala
        195                 200                 205

Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
    210                 215                 220

Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser Thr
225                 230                 235                 240

Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly Thr Thr
                245                 250                 255

Val Thr Val Ser Ala Ala Ala Ala Val Val Pro Val Leu Gln Lys Val
            260                 265                 270

Asn Ser Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser Pro Val His
        275                 280                 285

Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg
    290                 295                 300
```

```
Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
305                 310                 315                 320

Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Pro Leu Leu Ser Leu Ile
                325                 330                 335

Ile Thr Leu Ile Cys Tyr His Arg Ser Arg Asn Ser Arg Arg Asn Arg
            340                 345                 350

Leu Leu Gln Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Leu
        355                 360                 365

Thr Arg Lys Pro Tyr Gln Pro Tyr Ala Pro Ala Arg Asp Phe Ala Ala
    370                 375                 380

Tyr Arg Pro Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln
385                 390                 395                 400

Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser
                405                 410                 415

Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu
            420                 425                 430

Arg Ala Lys Phe Ser Arg Ser Ala Glu Thr Ala Ala Asn Leu Gln Asp
        435                 440                 445

Pro Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
    450                 455                 460

Asp Val Leu Glu Lys Lys Arg Ala Arg Asp Pro Glu Met Gly Gly Lys
465                 470                 475                 480

Gln Gln Arg Arg Arg Asn Pro Gln Glu Gly Val Tyr Asn Ala Leu Gln
                485                 490                 495

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Thr Lys Gly Glu
```

500 505 510

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
515 520 525

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Thr Leu Ala Pro
530 535 540

Arg
545

<210> 3
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> MCS DNA segment encoding a stop codon and a restriction enzyme site (DNA segment #2)

<220>
<221> misc_feature
<222> (1)..(3)
<223> stop codon

<220>
<221> misc_feature
<222> (38)..(43)
<223> restriction site (Sal I)

<400> 3
tgaaagctta aaccagttaa ctggaaaacg cgtaaagtcg ac 42

<210> 4
<211> 1011
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment of IL15LSP_F2A_CCL19 (DNA segment #3)

<220>

<221> CDS
<222> (7)..(969)
<223> nucleic acid sequence encoding 1st F2A; a fusion protein "IL15LSP" comprising mouse IL-15 LSP and mouse IL-15; 2nd F2A; and CCL19

<220>
<221> misc_feature
<222> (7)..(81)
<223> F2A peptide

<220>
<221> misc_feature
<222> (82)..(168)
<223> mouse IL-15 LSP

<220>
<221> misc_feature
<222> (169)..(567)
<223> mouse IL-15

<220>
<221> misc_feature
<222> (568)..(642)
<223> mouse F2A

<220>
<221> misc_feature
<222> (646)..(969)
<223> mouse CCL19

<220>
<221> misc_feature
<222> (970)..(972)
<223> stop codon

<220>
<221> misc_feature
<222> (1006)..(1011)
<223> restriction site (Sal I)

<400> 4
gaattc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag 48
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10

ctg gcc gga gac gtg gag agc aac cct ggc cct atg aag atc ctg aag 96
Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Lys Ile Leu Lys
15 20 25 30

```
ccc tac atg agg aac acc agc atc tcc tgt tac ctc tgt ttc ctg ctg        144
Pro Tyr Met Arg Asn Thr Ser Ile Ser Cys Tyr Leu Cys Phe Leu Leu
               35                  40                  45

aac agc cac ttc ctg acc gag gcc ggc atc cac gtg ttc atc ctg ggc        192
Asn Ser His Phe Leu Thr Glu Ala Gly Ile His Val Phe Ile Leu Gly
            50                  55                  60

tgc gtg tcc gtg ggc ctg cct aag acc gag gcc aac tgg atc gac gtg        240
Cys Val Ser Val Gly Leu Pro Lys Thr Glu Ala Asn Trp Ile Asp Val
        65                  70                  75

aga tac gac ctg gag aag atc gag agc ctg atc cag agc atc cac atc        288
Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu Ile Gln Ser Ile His Ile
    80                  85                  90

gac acc aca ctg tac acc gac agc gac ttc cac ccc agc tgc aag gtg        336
Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe His Pro Ser Cys Lys Val
95                  100                 105                 110

acc gcc atg aac tgc ttt ctg ctg gag ctg cag gtg atc ctg cac gag        384
Thr Ala Met Asn Cys Phe Leu Leu Glu Leu Gln Val Ile Leu His Glu
               115                 120                 125

tac agc aac atg acc ctg aac gag acc gtg aga aac gtg ctg tac ctg        432
Tyr Ser Asn Met Thr Leu Asn Glu Thr Val Arg Asn Val Leu Tyr Leu
            130                 135                 140

gcc aac tcc acc ctg agc agc aac aag aac gtg gcc gag agc ggc tgc        480
Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn Val Ala Glu Ser Gly Cys
        145                 150                 155

aag gag tgc gag gag ctc gag gag aaa acc ttc acc gag ttc ctg cag        528
Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr Phe Thr Glu Phe Leu Gln
    160                 165                 170

agc ttc atc agg atc gtc cag atg ttc atc aac acc agc ggc agc ggc        576
Ser Phe Ile Arg Ile Val Gln Met Phe Ile Asn Thr Ser Gly Ser Gly
175                 180                 185                 190

gtg aag cag acc ctg aac ttc gac ctg ctg aag ctg gcc gga gac gtg        624
Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
               195                 200                 205

gag agc aac cct ggc cca tgc atg gcc ccc agg gtg acc cct ctg ctg        672
Glu Ser Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu
            210                 215                 220
```

```
gcc ttc agc ctg ctg gtg ctg tgg acc ttc cct gcc cct acc ctg gga        720
Ala Phe Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly
        225                 230                 235

gga gcc aat gac gcc gag gac tgc tgc ctg agc gtg acc cag aga ccc        768
Gly Ala Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro
    240                 245                 250

atc ccc ggc aac atc gtg aag gcc ttc agg tac ctg ctg aac gag gac        816
Ile Pro Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp
255                 260                 265                 270

ggc tgc aga gtg cct gcc gtg gtg ttc acc acc ctg agg ggc tac cag        864
Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln
                275                 280                 285

ctg tgt gct ccc cct gac cag cct tgg gtg gac agg atc atc agg agg        912
Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg
            290                 295                 300

ctg aag aag agc agc gcc aag aac aag ggc aac agc acc agg agg agc        960
Leu Lys Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser
        305                 310                 315

ccc gtg agc tgaaagctta aaccagttaa ctggaaaacg cgtaaagtcg ac           1011
Pro Val Ser
    320
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<210> 5
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5

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


Gly Asp Val Glu Ser Asn Pro Gly Pro Met Lys Ile Leu Lys Pro Tyr
            20                  25                  30


Met Arg Asn Thr Ser Ile Ser Cys Tyr Leu Cys Phe Leu Leu Asn Ser
        35                  40                  45
```

```
His Phe Leu Thr Glu Ala Gly Ile His Val Phe Ile Leu Gly Cys Val
    50                  55                  60

Ser Val Gly Leu Pro Lys Thr Glu Ala Asn Trp Ile Asp Val Arg Tyr
65                  70                  75                  80

Asp Leu Glu Lys Ile Glu Ser Leu Ile Gln Ser Ile His Ile Asp Thr
                85                  90                  95

Thr Leu Tyr Thr Asp Ser Asp Phe His Pro Ser Cys Lys Val Thr Ala
            100                 105                 110

Met Asn Cys Phe Leu Leu Glu Leu Gln Val Ile Leu His Glu Tyr Ser
        115                 120                 125

Asn Met Thr Leu Asn Glu Thr Val Arg Asn Val Leu Tyr Leu Ala Asn
    130                 135                 140

Ser Thr Leu Ser Ser Asn Lys Asn Val Ala Glu Ser Gly Cys Lys Glu
145                 150                 155                 160

Cys Glu Glu Leu Glu Glu Lys Thr Phe Thr Glu Phe Leu Gln Ser Phe
                165                 170                 175

Ile Arg Ile Val Gln Met Phe Ile Asn Thr Ser Gly Ser Gly Val Lys
            180                 185                 190

Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
        195                 200                 205

Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu Ala Phe
    210                 215                 220

Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly Gly Ala
225                 230                 235                 240
```

```
Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro Ile Pro
                245                 250                 255

Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp Gly Cys
            260                 265                 270

Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln Leu Cys
        275                 280                 285

Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg Leu Lys
    290                 295                 300

Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser Pro Val
305                 310                 315                 320

Ser
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<210> 6
<211> 1581
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment of sIL15RA_F2A_CCL19 (DNA segment #4)

<220>
<221> CDS
<222> (7)..(1539)
<223> nucleic acid sequence encoding 1st F2A; a fusion protein "sIL15RA" comprising IL-2SP, IL-15, a linker and IL-15Ra extracellular domain; 2nd F2A; and CCL19

<220>
<221> misc_feature
<222> (7)..(81)
<223> F2A peptide

<220>
<221> misc_feature
<222> (82)..(141)

<223> mouse IL-2 SP

<220>
<221> misc_feature
<222> (142)..(540)
<223> mouse IL-15

<220>
<221> misc_feature
<222> (541)..(618)
<223> linker

<220>
<221> misc_feature
<222> (619)..(1137)
<223> mouse IL-15Ra extracellular domain

<220>
<221> misc_feature
<222> (1138)..(1212)
<223> F2A

<220>
<221> misc_feature
<222> (1216)..(1539)
<223> mouse CCL19

<220>
<221> misc_feature
<222> (1540)..(1542)
<223> stop codon

<220>
<221> misc_feature
<222> (1576)..(1581)
<223> restriction site (Sal I)

<400> 6
gaattc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag 48
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10

ctg gcc gga gac gtg gag agc aac cct ggc cct atg tat tcc atg cag 96
Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Tyr Ser Met Gln
15 20 25 30

ctg gcc agc tgt gtg acc ctg aca ctg gtg ctg ctg gtg aac agc ggc 144
Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu Leu Val Asn Ser Gly
35 40 45

```
atc cac gtg ttc att ctg gga tgc gtc tcc gtg ggc ctc ccc aag acc        192
Ile His Val Phe Ile Leu Gly Cys Val Ser Val Gly Leu Pro Lys Thr
            50                  55                  60

gag gct aac tgg atc gac gtc agg tac gac ctg gag aag atc gaa agc        240
Glu Ala Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser
        65                  70                  75

ctg atc cag tcc atc cac atc gat aca acc ctg tac aca gat tcc gac        288
Leu Ile Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp
    80                  85                  90

ttc cac ccc tcc tgt aag gtc acc gcc atg aac tgc ttc ctc ctg gaa        336
Phe His Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu
95                  100                 105                 110

ctc cag gtc atc ctg cac gag tac tcc aac atg acc ctg aac gaa acc        384
Leu Gln Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr
                115                 120                 125

gtg agg aat gtg ctg tac ctc gcc aac tcc aca ctg agc tcc aat aag        432
Val Arg Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys
            130                 135                 140

aac gtg gct gag agc ggc tgc aag gag tgt gag gag ctg gaa gag aag        480
Asn Val Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys
        145                 150                 155

acc ttc acc gag ttc ctg cag agc ttc atc agg atc gtg cag atg ttc        528
Thr Phe Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe
    160                 165                 170

atc aac aca agc tcc ggc gga gga tcc gga gga gga gga agc gga ggc        576
Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
175                 180                 185                 190

ggc ggc tcc gga ggc gga gga agc gga gga gga agc ctg caa gga acc        624
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Thr
                195                 200                 205

acc tgt ccc cct ccc gtg tcc atc gag cac gcc gac atc agg gtg aag        672
Thr Cys Pro Pro Pro Val Ser Ile Glu His Ala Asp Ile Arg Val Lys
            210                 215                 220

aac tac tcc gtc aac agc agg gaa agg tac gtg tgc aac tcc ggc ttt        720
Asn Tyr Ser Val Asn Ser Arg Glu Arg Tyr Val Cys Asn Ser Gly Phe
        225                 230                 235
```

```
aag agg aag gcc ggc acc agc acc ctc atc gag tgc gtg atc aac aag        768
Lys Arg Lys Ala Gly Thr Ser Thr Leu Ile Glu Cys Val Ile Asn Lys
    240                 245                 250

aac aca aac gtg gcc cac tgg acc acc ccc agc ctg aag tgt att aga        816
Asn Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
255                 260                 265                 270

gac ccc agc ctg gct cat tac agc ccc gtg ccc aca gtg gtg aca ccc        864
Asp Pro Ser Leu Ala His Tyr Ser Pro Val Pro Thr Val Val Thr Pro
                275                 280                 285

aag gtg aca agc cag cct gag agc cct agc cct agc gcc aaa gag ccc        912
Lys Val Thr Ser Gln Pro Glu Ser Pro Ser Pro Ser Ala Lys Glu Pro
            290                 295                 300

gag gcc ttt tcc ccc aag tcc gac acc gcc atg acc acc gag aca gcc        960
Glu Ala Phe Ser Pro Lys Ser Asp Thr Ala Met Thr Thr Glu Thr Ala
        305                 310                 315

atc atg cct ggc agc aga ctg acc cct agc cag acc aca tcc gct ggc       1008
Ile Met Pro Gly Ser Arg Leu Thr Pro Ser Gln Thr Thr Ser Ala Gly
    320                 325                 330

acc aca ggc acc ggc tcc cac aag agc tcc aga gcc cct agc ctg gct       1056
Thr Thr Gly Thr Gly Ser His Lys Ser Ser Arg Ala Pro Ser Leu Ala
335                 340                 345                 350

gcc aca atg aca ctg gaa cct acc gcc tcc acc agc ctc aga atc aca       1104
Ala Thr Met Thr Leu Glu Pro Thr Ala Ser Thr Ser Leu Arg Ile Thr
                355                 360                 365

gag atc tcc ccc cac agc agc aag atg acc aag ggc agc ggc gtg aag       1152
Glu Ile Ser Pro His Ser Ser Lys Met Thr Lys Gly Ser Gly Val Lys
            370                 375                 380

cag acc ctg aac ttc gac ctg ctg aag ctg gcc gga gac gtg gag agc       1200
Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
        385                 390                 395

aac cct ggc cca tgc atg gcc ccc agg gtg acc cct ctg ctg gcc ttc       1248
Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu Ala Phe
    400                 405                 410

agc ctg ctg gtg ctg tgg acc ttc cct gcc cct acc ctg gga gga gcc       1296
Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly Gly Ala
415                 420                 425                 430

aat gac gcc gag gac tgc tgc ctg agc gtg acc cag aga ccc atc ccc       1344
```

```
Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro Ile Pro
                435                 440                 445

ggc aac atc gtg aag gcc ttc agg tac ctg ctg aac gag gac ggc tgc       1392
Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp Gly Cys
            450                 455                 460

aga gtg cct gcc gtg gtg ttc acc acc ctg agg ggc tac cag ctg tgt       1440
Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln Leu Cys
        465                 470                 475

gct ccc cct gac cag cct tgg gtg gac agg atc atc agg agg ctg aag       1488
Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg Leu Lys
    480                 485                 490

aag agc agc gcc aag aac aag ggc aac agc acc agg agg agc ccc gtg       1536
Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser Pro Val
495                 500                 505                 510

agc tgaaagctta aaccagttaa ctggaaaacg cgtaaagtcg ac                    1581
Ser
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<210> 7
<211> 511
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7

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


Gly Asp Val Glu Ser Asn Pro Gly Pro Met Tyr Ser Met Gln Leu Ala
            20                  25                  30


Ser Cys Val Thr Leu Thr Leu Val Leu Leu Val Asn Ser Gly Ile His
        35                  40                  45


Val Phe Ile Leu Gly Cys Val Ser Val Gly Leu Pro Lys Thr Glu Ala
    50                  55                  60
```

```
Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu Ile
65                  70                  75                  80

Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe His
                85                  90                  95

Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu Leu Gln
            100                 105                 110

Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr Val Arg
        115                 120                 125

Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn Val
    130                 135                 140

Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr Phe
145                 150                 155                 160

Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe Ile Asn
                165                 170                 175

Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Thr Thr Cys
        195                 200                 205

Pro Pro Pro Val Ser Ile Glu His Ala Asp Ile Arg Val Lys Asn Tyr
    210                 215                 220

Ser Val Asn Ser Arg Glu Arg Tyr Val Cys Asn Ser Gly Phe Lys Arg
225                 230                 235                 240

Lys Ala Gly Thr Ser Thr Leu Ile Glu Cys Val Ile Asn Lys Asn Thr
                245                 250                 255
```

```
Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro
            260                 265                 270

Ser Leu Ala His Tyr Ser Pro Val Pro Thr Val Val Thr Pro Lys Val
        275                 280                 285

Thr Ser Gln Pro Glu Ser Pro Ser Pro Ser Ala Lys Glu Pro Glu Ala
    290                 295                 300

Phe Ser Pro Lys Ser Asp Thr Ala Met Thr Thr Glu Thr Ala Ile Met
305                 310                 315                 320

Pro Gly Ser Arg Leu Thr Pro Ser Gln Thr Thr Ser Ala Gly Thr Thr
                325                 330                 335

Gly Thr Gly Ser His Lys Ser Ser Arg Ala Pro Ser Leu Ala Ala Thr
            340                 345                 350

Met Thr Leu Glu Pro Thr Ala Ser Thr Ser Leu Arg Ile Thr Glu Ile
        355                 360                 365

Ser Pro His Ser Ser Lys Met Thr Lys Gly Ser Gly Val Lys Gln Thr
    370                 375                 380

Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro
385                 390                 395                 400

Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu Ala Phe Ser Leu
                405                 410                 415

Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly Gly Ala Asn Asp
            420                 425                 430

Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro Ile Pro Gly Asn
        435                 440                 445

Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp Gly Cys Arg Val
```

```
    450                 455                 460

Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln Leu Cys Ala Pro
465                 470                 475                 480

Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg Leu Lys Lys Ser
                485                 490                 495

Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser Pro Val Ser
            500                 505                 510
```

<210> 8
<211> 1755
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment of mbIL15RA_F2A_CCL19 (DNA segment #5)

<220>
<221> CDS
<222> (7)..(1713)
<223> nucleic acid sequence encoding 1st F2A; a fusion protein "mbIL15RA" comprising IL-2 SP, IL-15, a linker and IL-15Ra; 2nd F2A; and CCL19

<220>
<221> misc_feature
<222> (7)..(81)
<223> F2A peptide

<220>
<221> misc_feature
<222> (82)..(141)
<223> mouse IL-2 SP

<220>
<221> misc_feature
<222> (142)..(540)
<223> mouse IL-15

<220>
<221> misc_feature
<222> (541)..(618)

<223> linker

<220>
<221> misc_feature
<222> (619)..(1311)
<223> mouse IL-15Ra (full length)

<220>
<221> misc_feature
<222> (1312)..(1386)
<223> F2A peptide

<220>
<221> misc_feature
<222> (1390)..(1713)
<223> mouse CCL19

<220>
<221> misc_feature
<222> (1714)..(1716)
<223> stop codon

<220>
<221> misc_feature
<222> (1750)..(1755)
<223> restriction site (Sal I)

<400> 8
gaattc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag 48
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10

ctg gcc gga gac gtg gag agc aac cct ggc cct atg tat tcc atg cag 96
Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Tyr Ser Met Gln
15 20 25 30

ctg gcc agc tgt gtg acc ctg aca ctg gtg ctg ctg gtg aac agc ggc 144
Leu Ala Ser Cys Val Thr Leu Thr Leu Val Leu Leu Val Asn Ser Gly
35 40 45

atc cac gtg ttc att ctg gga tgc gtc tcc gtg ggc ctc ccc aag acc 192
Ile His Val Phe Ile Leu Gly Cys Val Ser Val Gly Leu Pro Lys Thr
50 55 60

gag gct aac tgg atc gac gtc agg tac gac ctg gag aag atc gaa agc 240
Glu Ala Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser
65 70 75

ctg atc cag tcc atc cac atc gat aca acc ctg tac aca gat tcc gac 288

```
Leu Ile Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp
    80                  85                  90

ttc cac ccc tcc tgt aag gtc acc gcc atg aac tgc ttc ctc ctg gaa        336
Phe His Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu
95                  100                 105                 110

ctc cag gtc atc ctg cac gag tac tcc aac atg acc ctg aac gaa acc        384
Leu Gln Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr
                115                 120                 125

gtg agg aat gtg ctg tac ctc gcc aac tcc aca ctg agc tcc aat aag        432
Val Arg Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys
            130                 135                 140

aac gtg gct gag agc ggc tgc aag gag tgt gag gag ctg gaa gag aag        480
Asn Val Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys
        145                 150                 155

acc ttc acc gag ttc ctg cag agc ttc atc agg atc gtg cag atg ttc        528
Thr Phe Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe
    160                 165                 170

atc aac aca agc tcc ggc gga gga tcc gga gga gga gga agc gga ggc        576
Ile Asn Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
175                 180                 185                 190

ggc ggc tcc gga ggc gga gga agc gga gga gga agc ctg caa gga acc        624
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Thr
                195                 200                 205

acc tgt ccc cct ccc gtg tcc atc gag cac gcc gac atc agg gtg aag        672
Thr Cys Pro Pro Pro Val Ser Ile Glu His Ala Asp Ile Arg Val Lys
            210                 215                 220

aac tac tcc gtc aac agc agg gaa agg tac gtg tgc aac tcc ggc ttt        720
Asn Tyr Ser Val Asn Ser Arg Glu Arg Tyr Val Cys Asn Ser Gly Phe
        225                 230                 235

aag agg aag gcc ggc acc agc acc ctc atc gag tgc gtg atc aac aag        768
Lys Arg Lys Ala Gly Thr Ser Thr Leu Ile Glu Cys Val Ile Asn Lys
    240                 245                 250

aac aca aac gtg gcc cac tgg acc acc ccc agc ctg aag tgt att aga        816
Asn Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg
255                 260                 265                 270

gac ccc agc ctg gct cat tac agc ccc gtg ccc aca gtg gtg aca ccc        864
Asp Pro Ser Leu Ala His Tyr Ser Pro Val Pro Thr Val Val Thr Pro
```

```
                275                 280                 285

aag gtg aca agc cag cct gag agc cct agc cct agc gcc aaa gag ccc        912
Lys Val Thr Ser Gln Pro Glu Ser Pro Ser Pro Ser Ala Lys Glu Pro
            290                 295                 300

gag gcc ttt tcc ccc aag tcc gac acc gcc atg acc acc gag aca gcc        960
Glu Ala Phe Ser Pro Lys Ser Asp Thr Ala Met Thr Thr Glu Thr Ala
        305                 310                 315

atc atg cct ggc agc aga ctg acc cct agc cag acc aca tcc gct ggc       1008
Ile Met Pro Gly Ser Arg Leu Thr Pro Ser Gln Thr Thr Ser Ala Gly
    320                 325                 330

acc aca ggc acc ggc tcc cac aag agc tcc aga gcc cct agc ctg gct       1056
Thr Thr Gly Thr Gly Ser His Lys Ser Ser Arg Ala Pro Ser Leu Ala
335                 340                 345                 350

gcc aca atg aca ctg gaa cct acc gcc tcc acc agc ctc aga atc aca       1104
Ala Thr Met Thr Leu Glu Pro Thr Ala Ser Thr Ser Leu Arg Ile Thr
                355                 360                 365

gag atc tcc ccc cac agc agc aag atg acc aag gtg gcc atc tcc acc       1152
Glu Ile Ser Pro His Ser Ser Lys Met Thr Lys Val Ala Ile Ser Thr
            370                 375                 380

tcc gtg ctg ctg gtg gga gcc ggc gtg gtc atg gcc ttt ctg gcc tgg       1200
Ser Val Leu Leu Val Gly Ala Gly Val Val Met Ala Phe Leu Ala Trp
        385                 390                 395

tac atc aag tcc agg cag cct agc caa cct tgc agg gtg gag gtg gaa       1248
Tyr Ile Lys Ser Arg Gln Pro Ser Gln Pro Cys Arg Val Glu Val Glu
    400                 405                 410

act atg gaa acc gtg ccc atg acc gtg agg gcc agc tcc aag gag gat       1296
Thr Met Glu Thr Val Pro Met Thr Val Arg Ala Ser Ser Lys Glu Asp
415                 420                 425                 430

gaa gac acc ggc gcc ggc agc ggc gtg aag cag acc ctg aac ttc gac       1344
Glu Asp Thr Gly Ala Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp
                435                 440                 445

ctg ctg aag ctg gcc gga gac gtg gag agc aac cct ggc cca tgc atg       1392
Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys Met
            450                 455                 460

gcc ccc agg gtg acc cct ctg ctg gcc ttc agc ctg ctg gtg ctg tgg       1440
Ala Pro Arg Val Thr Pro Leu Leu Ala Phe Ser Leu Leu Val Leu Trp
        465                 470                 475
```

```
acc ttc cct gcc cct acc ctg gga gga gcc aat gac gcc gag gac tgc       1488
Thr Phe Pro Ala Pro Thr Leu Gly Gly Ala Asn Asp Ala Glu Asp Cys
    480                 485                 490

tgc ctg agc gtg acc cag aga ccc atc ccc ggc aac atc gtg aag gcc       1536
Cys Leu Ser Val Thr Gln Arg Pro Ile Pro Gly Asn Ile Val Lys Ala
495                 500                 505                 510

ttc agg tac ctg ctg aac gag gac ggc tgc aga gtg cct gcc gtg gtg       1584
Phe Arg Tyr Leu Leu Asn Glu Asp Gly Cys Arg Val Pro Ala Val Val
                515                 520                 525

ttc acc acc ctg agg ggc tac cag ctg tgt gct ccc cct gac cag cct       1632
Phe Thr Thr Leu Arg Gly Tyr Gln Leu Cys Ala Pro Pro Asp Gln Pro
            530                 535                 540

tgg gtg gac agg atc atc agg agg ctg aag aag agc agc gcc aag aac       1680
Trp Val Asp Arg Ile Ile Arg Arg Leu Lys Lys Ser Ser Ala Lys Asn
        545                 550                 555

aag ggc aac agc acc agg agg agc ccc gtg agc tgaaagctta aaccagttaa     1733
Lys Gly Asn Ser Thr Arg Arg Ser Pro Val Ser
    560                 565

ctggaaaacg cgtaaagtcg ac                                              1755


<210>  9
<211>  569
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  9

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


Gly Asp Val Glu Ser Asn Pro Gly Pro Met Tyr Ser Met Gln Leu Ala
            20                  25                  30


Ser Cys Val Thr Leu Thr Leu Val Leu Leu Val Asn Ser Gly Ile His
        35                  40                  45
```

```
Val Phe Ile Leu Gly Cys Val Ser Val Gly Leu Pro Lys Thr Glu Ala
    50                  55                  60

Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu Ile
65                  70                  75                  80

Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe His
                85                  90                  95

Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu Leu Gln
            100                 105                 110

Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr Val Arg
        115                 120                 125

Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn Val
    130                 135                 140

Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr Phe
145                 150                 155                 160

Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe Ile Asn
                165                 170                 175

Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
            180                 185                 190

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Gly Thr Thr Cys
        195                 200                 205

Pro Pro Pro Val Ser Ile Glu His Ala Asp Ile Arg Val Lys Asn Tyr
    210                 215                 220

Ser Val Asn Ser Arg Glu Arg Tyr Val Cys Asn Ser Gly Phe Lys Arg
225                 230                 235                 240
```

```
Lys Ala Gly Thr Ser Thr Leu Ile Glu Cys Val Ile Asn Lys Asn Thr
                245                 250                 255

Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro
            260                 265                 270

Ser Leu Ala His Tyr Ser Pro Val Pro Thr Val Val Thr Pro Lys Val
        275                 280                 285

Thr Ser Gln Pro Glu Ser Pro Ser Pro Ser Ala Lys Glu Pro Glu Ala
    290                 295                 300

Phe Ser Pro Lys Ser Asp Thr Ala Met Thr Thr Glu Thr Ala Ile Met
305                 310                 315                 320

Pro Gly Ser Arg Leu Thr Pro Ser Gln Thr Thr Ser Ala Gly Thr Thr
                325                 330                 335

Gly Thr Gly Ser His Lys Ser Ser Arg Ala Pro Ser Leu Ala Ala Thr
            340                 345                 350

Met Thr Leu Glu Pro Thr Ala Ser Thr Ser Leu Arg Ile Thr Glu Ile
        355                 360                 365

Ser Pro His Ser Ser Lys Met Thr Lys Val Ala Ile Ser Thr Ser Val
    370                 375                 380

Leu Leu Val Gly Ala Gly Val Val Met Ala Phe Leu Ala Trp Tyr Ile
385                 390                 395                 400

Lys Ser Arg Gln Pro Ser Gln Pro Cys Arg Val Glu Val Glu Thr Met
                405                 410                 415

Glu Thr Val Pro Met Thr Val Arg Ala Ser Ser Lys Glu Asp Glu Asp
            420                 425                 430

Thr Gly Ala Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu
```

```
        435                 440                 445

Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys Met Ala Pro
    450                 455                 460

Arg Val Thr Pro Leu Leu Ala Phe Ser Leu Leu Val Leu Trp Thr Phe
465                 470                 475                 480

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

Ser Val Thr Gln Arg Pro Ile Pro Gly Asn Ile Val Lys Ala Phe Arg
            500                 505                 510

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

Thr Leu Arg Gly Tyr Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val
    530                 535                 540

Asp Arg Ile Ile Arg Arg Leu Lys Lys Ser Ser Ala Lys Asn Lys Gly
545                 550                 555                 560

Asn Ser Thr Arg Arg Ser Pro Val Ser
                565
```

<210> 10
<211> 1221
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment of sushiIL15_F2A_CCL19 (DNA segment #6)

<220>
<221> CDS
<222> (7)..(1179)
<223> nucleic acid sequence encoding 1st F2A; a fusion protein "sushiIL15" comprising IL-15Ra SP, a linker and IL-15; 2nd F2A;

and CCL19

<220>
<221> misc_feature
<222> (7)..(81)
<223> F2A peptide

<220>
<221> misc_feature
<222> (82)..(375)
<223> mouse IL-15Ra SP and sushi domain

<220>
<221> misc_feature
<222> (376)..(435)
<223> linker

<220>
<221> misc_feature
<222> (436)..(777)
<223> mouse IL-15

<220>
<221> misc_feature
<222> (778)..(852)
<223> F2A

<220>
<221> misc_feature
<222> (856)..(1179)
<223> mouse CCL19

<220>
<221> misc_feature
<222> (1180)..(1182)
<223> stop codon

<220>
<221> misc_feature
<222> (1216)..(1221)
<223> restriction site (Sal I)

<400> 10
gaattc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag 48
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10

ctg gcc gga gac gtg gag agc aac cct ggc cct atg gcc tcc cct cag 96
Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ala Ser Pro Gln

```
15                  20                  25                  30

ctg aga ggc tac ggc gtg cag gct atc ccc gtg ctg ctg ctg ctg ctg        144
Leu Arg Gly Tyr Gly Val Gln Ala Ile Pro Val Leu Leu Leu Leu Leu
                35                  40                  45

ctg ctg ctg ctg ctg cct ctg aga gtg acc cct ggc aca acc tgc cct        192
Leu Leu Leu Leu Leu Pro Leu Arg Val Thr Pro Gly Thr Thr Cys Pro
            50                  55                  60

cct ccc gtg agc atc gag cac gcc gac atc agg gtg aag aac tac tcc        240
Pro Pro Val Ser Ile Glu His Ala Asp Ile Arg Val Lys Asn Tyr Ser
        65                  70                  75

gtg aac agc agg gag agg tac gtg tgc aac agc ggc ttc aag agg aag        288
Val Asn Ser Arg Glu Arg Tyr Val Cys Asn Ser Gly Phe Lys Arg Lys
    80                  85                  90

gcc ggc acc agc acc ctg atc gag tgc gtg atc aac aag aac acc aac        336
Ala Gly Thr Ser Thr Leu Ile Glu Cys Val Ile Asn Lys Asn Thr Asn
95                  100                 105                 110

gtg gcc cac tgg acc acc ccc agc ctg aag tgc atc agg agc ggc ggc        384
Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Ser Gly Gly
                115                 120                 125

agc ggc ggc ggc ggc agc ggc ggc ggc agc ggc ggc ggc ggc agc ctg        432
Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu
            130                 135                 140

cag aac tgg atc gac gtc agg tac gac ctg gag aag atc gaa agc ctg        480
Gln Asn Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu
        145                 150                 155

atc cag tcc atc cac atc gat aca acc ctg tac aca gat tcc gac ttc        528
Ile Gln Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe
    160                 165                 170

cac ccc tcc tgt aag gtc acc gcc atg aac tgc ttc ctc ctg gaa ctc        576
His Pro Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu Leu
175                 180                 185                 190

cag gtc atc ctg cac gag tac tcc aac atg acc ctg aac gaa acc gtg        624
Gln Val Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr Val
                195                 200                 205

agg aat gtg ctg tac ctc gcc aac tcc aca ctg agc tcc aat aag aac        672
Arg Asn Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn
            210                 215                 220
```

```
gtg gct gag agc ggc tgc aag gag tgt gag gag ctg gaa gag aag acc        720
Val Ala Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr
        225                 230                 235

ttc acc gag ttc ctg cag agc ttc atc agg atc gtg cag atg ttc atc        768
Phe Thr Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe Ile
    240                 245                 250

aac aca agc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg        816
Asn Thr Ser Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu
255                 260                 265                 270

aag ctg gcc gga gac gtg gag agc aac cct ggc cca tgc atg gcc ccc        864
Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys Met Ala Pro
                275                 280                 285

agg gtg acc cct ctg ctg gcc ttc agc ctg ctg gtg ctg tgg acc ttc        912
Arg Val Thr Pro Leu Leu Ala Phe Ser Leu Leu Val Leu Trp Thr Phe
            290                 295                 300

cct gcc cct acc ctg gga gga gcc aat gac gcc gag gac tgc tgc ctg        960
Pro Ala Pro Thr Leu Gly Gly Ala Asn Asp Ala Glu Asp Cys Cys Leu
        305                 310                 315

agc gtg acc cag aga ccc atc ccc ggc aac atc gtg aag gcc ttc agg       1008
Ser Val Thr Gln Arg Pro Ile Pro Gly Asn Ile Val Lys Ala Phe Arg
    320                 325                 330

tac ctg ctg aac gag gac ggc tgc aga gtg cct gcc gtg gtg ttc acc       1056
Tyr Leu Leu Asn Glu Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr
335                 340                 345                 350

acc ctg agg ggc tac cag ctg tgt gct ccc cct gac cag cct tgg gtg       1104
Thr Leu Arg Gly Tyr Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val
                355                 360                 365

gac agg atc atc agg agg ctg aag aag agc agc gcc aag aac aag ggc       1152
Asp Arg Ile Ile Arg Arg Leu Lys Lys Ser Ser Ala Lys Asn Lys Gly
            370                 375                 380

aac agc acc agg agg agc ccc gtg agc tgaaagctta aaccagttaa            1199
Asn Ser Thr Arg Arg Ser Pro Val Ser
        385                 390

ctggaaaacg cgtaaagtcg ac                                            1221


<210>  11
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<211> 391
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11

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


Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ala Ser Pro Gln Leu Arg
            20                  25                  30


Gly Tyr Gly Val Gln Ala Ile Pro Val Leu Leu Leu Leu Leu Leu Leu
        35                  40                  45


Leu Leu Leu Pro Leu Arg Val Thr Pro Gly Thr Thr Cys Pro Pro Pro
    50                  55                  60


Val Ser Ile Glu His Ala Asp Ile Arg Val Lys Asn Tyr Ser Val Asn
65                  70                  75                  80


Ser Arg Glu Arg Tyr Val Cys Asn Ser Gly Phe Lys Arg Lys Ala Gly
                85                  90                  95


Thr Ser Thr Leu Ile Glu Cys Val Ile Asn Lys Asn Thr Asn Val Ala
            100                 105                 110


His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Ser Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Gln Asn
    130                 135                 140


Trp Ile Asp Val Arg Tyr Asp Leu Glu Lys Ile Glu Ser Leu Ile Gln
145                 150                 155                 160
```

```
Ser Ile His Ile Asp Thr Thr Leu Tyr Thr Asp Ser Asp Phe His Pro
                165                 170                 175

Ser Cys Lys Val Thr Ala Met Asn Cys Phe Leu Leu Glu Leu Gln Val
            180                 185                 190

Ile Leu His Glu Tyr Ser Asn Met Thr Leu Asn Glu Thr Val Arg Asn
        195                 200                 205

Val Leu Tyr Leu Ala Asn Ser Thr Leu Ser Ser Asn Lys Asn Val Ala
    210                 215                 220

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Thr Phe Thr
225                 230                 235                 240

Glu Phe Leu Gln Ser Phe Ile Arg Ile Val Gln Met Phe Ile Asn Thr
                245                 250                 255

Ser Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu
            260                 265                 270

Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Cys Met Ala Pro Arg Val
        275                 280                 285

Thr Pro Leu Leu Ala Phe Ser Leu Leu Val Leu Trp Thr Phe Pro Ala
    290                 295                 300

Pro Thr Leu Gly Gly Ala Asn Asp Ala Glu Asp Cys Cys Leu Ser Val
305                 310                 315                 320

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

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

Arg Gly Tyr Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Asp Arg
```

355 360 365

Ile Ile Arg Arg Leu Lys Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser
370 375 380

Thr Arg Arg Ser Pro Val Ser
385 390

<210> 12
<211> 1101
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment of IL-18_F2A_CCL19 (DNA segment #7)

<220>
<221> CDS
<222> (7)..(1059)
<223> nucleic acid sequence encoding 1st F2A; IL-18; 2nd F2A; and CCL19

<220>
<221> misc_feature
<222> (7)..(81)
<223> F2A peptide

<220>
<221> misc_feature
<222> (82)..(657)
<223> mouse IL-18

<220>
<221> misc_feature
<222> (658)..(732)
<223> F2A peptide

<220>
<221> misc_feature
<222> (736)..(1059)
<223> mouse CCL19

<220>
<221> misc_feature
<222> (1060)..(1062)
<223> stop codon

<220>
<221> misc_feature
<222> (1096)..(1101)
<223> restriction site (Sal I)

<400> 12
gaattc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag 48
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10

ctg gcc gga gac gtg gag agc aac cct ggc cct atg gcc gcc atg agc 96
Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ala Ala Met Ser
15 20 25 30

gag gac tcc tgc gtg aac ttt aag gag atg atg ttc atc gac aac acc 144
Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met Phe Ile Asp Asn Thr
35 40 45

ctg tac ttc atc ccc gag gaa aac ggc gac ctg gag agc gac aac ttc 192
Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu Glu Ser Asp Asn Phe
50 55 60

ggc agg ctg cac tgc acc acc gcc gtg atc agg aac atc aac gac cag 240
Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn Asp Gln
65 70 75

gtg ctg ttc gtg gac aag agg cag ccc gtg ttt gag gac atg acc gac 288
Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met Thr Asp
80 85 90

atc gac cag agc gcc agc gag ccc cag aca agg ctg atc atc tac atg 336
Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile Tyr Met
95 100 105 110

tac aag gac agc gag gtg agg ggc ctg gcc gtg aca ctg agc gtg aag 384
Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser Val Lys
115 120 125

gac agc aag atg agc acc ctg agc tgc aaa aac aag atc atc agc ttc 432
Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile Ser Phe
130 135 140

gag gag atg gac ccc ccc gag aac atc gac gac atc cag tcc gac ctg 480
Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser Asp Leu
145 150 155

atc ttc ttc caa aag agg gtg ccc ggc cac aac aag atg gag ttc gag 528
Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu Phe Glu

```
    160                 165                 170

agc agc ctg tat gag ggc cac ttc ctg gcc tgc cag aag gag gat gat        576
Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu Asp Asp
175                 180                 185                 190

gcc ttc aag ctg atc ctg aag aag aaa gat gag aac ggc gat aag agc        624
Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser
                195                 200                 205

gtg atg ttc acc ctg acc aac ctg cac cag tcc ggc agc ggc gtg aag        672
Val Met Phe Thr Leu Thr Asn Leu His Gln Ser Gly Ser Gly Val Lys
            210                 215                 220

cag acc ctg aac ttc gac ctg ctg aag ctg gcc gga gac gtg gag agc        720
Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
        225                 230                 235

aac cct ggc cca tgc atg gcc ccc agg gtg acc cct ctg ctg gcc ttc        768
Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu Ala Phe
    240                 245                 250

agc ctg ctg gtg ctg tgg acc ttc cct gcc cct acc ctg gga gga gcc        816
Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly Gly Ala
255                 260                 265                 270

aat gac gcc gag gac tgc tgc ctg agc gtg acc cag aga ccc atc ccc        864
Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro Ile Pro
                275                 280                 285

ggc aac atc gtg aag gcc ttc agg tac ctg ctg aac gag gac ggc tgc        912
Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp Gly Cys
            290                 295                 300

aga gtg cct gcc gtg gtg ttc acc acc ctg agg ggc tac cag ctg tgt        960
Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln Leu Cys
        305                 310                 315

gct ccc cct gac cag cct tgg gtg gac agg atc atc agg agg ctg aag       1008
Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg Leu Lys
    320                 325                 330

aag agc agc gcc aag aac aag ggc aac agc acc agg agg agc ccc gtg       1056
Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser Pro Val
335                 340                 345                 350

agc tgaaagctta aaccagttaa ctggaaaacg cgtaaagtcg ac                    1101
Ser
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<210> 13
<211> 351
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 13

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


Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ala Ala Met Ser Glu Asp
            20                  25                  30


Ser Cys Val Asn Phe Lys Glu Met Met Phe Ile Asp Asn Thr Leu Tyr
        35                  40                  45


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


Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn Asp Gln Val Leu
65                  70                  75                  80


Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met Thr Asp Ile Asp
                85                  90                  95


Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile Tyr Met Tyr Lys
            100                 105                 110


Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser Val Lys Asp Ser
        115                 120                 125


Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile Ser Phe Glu Glu
    130                 135                 140


Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser Asp Leu Ile Phe
```

```
145                 150                 155                 160

Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu Phe Glu Ser Ser
                165                 170                 175

Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu Asp Asp Ala Phe
            180                 185                 190

Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser Val Met
        195                 200                 205

Phe Thr Leu Thr Asn Leu His Gln Ser Gly Ser Gly Val Lys Gln Thr
    210                 215                 220

Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro
225                 230                 235                 240

Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu Ala Phe Ser Leu
                245                 250                 255

Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly Gly Ala Asn Asp
            260                 265                 270

Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro Ile Pro Gly Asn
        275                 280                 285

Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp Gly Cys Arg Val
    290                 295                 300

Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln Leu Cys Ala Pro
305                 310                 315                 320

Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg Leu Lys Lys Ser
                325                 330                 335

Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser Pro Val Ser
            340                 345                 350
```

<210> 14
<211> 1011
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment of IL-21_F2A_CCL19 (DNA segment #8)

<220>
<221> CDS
<222> (7)..(969)
<223> nucleic acid sequence encoding 1st F2A; IL-21; 2nd F2A; and CCL19

<220>
<221> misc_feature
<222> (7)..(81)
<223> F2A peptide

<220>
<221> misc_feature
<222> (82)..(567)
<223> mouse IL-21

<220>
<221> misc_feature
<222> (568)..(642)
<223> F2A peptide

<220>
<221> misc_feature
<222> (646)..(969)
<223> mouse CCL19

<220>
<221> misc_feature
<222> (970)..(972)
<223> stop codon

<220>
<221> misc_feature
<222> (1006)..(1011)
<223> restriction site (Sal I)

<400> 14
gaattc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag 48
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys

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       1               5                  10

ctg gcc gga gac gtg gag agc aac cct ggc cct atg gag agg acc ctg         96
Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Glu Arg Thr Leu
15                  20                  25                  30

gtg tgc ctg gtg gtg att ttc ctg ggc acc gtc gcc cat aag agc agc        144
Val Cys Leu Val Val Ile Phe Leu Gly Thr Val Ala His Lys Ser Ser
                35                  40                  45

ccc cag gga ccc gac aga ctg ctg atc agg ctg agg cac ctg atc gac        192
Pro Gln Gly Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile Asp
            50                  55                  60

atc gtg gag cag ctg aag atc tac gag aac gac ctg gac ccc gag ctg        240
Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu Leu
        65                  70                  75

ctg agc gct cct cag gac gtg aag gga cac tgc gag cac gcc gcc ttc        288
Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala Phe
    80                  85                  90

gcc tgt ttc cag aag gcc aag ctg aag cct tcc aac ccc ggc aac aac        336
Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn Pro Gly Asn Asn
95                  100                 105                 110

aag acc ttc atc atc gac ctg gtg gcc cag ctg agg aga agg ctg cct        384
Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu Pro
                115                 120                 125

gcc agg agg ggc gga aag aag cag aag cac atc gcc aag tgc ccc agc        432
Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro Ser
            130                 135                 140

tgc gac tcc tac gag aag agg acc ccc aag gag ttc ctg gag agg ctg        480
Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg Leu
        145                 150                 155

aag tgg ctg ctg cag aag gtg tgc aca ctg aac gcc ttc ctg agc ctg        528
Lys Trp Leu Leu Gln Lys Val Cys Thr Leu Asn Ala Phe Leu Ser Leu
    160                 165                 170

cct tgt tgc gtg agg gtg cct ccc gtg cct tcc gac agc ggc agc ggc        576
Pro Cys Cys Val Arg Val Pro Pro Val Pro Ser Asp Ser Gly Ser Gly
175                 180                 185                 190

gtg aag cag acc ctg aac ttc gac ctg ctg aag ctg gcc gga gac gtg        624
Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
                195                 200                 205
```

```
gag agc aac cct ggc cca tgc atg gcc ccc agg gtg acc cct ctg ctg        672
Glu Ser Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu
            210                 215                 220

gcc ttc agc ctg ctg gtg ctg tgg acc ttc cct gcc cct acc ctg gga        720
Ala Phe Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly
        225                 230                 235

gga gcc aat gac gcc gag gac tgc tgc ctg agc gtg acc cag aga ccc        768
Gly Ala Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro
    240                 245                 250

atc ccc ggc aac atc gtg aag gcc ttc agg tac ctg ctg aac gag gac        816
Ile Pro Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp
255                 260                 265                 270

ggc tgc aga gtg cct gcc gtg gtg ttc acc acc ctg agg ggc tac cag        864
Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln
                275                 280                 285

ctg tgt gct ccc cct gac cag cct tgg gtg gac agg atc atc agg agg        912
Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg
            290                 295                 300

ctg aag aag agc agc gcc aag aac aag ggc aac agc acc agg agg agc        960
Leu Lys Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser
        305                 310                 315

ccc gtg agc tgaaagctta aaccagttaa ctggaaaacg cgtaaagtcg ac           1011
Pro Val Ser
    320
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<210> 15
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15

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


Gly Asp Val Glu Ser Asn Pro Gly Pro Met Glu Arg Thr Leu Val Cys
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```
            20                  25                  30

Leu Val Val Ile Phe Leu Gly Thr Val Ala His Lys Ser Ser Pro Gln
        35                  40                  45

Gly Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile Asp Ile Val
    50                  55                  60

Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu Leu Leu Ser
65                  70                  75                  80

Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala Phe Ala Cys
                85                  90                  95

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

Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu Pro Ala Arg
        115                 120                 125

Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro Ser Cys Asp
    130                 135                 140

Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg Leu Lys Trp
145                 150                 155                 160

Leu Leu Gln Lys Val Cys Thr Leu Asn Ala Phe Leu Ser Leu Pro Cys
                165                 170                 175

Cys Val Arg Val Pro Pro Val Pro Ser Asp Ser Gly Ser Gly Val Lys
            180                 185                 190

Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
        195                 200                 205

Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu Ala Phe
    210                 215                 220
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```
Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly Gly Ala
225                 230                 235                 240


Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro Ile Pro
                245                 250                 255


Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp Gly Cys
            260                 265                 270


Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln Leu Cys
        275                 280                 285


Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg Leu Lys
    290                 295                 300


Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser Pro Val
305                 310                 315                 320


Ser
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<210> 16
<211> 1881
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA segment of scIL27_F2A_CCL19 (DNA segment #9)

<220>
<221> CDS
<222> (7)..(1839)
<223> nucleic acid sequence encoding 1st F2A; a fusion protein "scIL27" comprising EBI3, a linker and p28; 2nd F2A and CCL19

<220>
<221> misc_feature
<222> (7)..(81)
<223> F2A peptide

<220>
<221> misc_feature
<222> (82)..(765)
<223> mouse EBI3

<220>
<221> misc_feature
<222> (766)..(819)
<223> linker

<220>
<221> misc_feature
<222> (820)..(1437)
<223> mouse p28

<220>
<221> misc_feature
<222> (1438)..(1512)
<223> F2A peptide

<220>
<221> misc_feature
<222> (1516)..(1839)
<223> mouse CCL19

<220>
<221> misc_feature
<222> (1840)..(1842)
<223> stop codon

<220>
<221> misc_feature
<222> (1879)..(1881)
<223> restriction site (Sal I)

<400> 16
gaattc ggc agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag 48
Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10

ctg gcc gga gac gtg gag agc aac cct ggc cct atg agc aag ctc ctc 96
Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ser Lys Leu Leu
15 20 25 30

ttt ctg tcc ctg gcc ctg tgg gcc agc aga tcc cct ggc tac aca gaa 144
Phe Leu Ser Leu Ala Leu Trp Ala Ser Arg Ser Pro Gly Tyr Thr Glu
35 40 45

```
aca gcc ctg gtg gcc ctg tcc caa ccc aga gtg cag tgt cac gct tcc        192
Thr Ala Leu Val Ala Leu Ser Gln Pro Arg Val Gln Cys His Ala Ser
            50                  55                  60

agg tac ccc gtg gct gtg gac tgc agc tgg acc cct ctg caa gcc cct        240
Arg Tyr Pro Val Ala Val Asp Cys Ser Trp Thr Pro Leu Gln Ala Pro
        65                  70                  75

aat agc acc agg agc acc tcc ttc atc gcc acc tac aga ctg gga gtg        288
Asn Ser Thr Arg Ser Thr Ser Phe Ile Ala Thr Tyr Arg Leu Gly Val
    80                  85                  90

gcc acc cag cag cag agc cag cct tgc ctg cag agg tcc cct cag gcc        336
Ala Thr Gln Gln Gln Ser Gln Pro Cys Leu Gln Arg Ser Pro Gln Ala
95                  100                 105                 110

tcc aga tgc aca atc cct gat gtg cac ctg ttt agc acc gtg ccc tac        384
Ser Arg Cys Thr Ile Pro Asp Val His Leu Phe Ser Thr Val Pro Tyr
                115                 120                 125

atg ctg aac gtg aca gcc gtg cac cct gga gga gcc agc agc tcc ctc        432
Met Leu Asn Val Thr Ala Val His Pro Gly Gly Ala Ser Ser Ser Leu
            130                 135                 140

ctg gcc ttc gtc gcc gag aga atc atc aag cct gac ccc cct gag ggc        480
Leu Ala Phe Val Ala Glu Arg Ile Ile Lys Pro Asp Pro Pro Glu Gly
        145                 150                 155

gtg aga ctg aga aca gct ggc cag aga ctg cag gtg ctg tgg cac cct        528
Val Arg Leu Arg Thr Ala Gly Gln Arg Leu Gln Val Leu Trp His Pro
    160                 165                 170

ccc gcc tcc tgg cct ttc ccc gat atc ttc tcc ctg aag tac aga ctg        576
Pro Ala Ser Trp Pro Phe Pro Asp Ile Phe Ser Leu Lys Tyr Arg Leu
175                 180                 185                 190

agg tac agg aga aga ggc gct agc cac ttc aga cag gtg ggc ccc att        624
Arg Tyr Arg Arg Arg Gly Ala Ser His Phe Arg Gln Val Gly Pro Ile
                195                 200                 205

gag gct acc acc ttt acc ctc agg aat agc aag ccc cat gct aag tac        672
Glu Ala Thr Thr Phe Thr Leu Arg Asn Ser Lys Pro His Ala Lys Tyr
            210                 215                 220

tgt atc cag gtg tcc gcc cag gat ctg aca gac tac ggc aag ccc tcc        720
Cys Ile Gln Val Ser Ala Gln Asp Leu Thr Asp Tyr Gly Lys Pro Ser
        225                 230                 235

gac tgg agc ctg cct gga caa gtg gaa agc gct ccc cac aag cct gga        768
```

```
Asp Trp Ser Leu Pro Gly Gln Val Glu Ser Ala Pro His Lys Pro Gly
    240                 245                 250

agc aca tcc gga agc ggc aaa ccc ggc agc gga gag gga tcc acc aaa        816
Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys
255                 260                 265                 270

ggc ttc cct acc gac ccc ctg tct tta caa gaa ctg aga agg gag ttc        864
Gly Phe Pro Thr Asp Pro Leu Ser Leu Gln Glu Leu Arg Arg Glu Phe
                275                 280                 285

acc gtg agc ctg tat ctg gcc agg aag ctc ctc agc gag gtg cag ggc        912
Thr Val Ser Leu Tyr Leu Ala Arg Lys Leu Leu Ser Glu Val Gln Gly
            290                 295                 300

tat gtg cac agc ttc gcc gaa agc agg ctg ccc ggc gtg aac ctg gat        960
Tyr Val His Ser Phe Ala Glu Ser Arg Leu Pro Gly Val Asn Leu Asp
        305                 310                 315

ctg ctg ccc ctg ggc tac cac ctg cct aac gtg tcc ctg acc ttc cag       1008
Leu Leu Pro Leu Gly Tyr His Leu Pro Asn Val Ser Leu Thr Phe Gln
    320                 325                 330

gct tgg cat cac ctg tcc gac tcc gag agg ctc tgc ttt ctg gcc acc       1056
Ala Trp His His Leu Ser Asp Ser Glu Arg Leu Cys Phe Leu Ala Thr
335                 340                 345                 350

acc ctg agg ccc ttc cct gcc atg ctg gga gga ctg ggc acc cag gga       1104
Thr Leu Arg Pro Phe Pro Ala Met Leu Gly Gly Leu Gly Thr Gln Gly
                355                 360                 365

acc tgg acc agc agc gag agg gaa cag ctg tgg gcc atg aga ctg gac       1152
Thr Trp Thr Ser Ser Glu Arg Glu Gln Leu Trp Ala Met Arg Leu Asp
            370                 375                 380

ctg agg gat ctg cac aga cac ctg agg ttc cag gtg ctg gcc gcc ggc       1200
Leu Arg Asp Leu His Arg His Leu Arg Phe Gln Val Leu Ala Ala Gly
        385                 390                 395

ttc aag tgt agc aaa gag gag gag gac aaa gaa gaa gaa gaa gag gaa       1248
Phe Lys Cys Ser Lys Glu Glu Glu Asp Lys Glu Glu Glu Glu Glu Glu
    400                 405                 410

gaa gag gaa gag aag aaa ctc ccc ctg gga gcc ctg gga ggc cct aat       1296
Glu Glu Glu Glu Lys Lys Leu Pro Leu Gly Ala Leu Gly Gly Pro Asn
415                 420                 425                 430

cag gtg tcc tcc cag gtg tcc tgg cct cag ctg ctg tat acc tac cag       1344
Gln Val Ser Ser Gln Val Ser Trp Pro Gln Leu Leu Tyr Thr Tyr Gln
```

```
                435                 440                 445

ctg ctg cac agc ctg gag ctg gtg ctg tcc agg gct gtg agg gac ctg       1392
Leu Leu His Ser Leu Glu Leu Val Leu Ser Arg Ala Val Arg Asp Leu
            450                 455                 460

ctc ctg ctg agc ctg cct aga agg cct ggc agc gct tgg gac tcc ggc       1440
Leu Leu Leu Ser Leu Pro Arg Arg Pro Gly Ser Ala Trp Asp Ser Gly
        465                 470                 475

agc ggc gtg aag cag acc ctg aac ttc gac ctg ctg aag ctg gcc gga       1488
Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
    480                 485                 490

gac gtg gag agc aac cct ggc cca tgc atg gcc ccc agg gtg acc cct       1536
Asp Val Glu Ser Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro
495                 500                 505                 510

ctg ctg gcc ttc agc ctg ctg gtg ctg tgg acc ttc cct gcc cct acc       1584
Leu Leu Ala Phe Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr
                515                 520                 525

ctg gga gga gcc aat gac gcc gag gac tgc tgc ctg agc gtg acc cag       1632
Leu Gly Gly Ala Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln
            530                 535                 540

aga ccc atc ccc ggc aac atc gtg aag gcc ttc agg tac ctg ctg aac       1680
Arg Pro Ile Pro Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn
        545                 550                 555

gag gac ggc tgc aga gtg cct gcc gtg gtg ttc acc acc ctg agg ggc       1728
Glu Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly
    560                 565                 570

tac cag ctg tgt gct ccc cct gac cag cct tgg gtg gac agg atc atc       1776
Tyr Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile
575                 580                 585                 590

agg agg ctg aag aag agc agc gcc aag aac aag ggc aac agc acc agg       1824
Arg Arg Leu Lys Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg
                595                 600                 605

agg agc ccc gtg agc tgaaagctta aaccagttaa ctggaaaacg cgtaaagtcg       1879
Arg Ser Pro Val Ser
            610

ac                                                                    1881
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<210> 17
<211> 611
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17

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


Gly Asp Val Glu Ser Asn Pro Gly Pro Met Ser Lys Leu Leu Phe Leu
            20                  25                  30


Ser Leu Ala Leu Trp Ala Ser Arg Ser Pro Gly Tyr Thr Glu Thr Ala
        35                  40                  45


Leu Val Ala Leu Ser Gln Pro Arg Val Gln Cys His Ala Ser Arg Tyr
    50                  55                  60


Pro Val Ala Val Asp Cys Ser Trp Thr Pro Leu Gln Ala Pro Asn Ser
65                  70                  75                  80


Thr Arg Ser Thr Ser Phe Ile Ala Thr Tyr Arg Leu Gly Val Ala Thr
                85                  90                  95


Gln Gln Gln Ser Gln Pro Cys Leu Gln Arg Ser Pro Gln Ala Ser Arg
            100                 105                 110


Cys Thr Ile Pro Asp Val His Leu Phe Ser Thr Val Pro Tyr Met Leu
        115                 120                 125


Asn Val Thr Ala Val His Pro Gly Gly Ala Ser Ser Ser Leu Leu Ala
    130                 135                 140


Phe Val Ala Glu Arg Ile Ile Lys Pro Asp Pro Pro Glu Gly Val Arg
145                 150                 155                 160
```

```
Leu Arg Thr Ala Gly Gln Arg Leu Gln Val Leu Trp His Pro Pro Ala
                165                 170                 175

Ser Trp Pro Phe Pro Asp Ile Phe Ser Leu Lys Tyr Arg Leu Arg Tyr
            180                 185                 190

Arg Arg Arg Gly Ala Ser His Phe Arg Gln Val Gly Pro Ile Glu Ala
        195                 200                 205

Thr Thr Phe Thr Leu Arg Asn Ser Lys Pro His Ala Lys Tyr Cys Ile
    210                 215                 220

Gln Val Ser Ala Gln Asp Leu Thr Asp Tyr Gly Lys Pro Ser Asp Trp
225                 230                 235                 240

Ser Leu Pro Gly Gln Val Glu Ser Ala Pro His Lys Pro Gly Ser Thr
                245                 250                 255

Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Phe
            260                 265                 270

Pro Thr Asp Pro Leu Ser Leu Gln Glu Leu Arg Arg Glu Phe Thr Val
        275                 280                 285

Ser Leu Tyr Leu Ala Arg Lys Leu Leu Ser Glu Val Gln Gly Tyr Val
    290                 295                 300

His Ser Phe Ala Glu Ser Arg Leu Pro Gly Val Asn Leu Asp Leu Leu
305                 310                 315                 320

Pro Leu Gly Tyr His Leu Pro Asn Val Ser Leu Thr Phe Gln Ala Trp
                325                 330                 335

His His Leu Ser Asp Ser Glu Arg Leu Cys Phe Leu Ala Thr Thr Leu
            340                 345                 350
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Arg Pro Phe Pro Ala Met Leu Gly Gly Leu Gly Thr Gln Gly Thr Trp
        355                 360                 365

Thr Ser Ser Glu Arg Glu Gln Leu Trp Ala Met Arg Leu Asp Leu Arg
    370                 375                 380

Asp Leu His Arg His Leu Arg Phe Gln Val Leu Ala Ala Gly Phe Lys
385                 390                 395                 400

Cys Ser Lys Glu Glu Glu Asp Lys Glu Glu Glu Glu Glu Glu Glu Glu
                405                 410                 415

Glu Glu Lys Lys Leu Pro Leu Gly Ala Leu Gly Gly Pro Asn Gln Val
            420                 425                 430

Ser Ser Gln Val Ser Trp Pro Gln Leu Leu Tyr Thr Tyr Gln Leu Leu
        435                 440                 445

His Ser Leu Glu Leu Val Leu Ser Arg Ala Val Arg Asp Leu Leu Leu
    450                 455                 460

Leu Ser Leu Pro Arg Arg Pro Gly Ser Ala Trp Asp Ser Gly Ser Gly
465                 470                 475                 480

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
                485                 490                 495

Glu Ser Asn Pro Gly Pro Cys Met Ala Pro Arg Val Thr Pro Leu Leu
            500                 505                 510

Ala Phe Ser Leu Leu Val Leu Trp Thr Phe Pro Ala Pro Thr Leu Gly
        515                 520                 525

Gly Ala Asn Asp Ala Glu Asp Cys Cys Leu Ser Val Thr Gln Arg Pro
    530                 535                 540

Ile Pro Gly Asn Ile Val Lys Ala Phe Arg Tyr Leu Leu Asn Glu Asp
```

545 550 555 560

Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr Leu Arg Gly Tyr Gln
565 570 575

Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Asp Arg Ile Ile Arg Arg
580 585 590

Leu Lys Lys Ser Ser Ala Lys Asn Lys Gly Asn Ser Thr Arg Arg Ser
595 600 605

Pro Val Ser
610

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<212> PRT
<213> Homo sapiens

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<223> Signal peptide

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<220>
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<223> Interleukin-15

<400> 18

Met Arg Ile Ser Lys Pro His Leu Arg Ser Ile Ser Ile Gln Cys Tyr
1 5 10 15

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

```
Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
        35                  40                  45

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
    50                  55                  60

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
65                  70                  75                  80

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
                85                  90                  95

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
            100                 105                 110

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
        115                 120                 125

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
    130                 135                 140

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
145                 150                 155                 160

Thr Ser
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<223> Sushi domain

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<223> Helical domain

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Met Ala Pro Arg Arg Ala Arg Gly Cys Arg Thr Leu Gly Leu Pro Ala
1               5                   10                  15


Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Ala Thr Arg Gly Ile Thr
            20                  25                  30


Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser
        35                  40                  45


Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys
    50                  55                  60


Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala
65                  70                  75                  80


Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp
                85                  90                  95
```

```
Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr
            100                 105                 110

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

Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala
    130                 135                 140

Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr
145                 150                 155                 160

Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser
                165                 170                 175

Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln
            180                 185                 190

Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr Val Ala Ile
        195                 200                 205

Ser Thr Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu
    210                 215                 220

Ala Cys Tyr Leu Lys Ser Arg Gln Thr Pro Pro Leu Ala Ser Val Glu
225                 230                 235                 240

Met Glu Ala Met Glu Ala Leu Pro Val Thr Trp Gly Thr Ser Ser Arg
                245                 250                 255

Asp Glu Asp Leu Glu Asn Cys Ser His His Leu
            260                 265
```