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(75) **Inventor/Applicant** *(for US only)*: **SHEPPARD, Paul, O.** [US/US]; 13532 278th Drive NE, Granite Falls, WA 98252 (US).

(74) **Agents: WALSH, Brian, J.** et al.; 1201 Eastlake Avenue East, Seattle, WA 98102 (US).

(81) **Designated States** *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

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- *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

Published:
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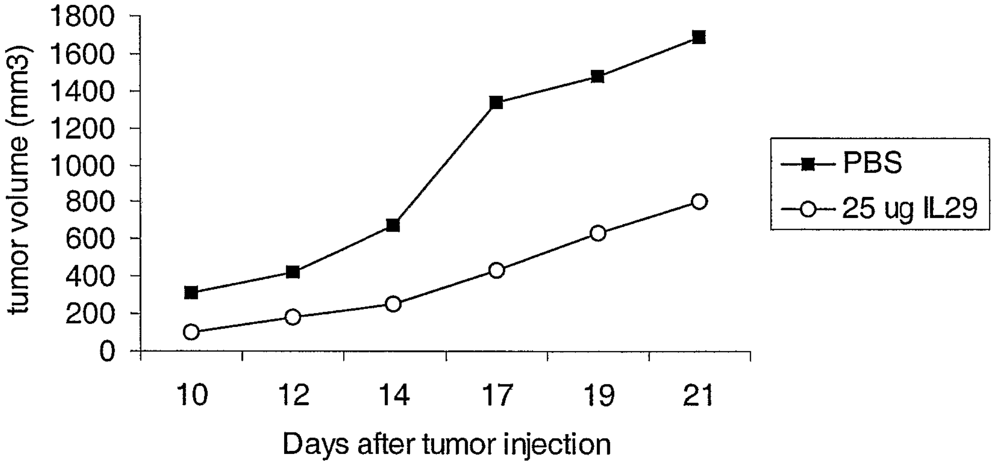
[Continued on next page]

(54) Title: USE OF TRUNCATED CYSTEINE IL28 AND IL29 MUTANTS TO TREAT CANCERS AND AUTOIMMUNE DISORDERS



(57) **Abstract:** Methods for treating patients with cancer and autoimmune disorders using IL-28 and IL-29 molecules. The IL-28 and IL-29 molecules include polypeptides that have homology to the human IL-28 or IL-29 polypeptide sequence and proteins fused to a polypeptide with IL-28 and IL-29 functional activity. The molecules can be used as a monotherapy or in combination with other known cancer and/or autoimmune therapeutics.

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2006/028106

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K38/20 A61P35/00 A61P43/00 A61P19/02 A61P17/06
A61P25/00 A61P1/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K A61P C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, BIOSIS, EMBASE, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2005/023862 A (ZYMOGENETICS INC [US]; BRADY LOWELL J [US]; KLUCHER KEVIN M [US]; CHAN) 17 March 2005 (2005-03-17) claims, page 57, line 4 - page 60, line 29 page 45, line 1 - page 46, line 22	1-33
X	US 2005/037012 A1 (BRADY LOWELL J [US] ET AL) 17 February 2005 (2005-02-17) claims paragraphs [0139] - [0146], [0107] - [0115]	1-33
X	WO 02/086087 A (ZYMOGENETICS INC [US]) 31 October 2002 (2002-10-31) claims page 40, line 1 - line 4 page 49, line 9 - page 52, line 22	9-27, 29-33

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☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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"&" document member of the same patent family

Date of the actual completion of the international search 12 March 2007	Date of mailing of the international search report 23/03/2007
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31–70) 340–2040, Tx. 31 651 epo nl, Fax: (+31–70) 340–3016	Authorized officer Böhmerova, Eva

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2006/028106

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 02/092762 A (IMMUNEX CORP [US]; BAUM PETER R [US]; MOSLEY BRUCE A [US]; KETCHEM RAN) 21 November 2002 (2002-11-21) claims page 44, line 9 - line 17	29-31
X	WO 03/066002 A (UNIV NEW JERSEY MED [US]; KOTENKO SERGEI [US]; GALLAGHER GRANT [US]) 14 August 2003 (2003-08-14) page 178, paragraph 3 - page 179, paragraph 2 page 189, paragraph 2 - page 191, paragraph 2 page 209, paragraph 1 - paragraph 2	9-27, 29-33
A	FRANCIS G E ET AL: "PEGYLATION OF CYTOKINES AND OTHER THERAPEUTIC PROTEINS AND PEPTIDES: THE IMPORTANCE OF BIOLOGICAL OPTIMISATION OF COUPLING TECHNIQUES" INTERNATIONAL JOURNAL OF HEMATOLOGY, ELSEVIER SCIENCE PUBLISHERS, NL, vol. 68, no. 1, July 1998 (1998-07), pages 1-18, XP000791226 ISSN: 0925-5710 the whole document	1-6
P,X	WO 2006/012644 A (ZYMOGENETICS INC [US]; DOYLE SEAN [US]; KLUCHER KEVIN M [US]; SIVAKUMA) 2 February 2006 (2006-02-02) the whole document	1-33

CLAIMS

What is claimed is:

1. A method of treating cancer comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

2. The method of claim 1 wherein the polypeptide further comprises polyethylene glycol.

3. The method of claim 2 wherein the polyethylene glycol is covalently linked amino-terminally to the polypeptide.

4. The method of claim 2 wherein the polyethylene glycol is about 20kD, 30kD, or 40 kD.

5. The method of claim 2 wherein the polyethylene glycol is linear or branched.

6. The method of claim 2 wherein the polyethylene glycol is monomethoxy-PEG propionaldehyde.

7. The method of claim 1 wherein the patient is a mammal.

8. The method of claim 7 wherein the patient is a human.

9. A method of treating cancer comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer,

melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

10. A method of treating cancer comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175; and

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

11. A method of treating cancer comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide;

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

12. The method of claim 11 wherein the second polypeptide is an Interferon.

13. The method of claim 12 wherein the second polypeptide is Interferon-alpha, Interferon-beta, or Interferon-gamma.

14. A method of inhibiting the progressive of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95%

sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

15. A method of inhibiting the progression of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide;

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

16. A method of delaying the onset of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

17. A method of delaying the onset of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide;

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

18. A method of reducing the severity of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

19. A method of reducing the severity of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide;

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

20. A method of inhibiting at least one of the conditions or symptoms of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's

lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

21. A method of inhibiting at least one of the conditions or symptoms of cancer comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide;

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of B-cell lymphomas, chronic lymphocytic leukemia, acute lymphocytic leukemia, Non-Hodgkin's lymphomas, multiple myeloma, acute myelocytic leukemia, chronic myelocytic leukemia, renal cell carcinoma, hepatocellular carcinoma, cervical cancer, melanoma, thyroid carcinoma, malignant gliomas, breast cancer, colon cancer, lung cancer, pancreatic cancer, prostate cancer, stomach cancer, ovarian cancer, testicular cancer, Kaposi's sarcoma, and bone cancer.

22. A method of inhibiting at least one of the conditions or symptoms of non-Hogkin's lymphoma comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the at least one of the conditions or symptoms is selected from the group of painless swelling of a lymph node in the neck, armpit or groin, night sweats, unexplained fever, weight loss, and excessive tiredness.

23. A method of inhibiting at least one of the conditions or symptoms of non-Hodgkin's lymphoma comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide; and

a pharmaceutically acceptable vehicle;

wherein the at least one of the conditions or symptoms is selected from the group of painless swelling of a lymph node in the neck, armpit or groin, night sweats, unexplained fever, weight loss, and excessive tiredness.

24. A method of inhibiting at least one of the conditions or symptoms of multiple myeloma comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the at least one of the conditions or symptoms is selected from the group of back pain, loss of height, anaemia, kidney damage, repeated respiratory infections, and hypercalcaemia.

25. A method of inhibiting at least one of the conditions or symptoms of multiple myeloma comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide; and

a pharmaceutically acceptable vehicle;

wherein the at least one of the conditions or symptoms is selected from the group of back pain, loss of height, anaemia, kidney damage, repeated respiratory infections, and hypercalcaemia.

26. A method of inhibiting at least one of the conditions or symptoms of head and neck tumours comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the at least one of the conditions or symptoms is selected from the group of an ulcer or sore area in the head or neck that does not heal within a few weeks, difficulty in swallowing, trouble with breathing or speaking, a numb feeling in the mouth, nose bleeds, persistent earache, difficulty in hearing, and swelling or lump in the mouth or neck.

27. A method of inhibiting at least one of the conditions or symptoms of head and neck tumours comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide; and

a pharmaceutically acceptable vehicle;

wherein the at least one of the conditions or symptoms is selected from the group of an ulcer or sore area in the head or neck that does not heal within a few weeks, difficulty in swallowing, trouble with breathing or speaking, a numb feeling in the mouth, nose bleeds, persistent earache, difficulty in hearing, and swelling or lump in the mouth or neck.

28. A method of treating an autoimmune disorder comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the autoimmune disorder is selected from the group of multiple sclerosis, arthritis, rheumatoid arthritis, ulcerative colitis, Crohn's disease, systemic lupus erythematosus, and psoriasis.

29. A method of treating an autoimmune disorder comprising administering to a patient in need thereof a therapeutically effective amount of a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175, wherein the autoimmune disorder is selected from the group of multiple sclerosis, arthritis, rheumatoid arthritis, ulcerative colitis, Crohn's disease, systemic lupus erythematosus, and psoriasis.

30. A method of an autoimmune disorder comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide;

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of multiple sclerosis, arthritis, rheumatoid arthritis, ulcerative colitis, Crohn's disease, systemic lupus erythematosus, and psoriasis.

31. A method of inhibiting the progression of an autoimmune disorder comprising administering to a patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a second polypeptide;

a pharmaceutically acceptable vehicle; and

wherein the cancer is selected from the group of multiple sclerosis, arthritis, rheumatoid arthritis, ulcerative colitis, Crohn's disease, systemic lupus erythematosus, and psoriasis.

32. A method of delaying a multiple sclerosis relapse in a patient comprising administering to the patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

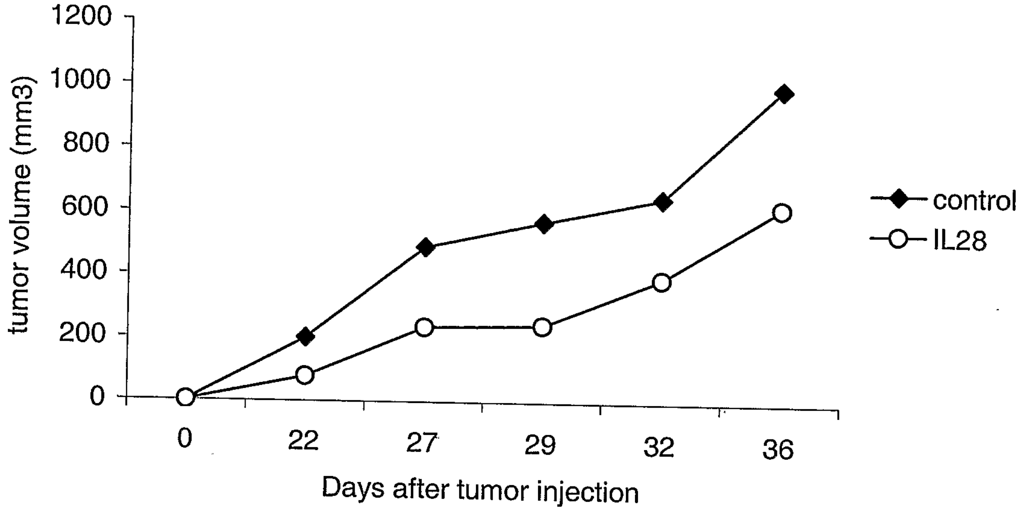
a pharmaceutically acceptable vehicle.

33. A method of reducing the severity of a multiple sclerosis relapse in a patient comprising administering to the patient in need thereof a therapeutically effective amount of a formulation comprising:

a polypeptide having at least 95% sequence identity with a sequence selected from the group of SEQ ID NOs:163, 165, 167, 169, 171, 173 and 175;

a pharmaceutically acceptable vehicle.

Sheet 1 of 8



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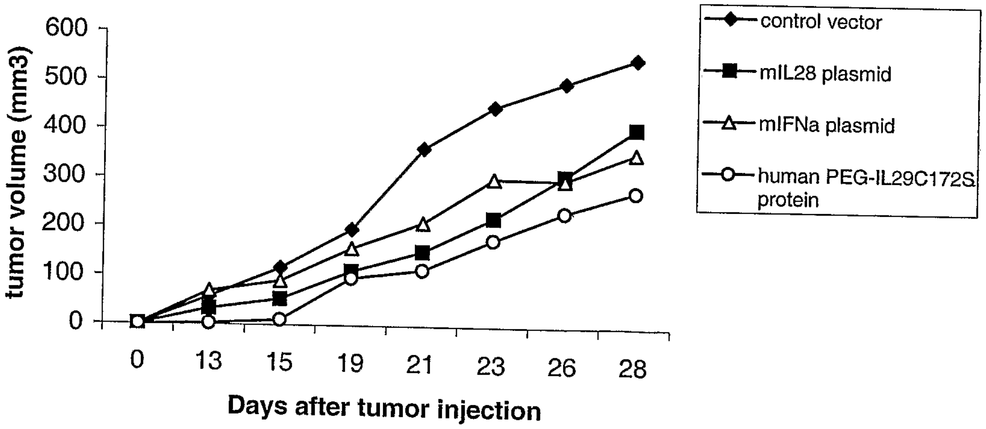

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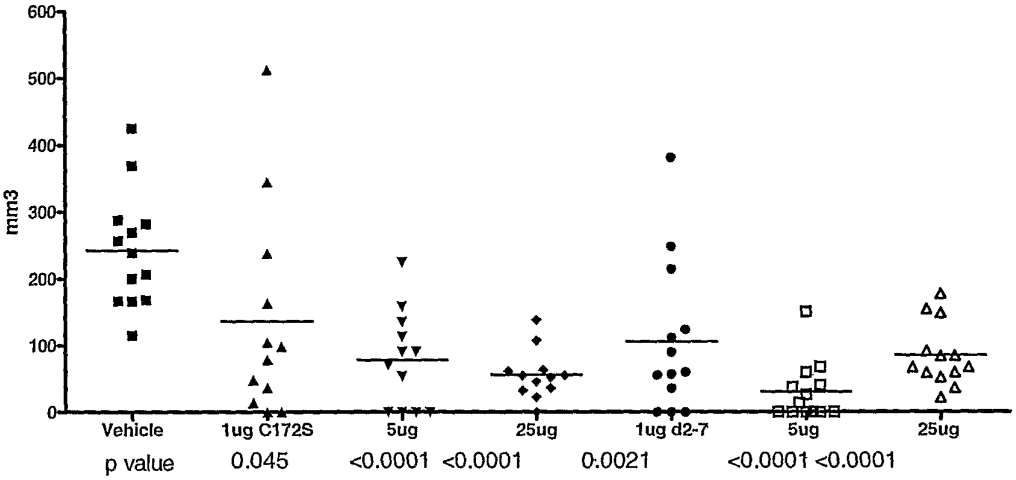

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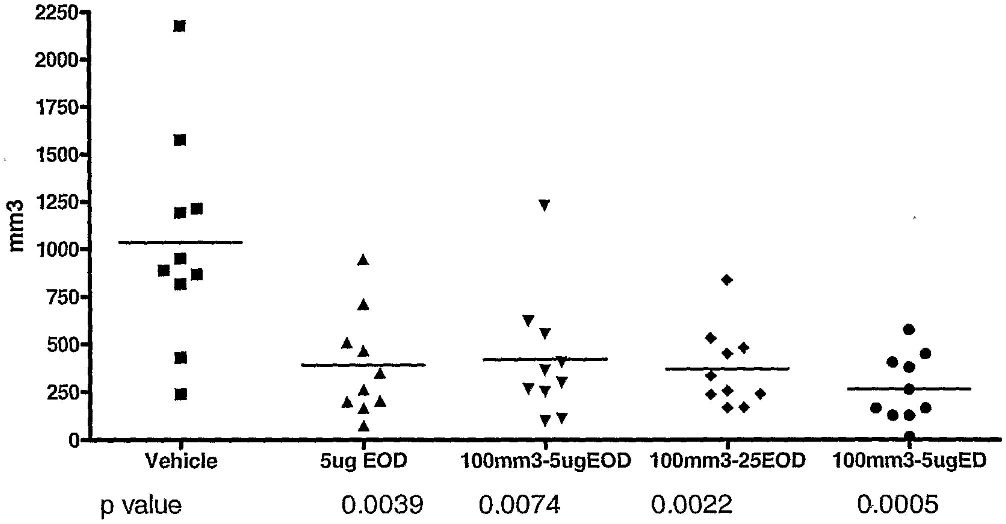

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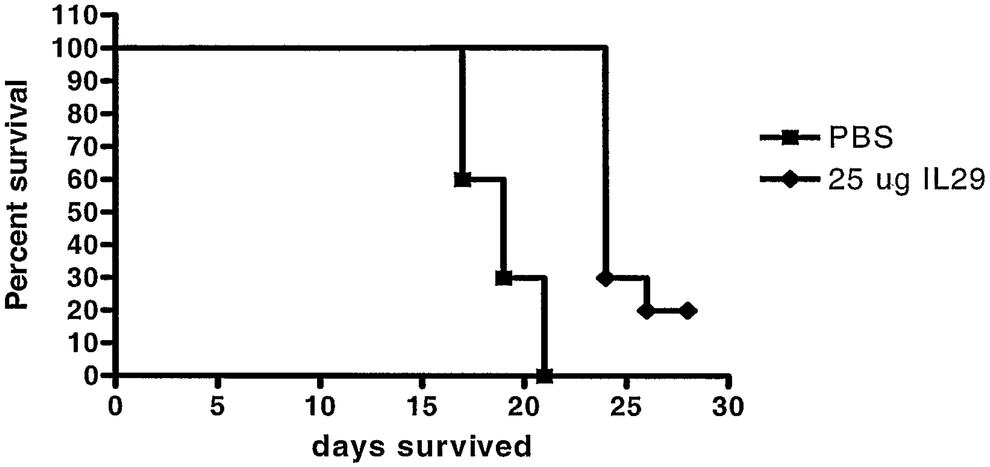

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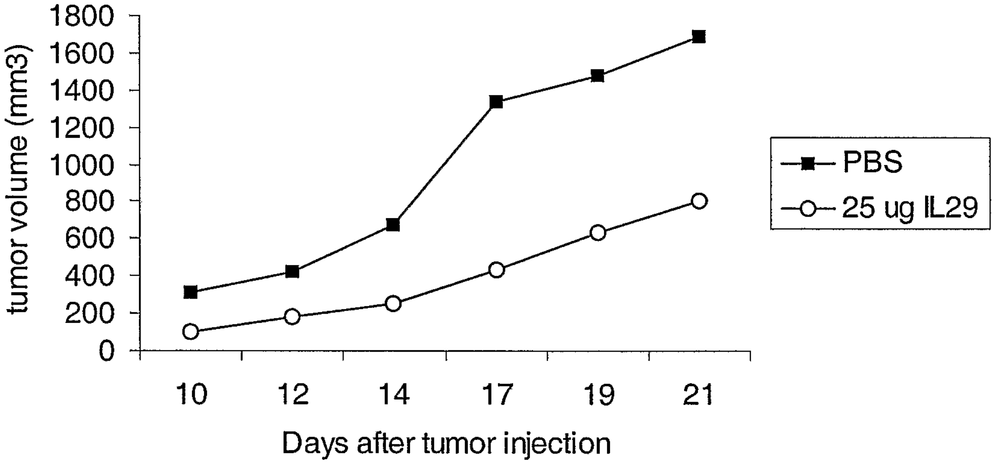

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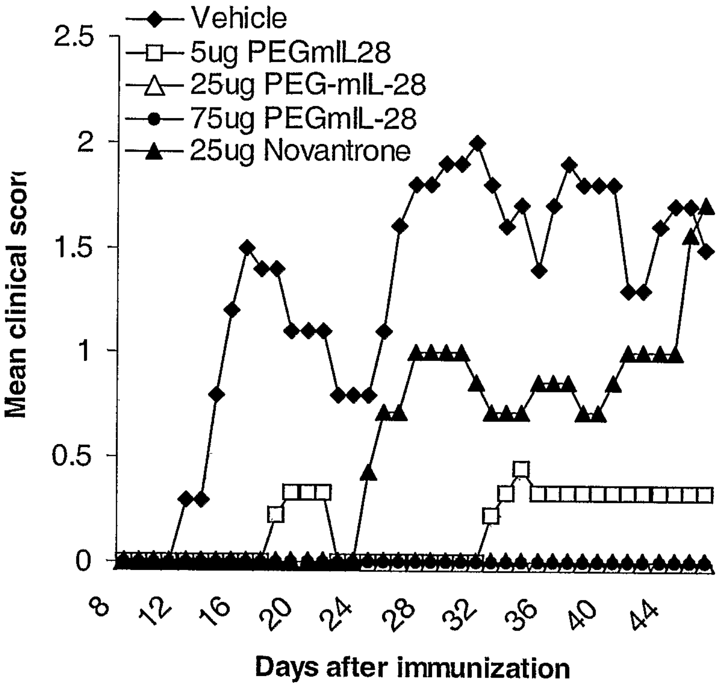

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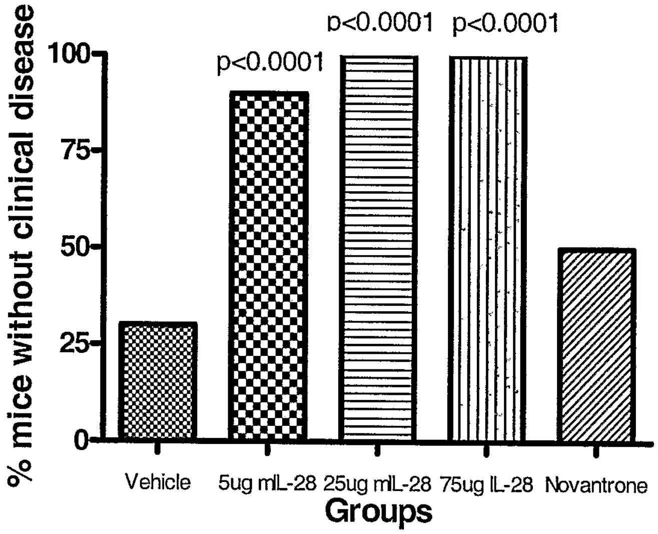

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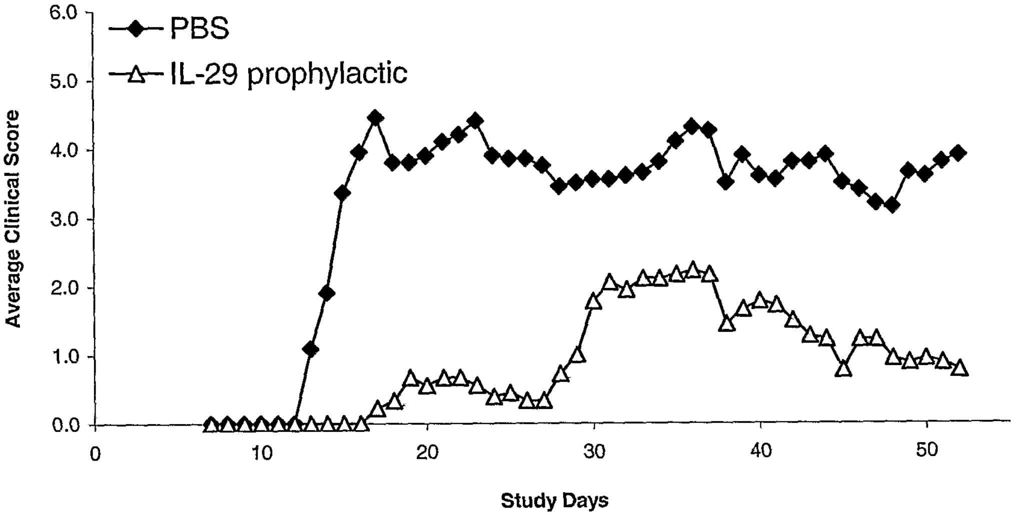

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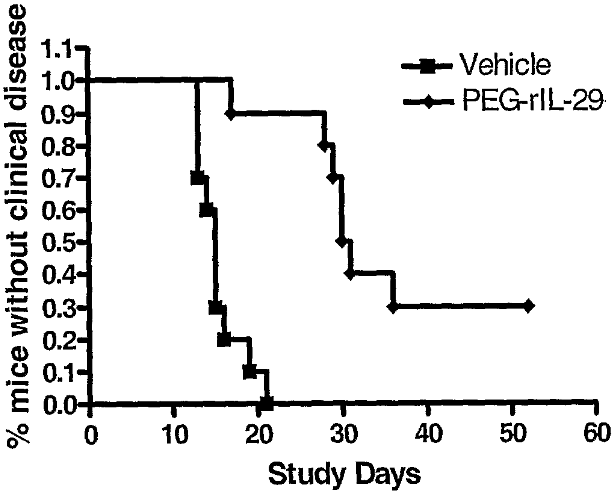

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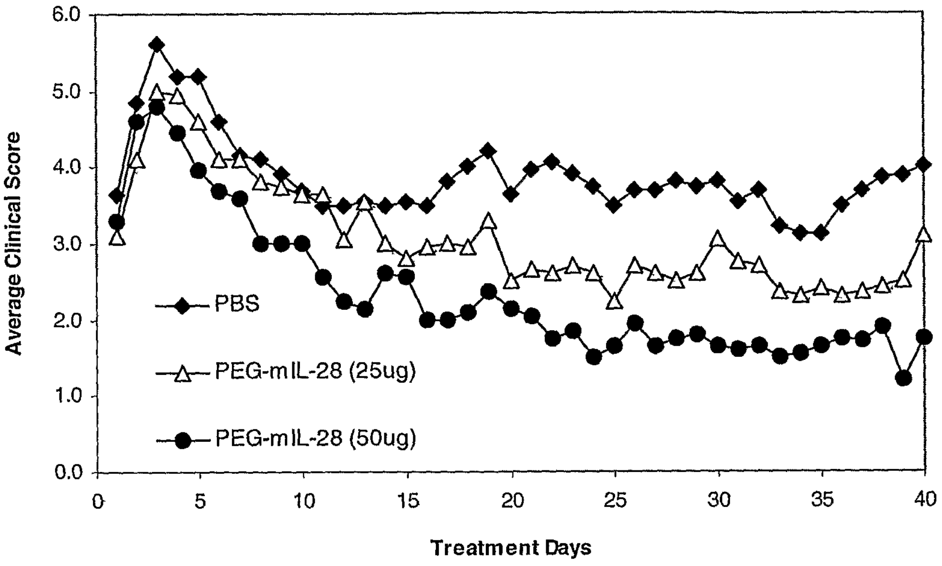
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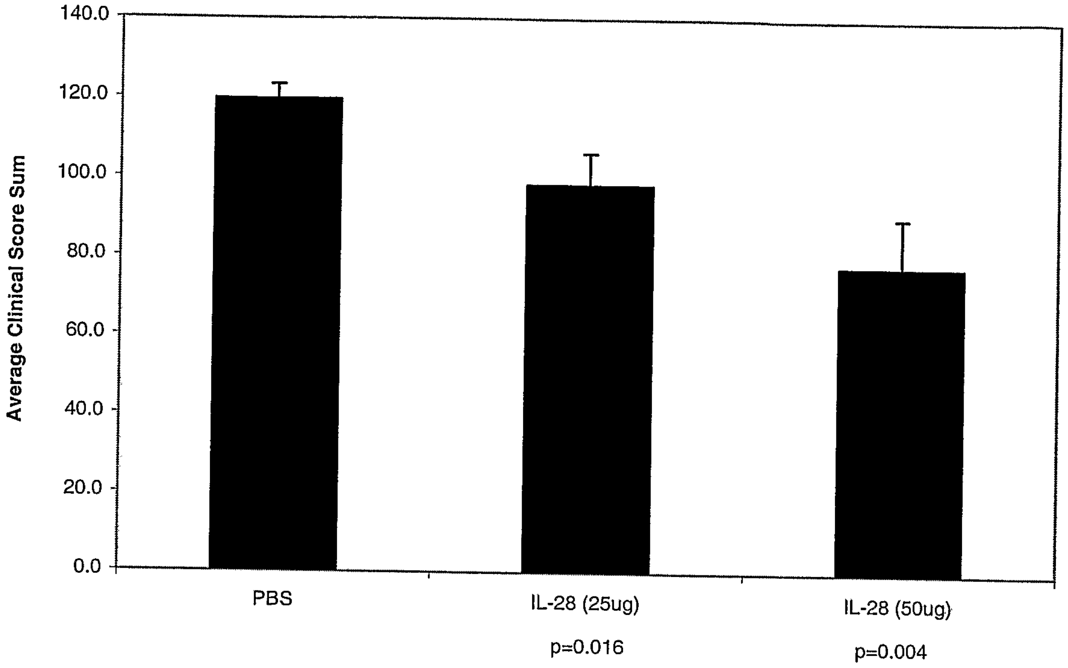
Figure 10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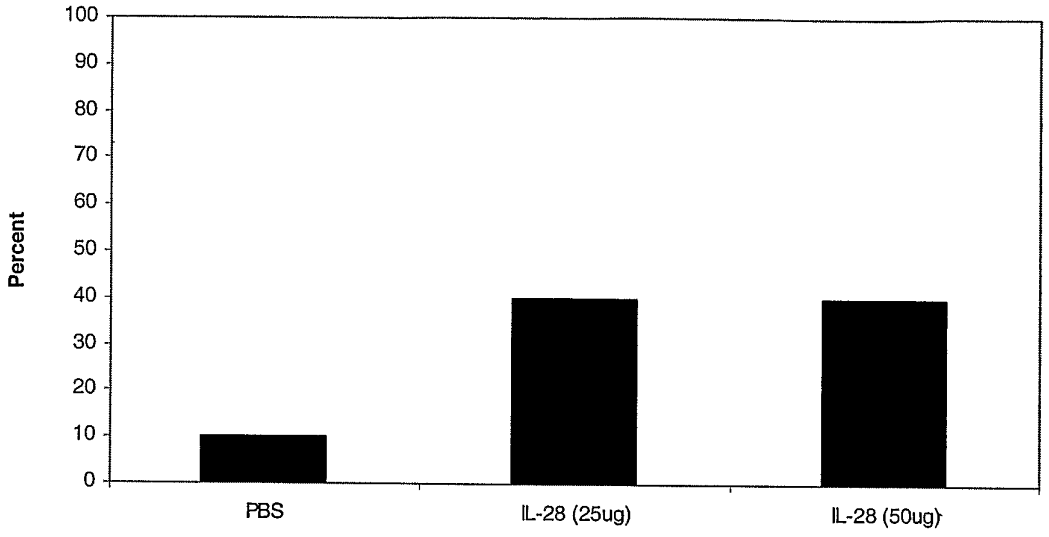

Figure 12

SEQUENCE LISTING

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                                                          -25

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Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met Ala Ala
            -20                 -15                 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cac ggg gct   154
Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His Gly Ala
         -5                  1               5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct   202
Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
 10                  15                  20                  25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag   250
Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
                 30                  35                  40

tcg ctt ctg ctg aag gac tgc agg tgc cac tcc cgc ctc ttc ccc agg   298
Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe Pro Arg
             45                  50                  55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc atg gct ttg   346
```

```
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met Ala Leu
         60                  65                  70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac     394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
     75                  80                  85

act gac cca gcc ctg gtg gac gtc ttg gac cag ccc ctt cac acc ctg     442
Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His Thr Leu
 90                  95                  100                 105

cac cat atc ctc tcc cag ttc cgg gcc tgt atc cag cct cag ccc acg     490
His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr
                110                 115                 120

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg tac cgg ctc     538
Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr Arg Leu
            125                 130                 135

cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc     586
Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val
        140                 145                 150

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc     634
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala
    155                 160                 165

agt ggg gac ctg tgt gtc tga ccctcccacc agtcatgcaa cctgagattt        685
Ser Gly Asp Leu Cys Val  *
170                 175

tatttataaa ttagccactt gtcttaattt attgccaccc agtcgctat               734

<210> 2
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(25)

<400> 2
Met Lys Leu Asp Met Thr Gly Asp Cys Thr Pro Val Leu Val Leu Met
-25                 -20                 -15                 -10
Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu His
                -5                       1           5
Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser
         10                  15                  20
Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu
     25                  30                  35
Glu Glu Ser Leu Leu Leu Lys Asp Cys Arg Cys His Ser Arg Leu Phe
40                   45                  50                  55
Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Met
                 60                  65                  70
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr
             75                  80                  85
Ala Asp Thr Asp Pro Ala Leu Val Asp Val Leu Asp Gln Pro Leu His
         90                  95                  100
Thr Leu His His Ile Leu Ser Gln Phe Arg Ala Cys Ile Gln Pro Gln
    105                 110                 115
```

```
Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu Tyr
120                 125                 130                 135
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala
                140                 145                 150
Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys
            155                 160                 165
Val Ala Ser Gly Asp Leu Cys Val
        170                 175


<210> 3
<211> 856
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (98)...(154)

<221> mat_peptide
<222> (155)...(700)

<221> CDS
<222> (98)...(700)

<400> 3
aattaccttt tcactttaca cacatcatct tggattgccc attttgcgtg gctaaaaagc 60
agagccatgc cgctggggaa gcagttgcga tttagcc atg gct gca gct tgg acc  115
                                         Met Ala Ala Ala Trp Thr
                                                         -15

gtg gtg ctg gtg act ttg gtg cta ggc ttg gcc gtg gca ggc cct gtc   163
Val Val Leu Val Thr Leu Val Leu Gly Leu Ala Val Ala Gly Pro Val
           -10                 -5                   1

ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg   211
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
     5                  10                  15

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg   259
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
 20                  25                  30                  35

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct   307
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
                 40                  45                  50

cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag   355
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
             55                  60                  65

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg   403
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
         70                  75                  80

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt   451
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
     85                  90                  95

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct   499
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
```

```
100                 105                 110                 115

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg    547
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
                120                 125                 130

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag    595
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
            135                 140                 145

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa    643
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
        150                 155                 160

tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca acc cac cct gag    691
Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr His Pro Glu
    165                 170                 175

tcc acc tga caccccacac cttatttatg cgctgagccc tactccttcc            740
Ser Thr  *
180

ttaatttatt tcctctcacc ctttatttat gaagctgcag ccctgactga gacatagggc 800
tgagtttatt gttttacttt tatacattat gcacaaataa acaacaagga attgga     856

<210> 4
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(19)

<400> 4
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
                -15                 -10                 -5
Ala Val Ala Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys
             1               5                  10
Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala
    15                  20                  25
Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys
30                  35                  40                  45
Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg
                50                  55                  60
Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala
            65                  70                  75
Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp
        80                  85                  90
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
    95                  100                 105
Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly
110                 115                 120                 125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
                130                 135                 140
Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
            145                 150                 155
Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg
        160                 165                 170
Thr Ser Thr His Pro Glu Ser Thr
    175                 180
```

```
<210> 5
<211> 734
<212> DNA
<213> Homo sapiens

<220>
<221> sig_peptide
<222> (53)...(127)

<221> mat_peptide
<222> (128)...(655)

<221> CDS
<222> (53)...(655)

<400> 5
tgggtgacag cctcagagtg tttcttctgc tgacaaagac cagagatcag ga atg aaa 58
                                                          Met Lys
                                                          -25

cta gac atg acc ggg gac tgc atg cca gtg ctg gtg ctg atg gcc gca   106
Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met Ala Ala
            -20                 -15                 -10

gtg ctg acc gtg act gga gca gtt cct gtc gcc agg ctc cgc ggg gct   154
Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg Gly Ala
         -5                 1               5

ctc ccg gat gca agg ggc tgc cac ata gcc cag ttc aag tcc ctg tct   202
Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser Leu Ser
 10                  15                  20                  25

cca cag gag ctg cag gcc ttt aag agg gcc aaa gat gcc tta gaa gag   250
Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu
                 30                  35                  40

tcg ctt ctg ctg aag gac tgc aag tgc cgc tcc cgc ctc ttc ccc agg   298
Ser Leu Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg
             45                  50                  55

acc tgg gac ctg agg cag ctg cag gtg agg gag cgc ccc gtg gct ttg   346
Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val Ala Leu
         60                  65                  70

gag gct gag ctg gcc ctg acg ctg aag gtt ctg gag gcc acc gct gac   394
Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr Ala Asp
     75                  80                  85

act gac cca gcc ctg ggg gat gtc ttg gac cag ccc ctt cac acc ctg   442
Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His Thr Leu
 90                  95                 100                 105

cac cat atc ctc tcc cag ctc cgg gcc tgt atc cag cct cag ccc acg   490
His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr
                110                 115                 120

gca ggg ccc agg acc cgg ggc cgc ctc cac cat tgg ctg cac cgg ctc   538
Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His Arg Leu
            125                 130                 135
```

```
cag gag gcc cca aaa aag gag tcc cct ggc tgc ctc gag gcc tct gtc    586
Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala Ser Val
        140                 145                 150

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctg aat tgt gtt gcc    634
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys Val Ala
    155                 160                 165

agc ggg gac ctg tgt gtc tga cccttccgcc agtcatgcaa cctgagattt      685
Ser Gly Asp Leu Cys Val  *
170                 175

tatttataaa ttagccactt ggcttaattt attgccaccc agtcgctat              734

<210> 6
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(25)

<400> 6
Met Lys Leu Asp Met Thr Gly Asp Cys Met Pro Val Leu Val Leu Met
-25                 -20                 -15                 -10
Ala Ala Val Leu Thr Val Thr Gly Ala Val Pro Val Ala Arg Leu Arg
                -5                   1               5
Gly Ala Leu Pro Asp Ala Arg Gly Cys His Ile Ala Gln Phe Lys Ser
        10                  15                  20
Leu Ser Pro Gln Glu Leu Gln Ala Phe Lys Arg Ala Lys Asp Ala Leu
    25                  30                  35
Glu Glu Ser Leu Leu Leu Lys Asp Cys Lys Cys Arg Ser Arg Leu Phe
40                  45                  50                  55
Pro Arg Thr Trp Asp Leu Arg Gln Leu Gln Val Arg Glu Arg Pro Val
                60                  65                  70
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Thr
            75                  80                  85
Ala Asp Thr Asp Pro Ala Leu Gly Asp Val Leu Asp Gln Pro Leu His
        90                  95                  100
Thr Leu His His Ile Leu Ser Gln Leu Arg Ala Cys Ile Gln Pro Gln
    105                 110                 115
Pro Thr Ala Gly Pro Arg Thr Arg Gly Arg Leu His His Trp Leu His
120                 125                 130                 135
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Pro Gly Cys Leu Glu Ala
                140                 145                 150
Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Asn Cys
            155                 160                 165
Val Ala Ser Gly Asp Leu Cys Val
        170                 175


<210> 7
<211> 633
<212> DNA
<213> Mus musculus

<220>
<221> sig_peptide
<222> (22)...(105)
```

```
<221> mat_peptide
<222> (106)...(630)

<221> CDS
<222> (22)...(630)

<400> 7
tcacagaccc cggagagcaa c atg aag cca gaa aca gct ggg ggc cac atg      51
                        Met Lys Pro Glu Thr Ala Gly Gly His Met
                                    -25                 -20

ctc ctc ctg ctg ttg cct ctg ctg ctg gcc gca gtg ctg aca aga acc      99
Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr
            -15                 -10                 -5

caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag     147
Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys
        1               5                   10

gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag     195
Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln
 15                 20                  25                  30

gcc ttc aaa aag gcc aag gat gcc atc gag aag agg ctg ctt gag aag     243
Ala Phe Lys Lys Ala Lys Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys
                35                  40                  45

gac ctg agg tgc agt tcc cac ctc ttc ccc agg gcc tgg gac ctg aag     291
Asp Leu Arg Cys Ser Ser His Leu Phe Pro Arg Ala Trp Asp Leu Lys
            50                  55                  60

cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc     339
Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala
        65                  70                  75

ctg acc ctg aag gtc tgg gag aac atg act gac tca gcc ctg gcc acc     387
Leu Thr Leu Lys Val Trp Glu Asn Met Thr Asp Ser Ala Leu Ala Thr
    80                  85                  90

atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg     435
Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu
 95                 100                 105                 110

cag acc tgt aca cag ctt cag gcc aca gca gag ccc agg tcc ccg agc     483
Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser
                115                 120                 125

cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag     531
Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys
            130                 135                 140

gag acc cct ggc tgc ctg gag gcc tct gtc acc tcc aac ctg ttt cgc     579
Glu Thr Pro Gly Cys Leu Glu Ala Ser Val Thr Ser Asn Leu Phe Arg
        145                 150                 155

ctg ctc acc cgg gac ctc aag tgt gtg gcc aat gga gac cag tgt gtc     627
Leu Leu Thr Arg Asp Leu Lys Cys Val Ala Asn Gly Asp Gln Cys Val
    160                 165                 170

tga cct                                                             633
```

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*



<210> 8
<211> 202
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
<222> (1)...(28)

<400> 8
Met Lys Pro Glu Thr Ala Gly Gly His Met Leu Leu Leu Leu Leu Pro
            -25                 -20                 -15
Leu Leu Leu Ala Ala Val Leu Thr Arg Thr Gln Ala Asp Pro Val Pro
        -10                 -5                   1
Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln
 5                  10                  15                  20
Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys
                25                  30                  35
Asp Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Leu Arg Cys Ser Ser
            40                  45                  50
His Leu Phe Pro Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu
        55                  60                  65
Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp
    70                  75                  80
Glu Asn Met Thr Asp Ser Ala Leu Ala Thr Ile Leu Gly Gln Pro Leu
85                  90                  95                  100
His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu
                105                 110                 115
Gln Ala Thr Ala Glu Pro Arg Ser Pro Ser Arg Arg Leu Ser Arg Trp
            120                 125                 130
Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu
        135                 140                 145
Glu Ala Ser Val Thr Ser Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
    150                 155                 160
Lys Cys Val Ala Asn Gly Asp Gln Cys Val
165                 170


<210> 9
<211> 632
<212> DNA
<213> Mus musculus

<220>
<221> sig_peptide
<222> (22)...(105)

<221> mat_peptide
<222> (106)...(630)

<221> CDS
<222> (22)...(630)

<400> 9
tcacagaccc cggagagcaa c atg aag cca gaa aca gct ggg ggc cac atg    51
                        Met Lys Pro Glu Thr Ala Gly Gly His Met
                                    -25                 -20
```

```
ctc ctc ctg ctg ttg cct ctg ctg ctg gcc gca gtg ctg aca aga acc     99
Leu Leu Leu Leu Leu Pro Leu Leu Leu Ala Ala Val Leu Thr Arg Thr
            -15                 -10                  -5

caa gct gac cct gtc ccc agg gcc acc agg ctc cca gtg gaa gca aag    147
Gln Ala Asp Pro Val Pro Arg Ala Thr Arg Leu Pro Val Glu Ala Lys
         1               5                   10

gat tgc cac att gct cag ttc aag tct ctg tcc cca aaa gag ctg cag    195
Asp Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln
 15                  20                  25                  30

gcc ttc aaa aag gcc aag ggt gcc atc gag aag agg ctg ctt gag aag    243
Ala Phe Lys Lys Ala Lys Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys
                 35                  40                  45

gac atg agg tgc agt tcc cac ctc atc tcc agg gcc tgg gac ctg aag    291
Asp Met Arg Cys Ser Ser His Leu Ile Ser Arg Ala Trp Asp Leu Lys
             50                  55                  60

cag ctg cag gtc caa gag cgc ccc aag gcc ttg cag gct gag gtg gcc    339
Gln Leu Gln Val Gln Glu Arg Pro Lys Ala Leu Gln Ala Glu Val Ala
         65                  70                  75

ctg acc ctg aag gtc tgg gag aac ata aat gac tca gcc ctg acc acc    387
Leu Thr Leu Lys Val Trp Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr
     80                  85                  90

atc ctg ggc cag cct ctt cat aca ctg agc cac att cac tcc cag ctg    435
Ile Leu Gly Gln Pro Leu His Thr Leu Ser His Ile His Ser Gln Leu
 95                 100                 105                 110

cag acc tgt aca cag ctt cag gcc aca gca gag ccc aag ccc ccg agt    483
Gln Thr Cys Thr Gln Leu Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser
                115                 120                 125

cgc cgc ctc tcc cgc tgg ctg cac agg ctc cag gag gcc cag agc aag    531
Arg Arg Leu Ser Arg Trp Leu His Arg Leu Gln Glu Ala Gln Ser Lys
            130                 135                 140

gag act cct ggc tgc ctg gag gac tct gtc acc tcc aac ctg ttt caa    579
Glu Thr Pro Gly Cys Leu Glu Asp Ser Val Thr Ser Asn Leu Phe Gln
        145                 150                 155

ctg ctc ctc cgg gac ctc aag tgt gtg gcc agt gga gac cag tgt gtc    627
Leu Leu Leu Arg Asp Leu Lys Cys Val Ala Ser Gly Asp Gln Cys Val
    160                 165                 170

tga cc                                                             632
 *


<210> 10
<211> 202
<212> PRT
<213> Mus musculus

<220>
<221> SIGNAL
```

```
<222> (1)...(28)

<400> 10
Met Lys Pro Glu Thr Ala Gly Gly His Met Leu Leu Leu Leu Leu Pro
            -25                 -20                 -15
Leu Leu Leu Ala Ala Val Leu Thr Arg Thr Gln Ala Asp Pro Val Pro
        -10                 -5                   1
Arg Ala Thr Arg Leu Pro Val Glu Ala Lys Asp Cys His Ile Ala Gln
 5                  10                  15                  20
Phe Lys Ser Leu Ser Pro Lys Glu Leu Gln Ala Phe Lys Lys Ala Lys
                25                  30                  35
Gly Ala Ile Glu Lys Arg Leu Leu Glu Lys Asp Met Arg Cys Ser Ser
            40                  45                  50
His Leu Ile Ser Arg Ala Trp Asp Leu Lys Gln Leu Gln Val Gln Glu
        55                  60                  65
Arg Pro Lys Ala Leu Gln Ala Glu Val Ala Leu Thr Leu Lys Val Trp
    70                  75                  80
Glu Asn Ile Asn Asp Ser Ala Leu Thr Thr Ile Leu Gly Gln Pro Leu
85                  90                  95                  100
His Thr Leu Ser His Ile His Ser Gln Leu Gln Thr Cys Thr Gln Leu
                105                 110                 115
Gln Ala Thr Ala Glu Pro Lys Pro Pro Ser Arg Arg Leu Ser Arg Trp
            120                 125                 130
Leu His Arg Leu Gln Glu Ala Gln Ser Lys Glu Thr Pro Gly Cys Leu
        135                 140                 145
Glu Asp Ser Val Thr Ser Asn Leu Phe Gln Leu Leu Leu Arg Asp Leu
    150                 155                 160
Lys Cys Val Ala Ser Gly Asp Gln Cys Val
165                 170


<210> 11
<211> 520
<212> PRT
<213> Homo sapiens

<400> 11
Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1               5                  10                  15
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
            20                  25                  30
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
        35                  40                  45
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
    50                  55                  60
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
65                  70                  75                  80
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
                85                  90                  95
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
            100                 105                 110
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
        115                 120                 125
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
    130                 135                 140
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
145                 150                 155                 160
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
                165                 170                 175
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
            180                 185                 190
```

```
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
        195                 200                 205
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
    210                 215                 220
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
225                 230                 235                 240
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
                245                 250                 255
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
            260                 265                 270
Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
        275                 280                 285
Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
    290                 295                 300
Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
305                 310                 315                 320
Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
                325                 330                 335
Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
            340                 345                 350
Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
        355                 360                 365
Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
    370                 375                 380
Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
385                 390                 395                 400
Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
                405                 410                 415
Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
            420                 425                 430
Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
        435                 440                 445
Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
    450                 455                 460
Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
465                 470                 475                 480
Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
                485                 490                 495
Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
            500                 505                 510
Thr Leu Gly His Tyr Met Ala Arg
        515                 520
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<210> 12
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> mature protein of SEQ ID NO: 1, with 3' Met added

<221> CDS
<222> (1)...(531)

<400> 12

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atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc    48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc    96
```

```
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac      144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45

tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag      192
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg      240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg      288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                85                  90                  95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag      336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg      384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag      432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc      480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc      528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                                  531
 *


<210> 13
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> mature protein of SEQ ID NO: 1, with 3' Met added

<400> 13
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1               5                   10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
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```
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 14
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> mature protein of SEQ ID NO: 3, with 3' Met added

<221> CDS
<222> (1)...(549)

<400> 14
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc    48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                  10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc    96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg   144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc   192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg   240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta   288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc   336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc   384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct   432
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His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg tgt ctg aga acg tca 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
165 170 175

acc cac cct gag tcc acc tga caccccacac cttatttatg cgctgagccc 579
Thr His Pro Glu Ser Thr *
180

tactccttcc ttaatttatt tcctctcacc ctttatttat ga 621

<210> 15
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> mature protein of SEQ ID NO: 3, with 3' Met added

<400> 15
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 16
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> mature protein of SEQ ID NO: 5, with 3' Met added

<221> CDS

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<222> (1)...(531)

<400> 16
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc    48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc    96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
             20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac    144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
         35                  40                  45

tgc aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag    192
Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
     50                  55                  60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg    240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg    288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
                 85                  90                  95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag    336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg    384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag    432
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc    480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc    528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                                531
 *


<210> 17
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> mature protein of SEQ ID NO: 5, with 3' Met added

<400> 17
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Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Cys Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 18
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28A mutant C48S

<221> CDS
<222> (1)...(528)

<400> 18
gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc      48
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt      96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tcc     144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser
        35                  40                  45

agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg     192
Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
    50                  55                  60

cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg     240
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80

ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac     288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
                85                  90                  95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc     336
```

```
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
            100                 105                 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc    384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125

cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag    432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc    480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga    528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  *
                165                 170                 175
```

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<210> 19
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-28A mutant C48S

<400> 19
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Ser
        35                  40                  45
Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
                85                  90                  95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
            100                 105                 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175
```

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<210> 20
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C49S
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<221> CDS
<222> (1)...(531)

<400> 20
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc    48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc    96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
             20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac    144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
         35                  40                  45

tcc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag    192
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
     50                  55                  60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg    240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg    288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                 85                  90                  95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag    336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg    384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag    432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc    480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc    528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                                531
 *


<210> 21
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C49S
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<400> 21
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45
Ser Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
85 90 95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 22
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28A mutant C50S

<221> CDS
<222> (1)...(528)

<400> 22
gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc tgc 48
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
1 5 10 15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc 144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
35 40 45

agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50 55 60

cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg gac 288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
85 90 95

```
gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ttc    336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
            100                 105                 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc    384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125

cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag gag    432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc    480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160

ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc tga    528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  *
                165                 170                 175


<210> 23
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-28A mutant C50S

<400> 23
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
        35                  40                  45
Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
                85                  90                  95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
            100                 105                 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 24
<211> 531
<212> DNA
<213> Artificial Sequence
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<220>
<223> met IL-28A mutant C51S

<221> CDS
<222> (1)...(531)

<400> 24
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc    48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
1               5                   10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc    96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
                20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac    144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45

tgc agg tcc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag    192
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg    240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg    288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                85                  90                  95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag    336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg    384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag    432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc    480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc    528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                                531
 *


<210> 25
<211> 176
<212> PRT
<213> Artificial Sequence
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<220>
<223> met IL-28A mutant C51S

<400> 25
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Cys Arg Ser His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 26
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<221> CDS
<222> (1)...(546)

<400> 26
ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc cac      48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                   10                  15

atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc aaa      96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30

aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct     144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45

tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag     192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60

gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc ctg     240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg gat     288
```

```
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95

cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct tgc      336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac      384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct ggt      432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt      480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct acc      528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr
                165                 170                 175

cat ccg gaa tct acc taa                                              546
His Pro Glu Ser Thr  *
            180


<210> 27
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171S

<400> 27
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
1               5                   10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180
```

```
<210> 28
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> met IL-29 mutant C172S

<221> CDS
<222> (1)...(549)

<400> 28
atg ggt ccg gtt ccg acc tct aaa cca acc acc act ggt aaa ggt tgc       48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                   10                  15

cac atc ggt cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc       96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30

aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg      144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg      192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc      240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg      288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct      336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg      384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct      432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc      480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cgt gat ctg aaa tac gtt gct gat ggt aac ctg tct ctg cgt acc tct      528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser
                165                 170                 175

acc cat ccg gaa tct acc taa                                           549
Thr His Pro Glu Ser Thr  *
            180
```

<210> 29
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-29 mutant C172S

<400> 29
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Ser Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 30
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence of SEQ ID NO: 18

<221> misc_feature
<222> (1)...(525)
<223> n = A,T,C or G

<400> 30
gtnccngtng cnmgnytnca yggngcnytn ccngaygcnm gnggntgyca yathgcncar 60
ttyaarwsny tnwsnccnca rgarytncar gcnttyaarm gngcnaarga ygcnytngar 120
garwsnytny tnytnaarga ywsnmgntgy caywsnmgny tnttyccnmg nacntgggay 180
ytnmgncary tncargtnmg ngarmgnccn atggcnytng argcngaryt ngcnytnacn 240
ytnaargtny tngargcnac ngcngayacn gayccngcny tngtngaygt nytngaycar 300
ccnytncaya cnytncayca yathytnwsn carttymgng cntgyathca rccncarccn 360
acngcnggnc cnmgnacnmg nggnmgnytn caycaytggy tntaymgnyt ncargargcn 420
ccnaaraarg arwsnccngg ntgyytngar gcnwsngtna cnttyaayyt nttymgnytn 480
ytnacnmgng ayytnaaytg ygtngcnwsn ggngayytnt gygtn 525

<210> 31

<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence of SEQ ID NO: 20

<221> misc_feature
<222> (1)...(525)
<223> n = A,T,C or G

<400> 31
gtnccngtng cnmgnytnca yggngcnytn ccngaygcnm gnggntgyca yathgcncar 60
ttyaarwsny tnwsnccnca rgarytncar gcnttyaarm gngcnaarga ygcnytngar 120
garwsnytny tnytnaarga ywsnmgntgy caywsnmgny tnttyccnmg nacntgggay 180
ytnmgncary tncargtnmg ngarmgnccn atggcnytng argcngaryt ngcnytnacn 240
ytnaargtny tngargcnac ngcngayacn gayccngcny tngtngaygt nytngaycar 300
ccnytncaya cnytncayca yathytnwsn carttymgng cntgyathca rccncarccn 360
acngcnggnc cnmgnacnmg nggnmgnytn caycaytggy tntaymgnyt ncargargcn 420
ccnaaraarg arwsnccngg ntgyytngar gcnwsngtna cnttyaayyt nttymgnytn 480
ytnacnmgng ayytnaaytg ygtngcnwsn ggngayytnt gygtn 525

<210> 32
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence of SEQ ID NO: 22

<221> misc_feature
<222> (1)...(525)
<223> n = A,T,C or G

<400> 32
gtnccngtng cnmgnytnca yggngcnytn ccngaygcnm gnggntgyca yathgcncar 60
ttyaarwsny tnwsnccnca rgarytncar gcnttyaarm gngcnaarga ygcnytngar 120
garwsnytny tnytnaarga ywsnmgntgy caywsnmgny tnttyccnmg nacntgggay 180
ytnmgncary tncargtnmg ngarmgnccn atggcnytng argcngaryt ngcnytnacn 240
ytnaargtny tngargcnac ngcngayacn gayccngcny tngtngaygt nytngaycar 300
ccnytncaya cnytncayca yathytnwsn carttymgng cntgyathca rccncarccn 360
acngcnggnc cnmgnacnmg nggnmgnytn caycaytggy tntaymgnyt ncargargcn 420
ccnaaraarg arwsnccngg ntgyytngar gcnwsngtna cnttyaayyt nttymgnytn 480
ytnacnmgng ayytnaaytg ygtngcnwsn ggngayytnt gygtn 525

<210> 33
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence of SEQ ID NO: 24

<221> misc_feature
<222> (1)...(525)
<223> n = A,T,C or G

<400> 33
gtnccngtng cnmgnytnca yggngcnytn ccngaygcnm gnggntgyca yathgcncar 60
ttyaarwsny tnwsnccnca rgarytncar gcnttyaarm gngcnaarga ygcnytngar 120
garwsnytny tnytnaarga ywsnmgntgy caywsnmgny tnttyccnmg nacntgggay 180

```
ytnmgncary tncargtnmg ngarmgnccn atggcnytng argcngaryt ngcnytnacn 240
ytnaargtny tngargcnac ngcngayacn gayccngcny tngtngaygt nytngaycar 300
ccnytncaya cnytncayca yathytnwsn carttymgng cntgyathca rccncarccn 360
acngcnggnc cnmgnacnmg nggnmgnytn caycaytggy tntaymgnyt ncargargcn 420
ccnaaraarg arwsnccngg ntgyytngar gcnwsngtna cnttyaayyt nttymgnytn 480
ytnacnmgng ayytnaaytg ygtngcnwsn ggngayytnt gygtn                 525
```

<210> 34
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence of SEQ ID NO: 26

<221> misc_feature
<222> (1)...(525)
<223> n = A,T,C or G

<400> 34

```
gtnccngtng cnmgnytnca yggngcnytn ccngaygcnm gnggntgyca yathgcncar 60
ttyaarwsny tnwsnccnca rgarytncar gcnttyaarm gngcnaarga ygcnytngar 120
garwsnytny tnytnaarga ywsnmgntgy caywsnmgny tnttyccnmg nacntgggay 180
ytnmgncary tncargtnmg ngarmgnccn atggcnytng argcngaryt ngcnytnacn 240
ytnaargtny tngargcnac ngcngayacn gayccngcny tngtngaygt nytngaycar 300
ccnytncaya cnytncayca yathytnwsn carttymgng cntgyathca rccncarccn 360
acngcnggnc cnmgnacnmg nggnmgnytn caycaytggy tntaymgnyt ncargargcn 420
ccnaaraarg arwsnccngg ntgyytngar gcnwsngtna cnttyaayyt nttymgnytn 480
ytnacnmgng ayytnaaytg ygtngcnwsn ggngayytnt gygtn                 525
```

<210> 35
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence of SEQ ID NO: 28

<221> misc_feature
<222> (1)...(525)
<223> n = A,T,C or G

<400> 35

```
gtnccngtng cnmgnytnca yggngcnytn ccngaygcnm gnggntgyca yathgcncar 60
ttyaarwsny tnwsnccnca rgarytncar gcnttyaarm gngcnaarga ygcnytngar 120
garwsnytny tnytnaarga ywsnmgntgy caywsnmgny tnttyccnmg nacntgggay 180
ytnmgncary tncargtnmg ngarmgnccn atggcnytng argcngaryt ngcnytnacn 240
ytnaargtny tngargcnac ngcngayacn gayccngcny tngtngaygt nytngaycar 300
ccnytncaya cnytncayca yathytnwsn carttymgng cntgyathca rccncarccn 360
acngcnggnc cnmgnacnmg nggnmgnytn caycaytggy tntaymgnyt ncargargcn 420
ccnaaraarg arwsnccngg ntgyytngar gcnwsngtna cnttyaayyt nttymgnytn 480
ytnacnmgng ayytnaaytg ygtngcnwsn ggngayytnt gygtn                 525
```

<210> 36
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-28A mutant C48X

```
<221> VARIANT
<222> (48)...(48)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 36
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                   10                  15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
        35                  40                  45
Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
                85                  90                  95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
            100                 105                 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 37
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C49X

<221> VARIANT
<222> (49)...(49)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 37
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
```

```
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 38
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-28A mutant C50X

<221> VARIANT
<222> (50)...(50)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 38
Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
        35                  40                  45
Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val Asp
                85                  90                  95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Phe
            100                 105                 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 39
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> met IL-28A mutant C51X

<221> VARIANT
<222> (51)...(51)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 39
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
```

```
Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 40
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 mutant C171X

<221> VARIANT
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 40
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                  10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 41
<211> 182
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> met IL-29 mutant C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 41
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                  10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 42
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC40923

<400> 42
tccagggaat tcatataggc cggccaccat gaaactagac atgactggg                49

<210> 43
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC43152

<400> 43
ggggtgggta caaccccaga gctgttttaa ggcgcgcctc tagactattt ttagacacac 60
aggtccccac tggc                                                      74

<210> 44
<211> 50
<212> DNA
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<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC29740

<400> 44
ttgacaatta atcatcggct cgtataatgt gtggaattgt gagcggataa 50

<210> 45
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC29741

<400> 45
tctgatttaa tctgtatcag gctgaaaatc ttatctcatc cg 42

<210> 46
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC29736

<400> 46
gtggaattgt gagcggataa caatttcaca cagaattcat taaagaggag aaattaactc 60
cc 62

<210> 47
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC29738

<400> 47
gctgaaaatc ttatctcatc cgccaaaaca cccgggagtt aatttctcct ctttaatgaa 60
ttc 63

<210> 48
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44566

<400> 48
tcttccagag cgtcacgagc ttttttgaaa gaagccagtt cctgcggaga cagagatttg 60
aaacgaccga tgtggcaa 78

<210> 49
<211> 84
<212> DNA
<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC44565

<400> 49
tcgtgacgct ctggaagaat ctctgaaact gaaaaactgg tcttgctctt ctccggtttt 60
cccgggtaac tgggatctgc gtct 84

<210> 50
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44564

<400> 50
aacagaagct tccaggcaac cagcagattc ttttttcgga gcttcctgca gacgatgcag 60
ccagtggtgc a 71

<210> 51
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44563

<400> 51
aactggctct gaccctgaaa gttctggaag ctgctgcagg tcctgctctg gaagatgttc 60
tggatcagcc gct 73

<210> 52
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44562

<400> 52
tcagggtcag agccagttca gcttccagag caaccggacg ttcacgaacc tgcagcagac 60
gcagatccca gtta 74

<210> 53
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44561

<400> 53
tcagctgcag gcttgcattc aaccgcaacc gaccgctggt ccgcgtccgc gtggtcgtct 60
gcaccactgg ctgcat 76

<210> 54
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44560

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<400> 54
atgcaagcct gcagctgaga caggatgtgg tgcagagtgt gcagcggctg atccagaaca 60


<210> 55
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44559

<400> 55
atgggtccgg ttccgacctc taaaccaacc accactggta aaggttgcca catcggtcgt 60
tt                                                                62

<210> 56
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44558

<400> 56
ttaggtagat tccggatggg tagaggtacg caggcacagg ttaccatcag caacgtattt 60
cagat                                                             65

<210> 57
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44557

<400> 57
tgcctggaag cttctgttac cttcaacctg ttccgtctgc tgacccgtga tctgaaatac 60
gttgctgat                                                         69

<210> 58
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44340

<400> 58
cgttgctgat ggtaacctgt ctctgcgtac ctctacccat c                     41

<210> 59
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44341

<400> 59
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gatgggtaga ggtacgcaga gacaggttac catcagcaac g 41

<210> 60
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC41212

<400> 60
ctagaaataa ttttgtttaa ctttaagaag gagatatata tatgggccct gtccccactt 60
ccaagccc 68

<210> 61
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC41041

<400> 61
tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ttaggtggac tcagggtggg 60
ttgacgt 67

<210> 62
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC43431

<400> 62
ctagaaataa ttttgtttaa ctttaagaag gagatatata tatggttcct gtcgccaggc 60
tccac 65

<210> 63
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC43437

<400> 63
taatctgtat caggctgaaa atcttatctc atccgccaaa acatcagaca cacaggtccc 60
cactggc 67

<210> 64
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44327

<400> 64
gtggccgatg ggaacctgtc cctgagaacg tcaacccac 39

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<210> 65
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC44328

<400> 65
gtgggttgac gttctcaggg acaggttccc atcggccac                          39

<210> 66
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC45399

<400> 66
tcaggtccca ggtcctgggg aagaggcggg agtggcacct ggagtccttc agcagaagcg 60
actcttctaa ggcatctttg gcc                                         83

<210> 67
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> zcyto20 mature start from pYEL7b

<221> CDS
<222> (1)...(531)

<400> 67
atg gtt cct gtc gcc agg ctc cac ggg gct ctc ccg gat gca agg ggc   48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc   96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
             20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac   144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
         35                  40                  45

tgc agg tgc cac tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag   192
Cys Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
     50                  55                  60

ctg cag gtg agg gag cgc ccc atg gct ttg gag gct gag ctg gcc ctg   240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg gtg   288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                 85                  90                  95

gac gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag   336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
```

```
            100                 105                 110

ttc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg   384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg tac cgg ctc cag gag gcc cca aaa aag   432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc   480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agt ggg gac ctg tgt gtc   528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                               531
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<210> 68
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC45398

<400> 68
ggccaaagat gccttagaag agtcgcttct gctgaaggac tccaggtgcc actcccgcct 60
cttccccagg acctgggacc tga 83

<210> 69
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC45397

<400> 69
gctgcctcag gtcccaggtc ctggggaaga ggcgggagtg ggacctgcag tccttcagca 60
gaagcgactc ttctaaggca tct 83

<210> 70
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC45396

<400> 70
agatgcctta gaagagtcgc ttctgctgaa ggactgcagg tcccactccc gcctcttccc 60
caggacctgg gacctgaggc agc 83

<210> 71
<211> 1013

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (14)...(991)

<400> 71
ccagcgtccg tcc atg gcg tgg agc ctt ggg agc tgg ctg ggt ggc tgc       49
               Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys
                1               5                  10

ctg ctg gtg tca gca ttg gga atg gta cca cct ccc gaa aat gtc aga      97
Leu Leu Val Ser Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg
         15                  20                  25

atg aat tct gtt aat ttc aag aac att cta cag tgg gag tca cct gct     145
Met Asn Ser Val Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala
     30                  35                  40

ttt gcc aaa ggg aac ctg act ttc aca gct cag tac cta agt tat agg     193
Phe Ala Lys Gly Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg
 45                  50                  55                  60

ata ttc caa gat aaa tgc atg aat act acc ttg acg gaa tgt gat ttc     241
Ile Phe Gln Asp Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe
                 65                  70                  75

tca agt ctt tcc aag tat ggt gac cac acc ttg aga gtc agg gct gaa     289
Ser Ser Leu Ser Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu
             80                  85                  90

ttt gca gat gag cat tca gac tgg gta aac atc acc ttc tgt cct gtg     337
Phe Ala Asp Glu His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val
         95                 100                 105

gat gac acc att att gga ccc cct gga atg caa gta gaa gta ctt gct     385
Asp Asp Thr Ile Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala
    110                 115                 120

gat tct tta cat atg cgt ttc tta gcc cct aaa att gag aat gaa tac     433
Asp Ser Leu His Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr
125                 130                 135                 140

gaa act tgg act atg aag aat gtg tat aac tca tgg act tat aat gtg     481
Glu Thr Trp Thr Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val
                145                 150                 155

caa tac tgg aaa aac ggt act gat gaa aag ttt caa att act ccc cag     529
Gln Tyr Trp Lys Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln
            160                 165                 170

tat gac ttt gag gtc ctc aga aac ctg gag cca tgg aca act tat tgt     577
Tyr Asp Phe Glu Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys
        175                 180                 185

gtt caa gtt cga ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg     625
Val Gln Val Arg Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp
    190                 195                 200

agt gag cct gtc tgt gag caa aca acc cat gac gaa acg gtc ccc tcc     673
```

```
Ser Glu Pro Val Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
205                 210                 215                 220

tgg atg gtg gcc gtc atc ctc atg gcc tcg gtc ttc atg gtc tgc ctg     721
Trp Met Val Ala Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu
                225                 230                 235

gca ctc ctc ggc tgc ttc tcc ttg ctg tgg tgc gtt tac aag aag aca     769
Ala Leu Leu Gly Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr
            240                 245                 250

aag tac gcc ttc tcc cct agg aat tct ctt cca cag cac ctg aaa gag     817
Lys Tyr Ala Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu
        255                 260                 265

ttt ttg ggc cat cct cat cat aac aca ctt ctg ttt ttc tcc ttt cca     865
Phe Leu Gly His Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro
    270                 275                 280

ttg tcg gat gag aat gat gtt ttt gac aag cta agt gtc att gca gaa     913
Leu Ser Asp Glu Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu
285                 290                 295                 300

gac tct gag agc ggc aag cag aat cct ggt gac agc tgc agc ctc ggg     961
Asp Ser Glu Ser Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly
                305                 310                 315

acc ccg cct ggg cag ggg ccc caa agc tag gctctgagaa ggaaacacac       1011
Thr Pro Pro Gly Gln Gly Pro Gln Ser  *
            320                 325

tc                                                                  1013

<210> 72
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC40922

<400> 72
tccagggaat tcatataggc cggccaccat ggctgcagct tggaccgtg               49

<210> 73
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC43153

<400> 73
ggggtgggta caaccccaga gctgttttaa ggcgcgcctc tagactattt ttaggtggac 60
tcagggtggg t                                                      71

<210> 74
<211> 546
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> IL29 mutant C15X, Asn169

<221> CDS
<222> (1)...(546)

<221> variation
<222> (44)...(45)
<223> n = A, G, T, or C

<400> 74
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac    48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                   10                  15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag    96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt    144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag    192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg    240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac    288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt    336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac    384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc    432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga    480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc    528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                            546
His Pro Glu Ser Thr  *
            180


<210> 75
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```
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> IL29 mutant C15X, Asn169

<400> 75
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                  10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 76
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant C16X, Asn170

<221> CDS
<222> (1)...(549)

<221> variation
<222> (47)...(48)
<223> n = A, T, G, or C

<400> 76
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn      48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1               5                  10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc      96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
```

```
aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg     144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc     192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg     240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta     288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc     336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
             100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc     384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
         115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct     432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
     130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg     480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca     528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
                 165                 170                 175

acc cac cct gag tcc acc tga                                         549
Thr His Pro Glu Ser Thr  *
             180


<210> 77
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> Met IL29 mutant C16X, Asn170

<400> 77
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1               5                   10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45
```

```
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 78
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant C15X, Asp169

<221> CDS
<222> (1)...(546)

<221> variation
<222> (44)...(45)
<223> n = A, T, G, or C

<400> 78
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac   48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                  10                  15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag   96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt   144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag   192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg   240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac   288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt   336
```

```
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac      384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc      432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga      480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc      528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
            165                 170                 175

cac cct gag tcc acc tga                                              546
His Pro Glu Ser Thr  *
            180


<210> 79
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant C15X, Asp169

<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 79
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                  10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
            165                 170                 175
His Pro Glu Ser Thr
            180
```

```
<210> 80
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant C16X, Asp170

<221> CDS
<222> (1)...(549)

<221> variation
<222> (47)...(48)
<223> n = A, T, G, or C

<400> 80
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn      48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1               5                  10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc      96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg     144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc     192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg     240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta     288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc     336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc     384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct     432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg     480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca     528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
                165                 170                 175
```

```
acc cac cct gag tcc acc tga                                          549
Thr His Pro Glu Ser Thr  *
            180
```

<210> 81
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant C16X, Asp170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 81

```
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1               5                  10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180
```

<210> 82
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant Asp169, C171X

<221> CDS
<222> (1)...(546)

<221> variation
<222> (512)...(513)
<223> n = A, T, G, or C

<400> 82

```
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac     48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                  10                  15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag     96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt    144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag    192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg    240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac    288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt    336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac    384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc    432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga    480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc    528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                            546
His Pro Glu Ser Thr  *
            180
```

```
<210> 83
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant Asp169, C171X

<221> VARIANT
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn
```

```
<400> 83
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                   10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                   70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 84
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant Asp170, C172X

<221> CDS
<222> (1)...(549)

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 84
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc     48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                   10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc     96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg    144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc    192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg    240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
```

```
65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta   288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc   336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc   384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct   432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg   480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca   528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                       549
Thr His Pro Glu Ser Thr  *
            180


<210> 85
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant Asp170, C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 85
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1               5                   10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
```

```
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 86
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, Asn169, C171X

<221> CDS
<222> (1)...(546)

<221> variation
<222> (512)...(513)
<223> n = A, T, G, or C

<400> 86
ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac    48
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1               5                  10                  15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag    96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt   144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag   192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg   240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac   288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt   336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac   384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc   432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
```

```
tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga     480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc     528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                             546
His Pro Glu Ser Thr  *
            180
```

```
<210> 87
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, Asn169, C171X

<221> VARIANT
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 87
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1               5                  10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 88
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant T11P, Asn170, C172X

<221> CDS
```

```
<222> (1)...(549)

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 88
atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc   48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1               5                  10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc   96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg   144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc   192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg   240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta   288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc   336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc   384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct   432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg   480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca   528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                       549
Thr His Pro Glu Ser Thr  *
            180


<210> 89
<211> 182
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Met IL29 mutant T11P, Asn170, C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 89
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1               5                  10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 90
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, C15X, Asn169

<221> CDS
<222> (1)...(546)

<221> variation
<222> 30, 44, 45
<223> n = A, T, G, or C

<400> 90
ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac    48
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
 1               5                  10                  15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag    96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt    144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
```

```
tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag     192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg     240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac     288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt     336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac     384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc     432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga     480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc     528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                             546
His Pro Glu Ser Thr  *
            180


<210> 91
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, C15X, Asn169

<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 91
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
 1               5                  10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80
```

```
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 92
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant T11P, C16X, Asn170

<221> CDS
<222> (1)...(549)

<221> variation
<222> 33, 47, 48
<223> n = A, T, G, or C

<400> 92
atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn    48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1               5                  10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc    96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg    144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc    192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg    240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta    288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc    336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
             100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc    384
```

```
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
    115                     120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct    432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg    480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca    528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                        549
Thr His Pro Glu Ser Thr  *
            180


<210> 93
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant T11P, C16X, Asn170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 93
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1              5                   10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 94
<211> 546
```

```
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, Asp169, C171X

<221> CDS
<222> (1)...(546)

<221> variation
<222> 30, 512, 513
<223> n = A, T, G, or C

<400> 94
ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc cac   48
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1               5                   10                  15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag   96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt   144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag   192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg   240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac   288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt   336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac   384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc   432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga   480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc   528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                           546
His Pro Glu Ser Thr  *
            180
```

<210> 95
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, Asp169, C171X

<221> VARIANT
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 95

```
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys His
 1               5                  10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                   80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
            165                 170                 175
His Pro Glu Ser Thr
            180
```

<210> 96
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant T11P, Asp170, C172X

<221> CDS
<222> (1)...(549)

<221> variation
<222> 33, 515, 516
<223> n = A, T, G, or C

<400> 96

```
atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc tgc    48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1               5                  10                  15
```

```
cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc       96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg      144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc      192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg      240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta      288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc      336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc      384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct      432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg      480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca      528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                          549
Thr His Pro Glu Ser Thr  *
            180
```

<210> 97
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant T11P, Asp170, C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 97

```
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Cys
 1               5                  10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
```

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


<210> 98
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, C15X, Asp169

<221> CDS
<222> (1)...(546)

<221> variation
<222> 30, 44, 45
<223> n = A, T, G, or C

<400> 98
ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn cac      48
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
 1               5                  10                  15

att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag      96
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt     144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag     192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg     240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac     288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
```

```
                 85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt      336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac      384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc      432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga      480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc      528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                              546
His Pro Glu Ser Thr  *
            180


<210> 99
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant T10P, C15X, Asp169

<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 99
Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa His
 1               5                  10                  15
Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
```

```
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 100
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant T11P, C16X, Asp170

<221> CDS
<222> (1)...(549)

<221> variation
<222> 33, 47, 48
<223> n = A, T, G, or C

<400> 100
atg ggc cct gtc ccc act tcc aag ccc acc ccn act ggg aag ggc dnn      48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1               5                  10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc      96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg     144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc     192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg     240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta     288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc     336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc     384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct     432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg     480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
```

```
cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca     528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                         549
Thr His Pro Glu Ser Thr  *
            180


<210> 101
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant T11P, C16X, Asp170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 101
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Pro Thr Gly Lys Gly Xaa
 1               5                  10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 102
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant G18D, Asn169, C171X

<221> CDS
<222> (1)...(546)

<221> variation
<222> (512)...(513)
```

```
<223> n = A, T, G, or C

<400> 102
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac       48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                   10                  15

att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag       96
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt      144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag      192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg      240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac      288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt      336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac      384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc      432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga      480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc      528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                              546
His Pro Glu Ser Thr  *
            180


<210> 103
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant G18D, Asn169, C171X

<221> VARIANT
```

```
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 103
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                  10                  15
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 104
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant G19D, Asn170, C172X

<221> CDS
<222> (1)...(549)

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 104
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc      48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                  10                  15

cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc      96
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg      144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc      192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
```

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta 288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc 336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc 384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct 432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg 480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca 528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
165 170 175

acc cac cct gag tcc acc tga 549
Thr His Pro Glu Ser Thr *
180

<210> 105
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant G19D, Asn170, C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 105
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
1 5 10 15
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
20 25 30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
35 40 45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110

```
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 106
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant C15X, G18D, Asn169

<221> CDS
<222> (1)...(546)

<221> variation
<222> (44)...(45)
<223> n = A, T, G, or C

<400> 106
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac    48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                  10                  15

att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag    96
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt    144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag    192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg    240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac    288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt    336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac    384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc    432
```

```
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga      480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca acc      528
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                              546
His Pro Glu Ser Thr  *
            180


<210> 107
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant C15X, G18D, Asn169

<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 107
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                  10                  15
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 108
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
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```
<223> Met IL29 mutant C16X, G19D, Asn170

<221> CDS
<222> (1)...(549)

<221> variation
<222> (47)...(48)
<223> n = A, T, G, or C

<400> 108
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn    48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1               5                  10                  15

cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc    96
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg   144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc   192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg   240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta   288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc   336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc   384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct   432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg   480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg aay ctg tgt ctg aga acg tca   528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                       549
Thr His Pro Glu Ser Thr  *
            180


<210> 109
<211> 182
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```
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant C16X, G19D, Asn170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 109
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1               5                  10                  15
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Cys Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 110
<211> 546
<212> DNA
<213> qArtificial Sequence

<220>
<223> IL29 mutant G18D, Asp169, C171X

<221> CDS
<222> (1)...(546)

<221> variation
<222> (512)...(513)
<223> n = A, T, G, or C

<400> 110
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac    48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                  10                  15

att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag    96
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30
```

```
aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt    144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag    192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg    240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac    288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt    336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac    384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc    432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga    480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca acc    528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175

cac cct gag tcc acc tga                                            546
His Pro Glu Ser Thr  *
            180


<210> 111
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant G18D, Asp169, C171X

<221> VARIANT
<222> (171)...(171)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 111
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His
 1               5                   10                  15
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
```

```
    50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180


<210> 112
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant G19D, Asp170, C172X

<221> CDS
<222> (1)...(549)

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<400> 112
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc      48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                  10                  15

cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc      96
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg     144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc     192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg     240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                 70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta     288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc     336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
```

```
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc    384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct    432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg    480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg dnn ctg aga acg tca    528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                        549
Thr His Pro Glu Ser Thr  *
            180


<210> 113
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant G19D, Asp170, C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 113
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                  10                  15
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Xaa Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180
```

```
<210> 114
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> IL29 mutant C15X, G18D, Asp169

<221> CDS
<222> (1)...(546)

<221> variation
<222> (44)...(45)
<223> n = A, T, G, or C

<400> 114
ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn cac      48
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                  10                  15

att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag      96
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
            20                  25                  30

aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt     144
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
        35                  40                  45

tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag     192
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
    50                  55                  60

gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg     240
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
 65                  70                  75                  80

aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac     288
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                85                  90                  95

cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt     336
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110

atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac     384
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125

cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc     432
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140

tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga     480
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160

gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca acc     528
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175
```

```
cac cct gag tcc acc tga                                              546
His Pro Glu Ser Thr  *
            180
```

<210> 115
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> IL29 mutant C15X, G18D, Asp169

<221> VARIANT
<222> (15)...(15)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 115

```
Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa His
 1               5                  10                  15
Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys
             20                  25                  30
Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser
         35                  40                  45
Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln
     50                  55                  60
Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu
65                  70                  75                  80
Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp
                 85                  90                  95
Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys
            100                 105                 110
Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His
        115                 120                 125
His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly
    130                 135                 140
Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg
145                 150                 155                 160
Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser Thr
                165                 170                 175
His Pro Glu Ser Thr
            180
```

<210> 116
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL29 mutant C16X, G19D, Asp170

<221> CDS
<222> (1)...(549)

<221> variation
<222> (47)...(48)
<223> n = A, T, G, or C

<400> 116

```
atg ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc dnn      48
```

```
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1               5                   10                  15

cac att gay agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc      96
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg      144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc      192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg      240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta      288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc      336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc      384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct      432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg      480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg gay ctg tgt ctg aga acg tca      528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                          549
Thr His Pro Glu Ser Thr  *
            180
```

<210> 117
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Met IL29 mutant C16X, G19D, Asp170

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 117

```
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Xaa
 1              5                   10                  15
His Ile Asp Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asp Leu Cys Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180
```

<210> 118
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Signal sequence

<221> CDS
<222> (1)...(57)

<400> 118

```
atg gct gca gct tgg acc gtg gtg ctg gtg act ttg gtg cta ggc ttg     48
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1              5                   10                  15

gcc gtg gca                                                         57
Ala Val Ala
```

<210> 119
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal sequence

<400> 119

```
Met Ala Ala Ala Trp Thr Val Val Leu Val Thr Leu Val Leu Gly Leu
 1              5                   10                  15
Ala Val Ala
```

```
<210> 120
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Signal sequence

<221> CDS
<222> (1)...(66)

<400> 120
atg gtg ccc acc aca ttg gct tgg acc gtg gtg ctg gtg act ttg gtg      48
Met Val Pro Thr Thr Leu Ala Trp Thr Val Val Leu Val Thr Leu Val
 1               5                  10                  15

cta ggc ttg gcc gtg gca                                              66
Leu Gly Leu Ala Val Ala
            20


<210> 121
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal sequence

<400> 121
Met Val Pro Thr Thr Leu Ala Trp Thr Val Val Leu Val Thr Leu Val
 1               5                  10                  15
Leu Gly Leu Ala Val Ala
            20


<210> 122
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28B C48S

<221> CDS
<222> (1)...(528)

<221> variation
<222> (143)...(144)
<223> n = A, T, G, or C

<400> 122
gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc      48
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt      96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30
```

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn 144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
35 40 45

aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50 55 60

cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat 288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
115 120 125

cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag 432
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
130 135 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc 480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145 150 155 160

ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga 528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val *
165 170 175

<210> 123
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (48)...(48)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> IL-28B C48S

<400> 123
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
1 5 10 15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
35 40 45
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50 55 60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

```
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
                85                  90                  95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
            100                 105                 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 124
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-28B C49S

<221> CDS
<222> (1)...(531)

<221> variation
<222> (146)...(147)
<223> n = A, T, G, or C

<400> 124
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc    48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc    96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac   144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45

dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag   192
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg   240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg   288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag   336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg   384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
```

```
ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag      432
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc      480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc      528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                                  531
 *


<210> 125
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (49)...(49)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> Met IL-28B C49S

<400> 125
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                   80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 126
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
```

```
<223> IL-28B C50S

<221> CDS
<222> (1)...(528)

<221> variation
<222> (149)...(150)
<223> n = A, T, G, or C

<400> 126
gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc    48
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                   10                  15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt    96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
             20                  25                  30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc    144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
         35                  40                  45

aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg    192
Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
     50                  55                  60

cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg    240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg gat    288
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
                 85                  90                  95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc    336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
            100                 105                 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc    384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125

cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag gag    432
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc    480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160

ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga    528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  *
                165                 170                 175


<210> 127
<211> 175
<212> PRT
<213> Artificial Sequence
```

```
<220>
<221> VARIANT
<222> (50)...(50)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> IL-28B C50S

<400> 127
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
        35                  40                  45
Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly Asp
                85                  90                  95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
            100                 105                 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125
Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 128
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-28B C51S

<221> CDS
<222> (1)...(531)

<221> variation
<222> (152)...(153)
<223> n = A, T, G, or C

<400> 128
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc      48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc      96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac     144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45

tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag     192
```

```
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg      240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65                 70                  75                  80

acg ctg aag gtt ctg gag gcc acc gct gac act gac cca gcc ctg ggg      288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag      336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg      384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg cac cgg ctc cag gag gcc cca aaa aag      432
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc      480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc      528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                                  531
 *


<210> 129
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (51)...(51)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> Met IL-28B C51S

<400> 129
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95
```

Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
100 105 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
115 120 125
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
130 135 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145 150 155 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
165 170 175

<210> 130
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28B C48S T87S H135Y

<221> CDS
<222> (1)...(528)

<221> variation
<222> 143, 144, 261
<223> n = A, T, G, or C

<400> 130
gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc 48
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
1 5 10 15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt 96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
20 25 30

aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac dnn 144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
35 40 45

aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg 192
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
50 55 60

cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg 240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65 70 75 80

ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat 288
Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
85 90 95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc 336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
100 105 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc 384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
115 120 125

cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag 432

```
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc    480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160

ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga    528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  *
                165                 170                 175
```

<210> 131
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (48)...(48)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (87)...(87)
<223> Xaa = Ser

<223> IL-28B C48S T87S H135Y

<400> 131

```
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
            20                  25                  30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Xaa
        35                  40                  45
Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
                85                  90                  95
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
            100                 105                 110
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175
```

<210> 132
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-28B C49S T88S H136Y

```
<221> CDS
<222> (1)...(531)

<221> variation
<222> 146, 147, 264
<223> n = A, T, G, or C

<400> 132
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc   48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc   96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
             20                  25                  30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac   144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
         35                  40                  45

dnn aag tgc cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag   192
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
     50                  55                  60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg   240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg   288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
                 85                  90                  95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag   336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg   384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag   432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc   480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc   528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                               531
 *


<210> 133
<211> 176
<212> PRT
```

```
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (49)...(49)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (88)...(88)
<223> Xaa = Ser

<223> Met IL-28B C49S T88S H136Y

<400> 133
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 134
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-28B C50S T87S H135Y

<221> CDS
<222> (1)...(528)

<221> variation
<222> 149, 150, 261
<223> n = A, T, G, or C

<400> 134
gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc tgc    48
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15

cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc ttt    96
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
                20                  25                  30
```

```
aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac tgc    144
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
         35                  40                  45

aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag ctg    192
Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln Leu
     50                  55                  60

cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg acg    240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg gat    288
Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly Asp
                 85                  90                  95

gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag ctc    336
Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu
            100                 105                 110

cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg ggc    384
Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg Gly
        115                 120                 125

cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag gag    432
Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys Glu
    130                 135                 140

tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc ctc    480
Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu
145                 150                 155                 160

ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc tga    528
Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val  *
                165                 170                 175


<210> 135
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (50)...(50)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (87)...(87)
<223> Xaa = Ser

<223> IL-28B C50S T87S H135Y

<400> 135
Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly Cys
 1               5                  10                  15
His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala Phe
             20                  25                  30
Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp Cys
```

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

<210> 136
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Met IL-28B C51S T88S H136Y

<221> CDS
<222> (1)...(531)

<221> variation
<222> 152, 153, 264
<223> n = A, T, G, or C

<400> 136
atg gtt cct gtc gcc agg ctc cgc ggg gct ctc ccg gat gca agg ggc 48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1 5 10 15

tgc cac ata gcc cag ttc aag tcc ctg tct cca cag gag ctg cag gcc 96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
20 25 30

ttt aag agg gcc aaa gat gcc tta gaa gag tcg ctt ctg ctg aag gac 144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
35 40 45

tgc aag dnn cgc tcc cgc ctc ttc ccc agg acc tgg gac ctg agg cag 192
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
50 55 60

ctg cag gtg agg gag cgc ccc gtg gct ttg gag gct gag ctg gcc ctg 240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65 70 75 80

acg ctg aag gtt ctg gag gcc wsn gct gac act gac cca gcc ctg ggg 288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
85 90 95

gat gtc ttg gac cag ccc ctt cac acc ctg cac cat atc ctc tcc cag 336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln

```
            100                 105                 110

ctc cgg gcc tgt atc cag cct cag ccc acg gca ggg ccc agg acc cgg     384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggc cgc ctc cac cat tgg ctg tay cgg ctc cag gag gcc cca aaa aag     432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc cct ggc tgc ctc gag gcc tct gtc acc ttc aac ctc ttc cgc     480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctg aat tgt gtt gcc agc ggg gac ctg tgt gtc     528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175

tga                                                                 531
 *



<210> 137
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (51)...(51)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<221> VARIANT
<222> (88)...(88)
<223> Xaa = Ser

<223> Met IL-28B C51S T88S H136Y

<400> 137
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
```

```
                165                 170                 175


<210> 138
<211> 543
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C170X, truncated after N-terminal Methionine
      and Glycine

<221> variation
<222> (509)...(510)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(543)

<400> 138
cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att   48
Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile
 1               5                   10                  15

ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag   96
Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys
             20                  25                  30

gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc   144
Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys
         35                  40                  45

agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg   192
Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val
     50                  55                  60

agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag   240
Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys
 65                  70                  75                  80

gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag   288
Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln
                 85                  90                  95

ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc   336
Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile
            100                 105                 110

cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac   384
Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His
        115                 120                 125

tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc   432
Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys
    130                 135                 140

ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac   480
Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp
145                 150                 155                 160

ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac   528
```

```
Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His
                165                 170                 175

cct gag tcc acc tga                                                 543
Pro Glu Ser Thr  *
            180


<210> 139
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (170)...(170)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> IL-29 C170X, truncated after N-terminal Methionine
      and Glycine

<400> 139
Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile
 1               5                  10                  15
Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys
            20                  25                  30
Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys
        35                  40                  45
Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val
    50                  55                  60
Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys
65                  70                  75                  80
Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln
                85                  90                  95
Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile
            100                 105                 110
Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His
        115                 120                 125
Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys
    130                 135                 140
Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp
145                 150                 155                 160
Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His
                165                 170                 175
Pro Glu Ser Thr
            180


<210> 140
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C169X, truncated after N-terminal
      Methionine, Glycine, and Proline

<221> variation
<222> (506)...(507)
<223> n = A, T, G, or C
```

```
<221> CDS
<222> (1)...(540)

<400> 140
gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc      48
Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly
 1               5                   10                  15

agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc      96
Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala
             20                  25                  30

agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc     144
Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser
         35                  40                  45

tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg     192
Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg
     50                  55                  60

gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc     240
Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val
 65                  70                  75                  80

ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc     288
Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro
                 85                  90                  95

ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag     336
Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln
            100                 105                 110

cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg     384
Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp
        115                 120                 125

ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg     432
Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu
    130                 135                 140

gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc     480
Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
145                 150                 155                 160

aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct     528
Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro
                165                 170                 175

gag tcc acc tga                                                     540
Glu Ser Thr  *


<210> 141
<211> 179
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (169)...(169)
```

<223> Xaa = Ser, Ala, Thr, Val, or Asn

<223> L-29 C169X, truncated after N-terminal Methionine,
      Glycine, and Proline

<400> 141

```
Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly
 1               5                  10                  15
Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala
            20                  25                  30
Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser
        35                  40                  45
Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg
    50                  55                  60
Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val
65                  70                  75                  80
Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro
                85                  90                  95
Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln
            100                 105                 110
Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp
        115                 120                 125
Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu
    130                 135                 140
Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu
145                 150                 155                 160
Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro
                165                 170                 175
Glu Ser Thr
```

<210> 142
<211> 537
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C168X, truncated after N-terminal
      Methionine, Glycine, Proline, and Valine

<221> variation
<222> (503)...(504)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(537)

<400> 142

```
ccc act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg     48
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
 1               5                  10                  15

ttc aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg     96
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
            20                  25                  30

gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct    144
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
        35                  40                  45
```

```
cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag    192
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
     50                  55                  60

cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg    240
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
 65                  70                  75                  80

gag gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt    288
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
                 85                  90                  95

cac acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct    336
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
            100                 105                 110

cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg    384
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
        115                 120                 125

cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag    432
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
    130                 135                 140

gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa    480
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
145                 150                 155                 160

tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag    528
Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu
                165                 170                 175

tcc acc tga                                                        537
Ser Thr  *



<210> 143
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 C168X, truncated after N-terminal
      Methionine, Glycine, Proline, and Valine

<221> VARIANT
<222> (168)...(168)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 143
Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg
 1               5                  10                  15
Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg
            20                  25                  30
Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser
        35                  40                  45
Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu
    50                  55                  60
Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu
65                  70                  75                  80
```

```
Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu
                85                  90                  95
His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro
            100                 105                 110
Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu
        115                 120                 125
His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu
    130                 135                 140
Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys
145                 150                 155                 160
Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu
                165                 170                 175
Ser Thr
```

<210> 144
<211> 534
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C167X, truncated after N-terminal
Methionine, Glycine, Proline, Valine, and Proline

<221> variation
<222> (500)...(501)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(534)

<400> 144

```
act tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc    48
Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe
 1               5                  10                  15

aaa tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac    96
Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp
             20                  25                  30

gcc ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct    144
Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro
         35                  40                  45

gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc    192
Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg
     50                  55                  60

cct gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag    240
Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu
 65                  70                  75                  80

gcc gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac    288
Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His
                 85                  90                  95

acc ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag    336
Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln
             100                 105                 110
```

```
ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac      384
Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His
        115                 120                 125

cgg ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca      432
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala
    130                 135                 140

tct gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat      480
Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr
145                 150                 155                 160

gtg gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc      528
Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser
                165                 170                 175

acc tga                                                              534
Thr  *



<210> 145
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 C167X, truncated after N-terminal
      Methionine, Glycine, Proline, Valine, and Proline

<221> VARIANT
<222> (167)...(167)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 145
Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe
 1               5                  10                  15
Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp
            20                  25                  30
Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro
        35                  40                  45
Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg
    50                  55                  60
Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu
65                  70                  75                  80
Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His
                85                  90                  95
Thr Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln
            100                 105                 110
Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His
        115                 120                 125
Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala
    130                 135                 140
Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr
145                 150                 155                 160
Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser
                165                 170                 175
Thr
```

```
<210> 146
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C166X, truncated after N-terminal
      Methionine, Glycine, Proline, Valine, Proline, and
      Threonine

<221> variation
<222> (497)...(498)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(531)

<400> 146
tcc aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa      48
Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1               5                  10                  15

tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc      96
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
            20                  25                  30

ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc     144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
        35                  40                  45

ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct     192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
    50                  55                  60

gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc     240
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
65                  70                  75                  80

gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc     288
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
                85                  90                  95

ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc     336
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
            100                 105                 110

aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg     384
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
        115                 120                 125

ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct     432
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
    130                 135                 140

gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg     480
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
145                 150                 155                 160

gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc     528
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
                165                 170                 175
```

```
tga                                                               531
 *


<210> 147
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 C166X, truncated after N-terminal
      Methionine, Glycine, Proline, Valine, Proline, and
      Threonine

<221> VARIANT
<222> (166)...(166)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 147
Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1               5                  10                  15
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
            20                  25                  30
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
        35                  40                  45
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
    50                  55                  60
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
65                  70                  75                  80
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
                85                  90                  95
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
            100                 105                 110
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
        115                 120                 125
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
    130                 135                 140
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
145                 150                 155                 160
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
                165                 170                 175


<210> 148
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 C165X, truncated after N-terminal
      Methionine, Glycine, Proline, Valine, Proline,
      Threonine, and Serine

<221> variation
<222> (494)...(495)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(528)
```

```
<400> 148
aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa tct      48
Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser
 1               5                   10                  15

ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc ttg      96
Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu
             20                  25                  30

gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc ttc      144
Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe
         35                  40                  45

ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct gtg      192
Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val
     50                  55                  60

gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc gct      240
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala
 65                  70                  75                  80

gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc ctg      288
Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu
                 85                  90                  95

cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc aca      336
His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr
            100                 105                 110

gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg ctc      384
Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu
        115                 120                 125

cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct gtc      432
Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val
    130                 135                 140

acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg gcc      480
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala
145                 150                 155                 160

gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc tga      528
Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr  *
                165                 170                 175


<210> 149
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 C165X, truncated after N-terminal
      Methionine, Glycine, Proline, Valine, Proline,
      Threonine, and Serine

<221> VARIANT
<222> (165)...(165)
<223> Xaa = Ser, Ala, Thr, Val, or Asn
```

```
<400> 149
Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys Ser
 1               5                  10                  15
Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu
            20                  25                  30
Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val Phe
        35                  40                  45
Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro Val
    50                  55                  60
Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala Ala
65                  70                  75                  80
Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr Leu
                85                  90                  95
His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr
            100                 105                 110
Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg Leu
        115                 120                 125
Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser Val
    130                 135                 140
Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala
145                 150                 155                 160
Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
                165                 170                 175


<210> 150
<211> 552
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Leu insert after N-terminal Met, C173X

<221> variation
<222> (518)...(519)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(552)

<400> 150
atg ytn ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc    48
Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly
 1               5                  10                  15

tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc    96
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
            20                  25                  30

ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac    144
Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
        35                  40                  45

tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt    192
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
    50                  55                  60

ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg    240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
```

```
acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc     288
Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
                 85                  90                  95

cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag     336
Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
            100                 105                 110

gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc     384
Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
        115                 120                 125

ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc     432
Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
    130                 135                 140

gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc     480
Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
145                 150                 155                 160

acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg     528
Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
                165                 170                 175

tca acc cac cct gag tcc acc tga                                     552
Ser Thr His Pro Glu Ser Thr  *
            180


<210> 151
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 Leu insert after N-terminal Met, C173X

<221> VARIANT
<222> (173)...(173)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 151
Met Leu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly
 1               5                  10                  15
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
            20                  25                  30
Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
        35                  40                  45
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
                85                  90                  95
Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
            100                 105                 110
Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
        115                 120                 125
Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
    130                 135                 140
```

```
Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
145                 150                 155                 160
Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
                165                 170                 175
Ser Thr His Pro Glu Ser Thr
            180


<210> 152
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 G2L C172X

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(549)

<400> 152
atg ytn cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc    48
Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                   10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc    96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg    144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45

agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc    192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg    240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta    288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc    336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc    384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct    432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg    480
```

```
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca   528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                       549
Thr His Pro Glu Ser Thr  *
            180


<210> 153
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 G2L C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 153
Met Leu Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                  10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 154
<211> 552
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 Ile insert after N-terminal Met, C173X

<221> variation
<222> (518)...(519)
```

```
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(552)

<400> 154
atg ath ggc cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc    48
Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly
 1               5                  10                  15

tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc    96
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
            20                  25                  30

ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac    144
Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
        35                  40                  45

tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt    192
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
    50                  55                  60

ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg    240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80

acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc    288
Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
                85                  90                  95

cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag    336
Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
            100                 105                 110

gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc    384
Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
        115                 120                 125

ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc    432
Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
    130                 135                 140

gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc    480
Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
145                 150                 155                 160

acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg    528
Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
                165                 170                 175

tca acc cac cct gag tcc acc tga                                    552
Ser Thr His Pro Glu Ser Thr  *
            180


<210> 155
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
```

```
<223> IL-29 Ile insert after N-terminal Met, C173X

<221> VARIANT
<222> (173)...(173)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 155
Met Ile Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly
 1              5                   10                  15
Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser
            20                  25                  30
Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn
        35                  40                  45
Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val
                85                  90                  95
Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln
            100                 105                 110
Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg
        115                 120                 125
Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser
    130                 135                 140
Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu
145                 150                 155                 160
Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr
                165                 170                 175
Ser Thr His Pro Glu Ser Thr
            180


<210> 156
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 G2I C172X

<221> variation
<222> (515)...(516)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(549)

<400> 156
atg ath cct gtc ccc act tcc aag ccc acc aca act ggg aag ggc tgc      48
Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1              5                   10                  15

cac att ggc agg ttc aaa tct ctg tca cca cag gag cta gcg agc ttc      96
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg aaa aac tgg     144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45
```

```
agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg agg ctt ctc    192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60

cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg gcc ctg acg    240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag gac gtc cta    288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag ctc cag gcc    336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg ggc cgc ctc    384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag gag tcc gct    432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc ctc ctc acg    480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg aga acg tca    528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175

acc cac cct gag tcc acc tga                                        549
Thr His Pro Glu Ser Thr  *
            180


<210> 157
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 G2I C172X

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 157
Met Ile Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly Lys Gly Cys
 1               5                   10                  15
His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
             20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
         35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
     50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
```

```
                85                  90                  95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser
                165                 170                 175
Thr His Pro Glu Ser Thr
            180


<210> 158
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-29 after N-terminal Met amino acid residues 2-7
      deleted, C166X

<221> variation
<222> (497)...(498)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(531)

<400> 158
atg aag ccc acc aca act ggg aag ggc tgc cac att ggc agg ttc aaa   48
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1               5                   10                  15

tct ctg tca cca cag gag cta gcg agc ttc aag aag gcc agg gac gcc   96
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
             20                  25                  30

ttg gaa gag tca ctc aag ctg aaa aac tgg agt tgc agc tct cct gtc   144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
         35                  40                  45

ttc ccc ggg aat tgg gac ctg agg ctt ctc cag gtg agg gag cgc cct   192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
     50                  55                  60

gtg gcc ttg gag gct gag ctg gcc ctg acg ctg aag gtc ctg gag gcc   240
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
 65                  70                  75                  80

gct gct ggc cca gcc ctg gag gac gtc cta gac cag ccc ctt cac acc   288
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
                 85                  90                  95

ctg cac cac atc ctc tcc cag ctc cag gcc tgt atc cag cct cag ccc   336
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
            100                 105                 110

aca gca ggg ccc agg ccc cgg ggc cgc ctc cac cac tgg ctg cac cgg   384
```

```
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
        115                 120                 125

ctc cag gag gcc ccc aaa aag gag tcc gct ggc tgc ctg gag gca tct    432
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
    130                 135                 140

gtc acc ttc aac ctc ttc cgc ctc ctc acg cga gac ctc aaa tat gtg    480
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
145                 150                 155                 160

gcc gat ggg aac ctg dnn ctg aga acg tca acc cac cct gag tcc acc    528
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
                165                 170                 175

tga                                                                531
 *


<210> 159
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 after N-terminal Met amino acid residues 2-7
      deleted, C166X

<221> VARIANT
<222> (166)...(166)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 159
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1               5                  10                  15
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
            20                  25                  30
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
        35                  40                  45
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
    50                  55                  60
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
65                  70                  75                  80
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
                85                  90                  95
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
            100                 105                 110
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
        115                 120                 125
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
    130                 135                 140
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
145                 150                 155                 160
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
                165                 170                 175


<210> 160
<211> 558
<212> DNA
```

```
<213> Artificial Sequence

<220>
<223> IL-29 Glu, Ala, and Glu inserted after N-terminal
      Met, C175X

<221> variation
<222> (524)...(525)
<223> n = A, T, G, or C

<221> CDS
<222> (1)...(558)

<400> 160
atg gar gcn gar ggc cct gtc ccc act tcc aag ccc acc aca act ggg   48
Met Glu Ala Glu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly
 1               5                  10                  15

aag ggc tgc cac att ggc agg ttc aaa tct ctg tca cca cag gag cta   96
Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu
             20                  25                  30

gcg agc ttc aag aag gcc agg gac gcc ttg gaa gag tca ctc aag ctg   144
Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu
         35                  40                  45

aaa aac tgg agt tgc agc tct cct gtc ttc ccc ggg aat tgg gac ctg   192
Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu
     50                  55                  60

agg ctt ctc cag gtg agg gag cgc cct gtg gcc ttg gag gct gag ctg   240
Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu
 65                  70                  75                  80

gcc ctg acg ctg aag gtc ctg gag gcc gct gct ggc cca gcc ctg gag   288
Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu
                 85                  90                  95

gac gtc cta gac cag ccc ctt cac acc ctg cac cac atc ctc tcc cag   336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ctc cag gcc tgt atc cag cct cag ccc aca gca ggg ccc agg ccc cgg   384
Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg
        115                 120                 125

ggc cgc ctc cac cac tgg ctg cac cgg ctc cag gag gcc ccc aaa aag   432
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gag tcc gct ggc tgc ctg gag gca tct gtc acc ttc aac ctc ttc cgc   480
Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctc ctc acg cga gac ctc aaa tat gtg gcc gat ggg aac ctg dnn ctg   528
Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu
                165                 170                 175

aga acg tca acc cac cct gag tcc acc tga                           558
Arg Thr Ser Thr His Pro Glu Ser Thr  *
            180                 185
```

```
<210> 161
<211> 185
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-29 Glu, Ala, and Glu inserted after N-terminal
      Met, C175X

<221> VARIANT
<222> (175)...(175)
<223> Xaa = Ser, Ala, Thr, Val, or Asn

<400> 161
Met Glu Ala Glu Gly Pro Val Pro Thr Ser Lys Pro Thr Thr Thr Gly
 1               5                  10                  15
Lys Gly Cys His Ile Gly Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu
            20                  25                  30
Ala Ser Phe Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu
        35                  40                  45
Lys Asn Trp Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu
    50                  55                  60
Arg Leu Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu
65                  70                  75                  80
Ala Leu Thr Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Leu Gln Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Ala Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Lys Tyr Val Ala Asp Gly Asn Leu Xaa Leu
                165                 170                 175
Arg Thr Ser Thr His Pro Glu Ser Thr
            180                 185


<210> 162
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-28A C2 mutant for expression in E. coli

<221> CDS
<222> (1)...(528)

<221> variation
<222> (146)...(147)
<223> n = A, T, G or C

<400> 162
atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt      48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
```

```
tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct    96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
             20                  25                  30

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac    144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
         35                  40                  45

dnn cgt tgc cac tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag    192
Xaa Arg Cys His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
     50                  55                  60

ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg    240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt    288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                 85                  90                  95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag    336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt    384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa    432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt    480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt    528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175
```

<210> 163
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-28A C2 mutant for expression in E. coli

<221> VARIANT
<222> (49)...(49)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 163

```
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
           20                   25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
```

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


<210> 164
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-28A C3 mutant for expression in E. coli

<221> CDS
<222> (1)...(528)

<221> variation
<222> (152)...(153)
<223> n = A, T, G or C

<400> 164
atg gtt ccg gtt gct cgt ctg cac ggt gct ctg ccg gac gct cgt ggt   48
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct   96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
             20                  25                  30

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac   144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
         35                  40                  45

tgc cgt dnn cac tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag   192
Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
     50                  55                  60

ctg cag gtt cgt gaa cgt ccg atg gct ctg gaa gct gaa ctg gct ctg   240
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acc ctg aaa gtt ctg gaa gct acc gct gac acc gac ccg gct ctg gtt   288
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                 85                  90                  95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag   336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
```

```
            100                 105                 110

ttc cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt      384
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggt cgt ctg cac cac tgg ctg tac cgt ctg cag gaa gct ccg aaa aaa      432
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt      480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt      528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175



<210> 165
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-28A C3 mutant for expression in E. coli

<221> VARIANT
<222> (51)...(51)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 165
Met Val Pro Val Ala Arg Leu His Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Cys Arg Xaa His Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Met Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Thr Ala Asp Thr Asp Pro Ala Leu Val
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Phe Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Tyr Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 166
<211> 528
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Human IL-28B C2 mutant for expression in E. coli

<221> CDS
<222> (1)...(528)

<221> variation
<222> 146, 147, 264
<223> n = A, T, G or C

<400> 166
atg gtt ccg gtt gct cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt      48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                  10                  15

tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct      96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac     144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45

dnn aaa tgc cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag     192
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60

ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg     240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt     288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
                 85                  90                  95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag     336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ctg cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt     384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa     432
Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt     480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt     528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 167
<211> 176
<212> PRT
```

<213> Artificial Sequence

<220>
<223> Human IL-28B C2 mutant for expression in E. coli

<221> VARIANT
<222> (49)...(49)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT
<222> (88)...(88)
<223> Xaa = Thr or Ser

<221> VARIANT
<222> (136)...(136)
<223> Xaa = His or Tyr

```
<400> 167
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Xaa Lys Cys Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175
```

<210> 168
<211> 528
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-28B C3 mutant for expression in E. coli

<221> CDS
<222> (1)...(528)

<221> variation
<222> 152, 153, 264
<223> n = A, T, G or C

```
<400> 168
atg gtt ccg gtt gct cgt ctg cgt ggt gct ctg ccg gac gct cgt ggt    48
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
 1               5                   10                  15
```

```
tgc cac atc gct cag ttc aaa tct ctg tct ccg cag gaa ctg cag gct    96
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
             20                  25                  30

ttc aaa cgt gct aaa gac gct ctg gaa gaa tct ctg ctg ctg aaa gac    144
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
         35                  40                  45

tgc aaa dnn cgt tct cgt ctg ttc ccg cgt acc tgg gac ctg cgt cag    192
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
     50                  55                  60

ctg cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg    240
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
 65                  70                  75                  80

acc ctg aaa gtt ctg gaa gct wsn gct gac acc gac ccg gct ctg ggt    288
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
                 85                  90                  95

gac gtt ctg gac cag ccg ctg cac acc ctg cac cac atc ctg tct cag    336
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110

ctg cgt gct tgc atc cag ccg cag ccg acc gct ggt ccg cgt acc cgt    384
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125

ggt cgt ctg cac cac tgg ctg yay cgt ctg cag gaa gct ccg aaa aaa    432
Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140

gaa tct ccg ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt    480
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160

ctg ctg acc cgt gac ctg aac tgc gtt gct tct ggt gac ctg tgc gtt    528
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 169
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-28B C3 mutant for expression in E. coli

<221> VARIANT
<222> (51)...(51)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT
<222> (88)...(88)
<223> Xaa = Thr or Ser

<221> VARIANT
<222> (136)...(136)
```

```
<223> Xaa = His or Tyr

<400> 169
Met Val Pro Val Ala Arg Leu Arg Gly Ala Leu Pro Asp Ala Arg Gly
1               5                   10                  15
Cys His Ile Ala Gln Phe Lys Ser Leu Ser Pro Gln Glu Leu Gln Ala
            20                  25                  30
Phe Lys Arg Ala Lys Asp Ala Leu Glu Glu Ser Leu Leu Leu Lys Asp
        35                  40                  45
Cys Lys Xaa Arg Ser Arg Leu Phe Pro Arg Thr Trp Asp Leu Arg Gln
    50                  55                  60
Leu Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu
65                  70                  75                  80
Thr Leu Lys Val Leu Glu Ala Xaa Ala Asp Thr Asp Pro Ala Leu Gly
                85                  90                  95
Asp Val Leu Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln
            100                 105                 110
Leu Arg Ala Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Thr Arg
        115                 120                 125
Gly Arg Leu His His Trp Leu Xaa Arg Leu Gln Glu Ala Pro Lys Lys
    130                 135                 140
Glu Ser Pro Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg
145                 150                 155                 160
Leu Leu Thr Arg Asp Leu Asn Cys Val Ala Ser Gly Asp Leu Cys Val
                165                 170                 175


<210> 170
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-29 C1 mutant for expression in E. coli

<221> CDS
<222> (1)...(549)

<221> variation
<222> 33, 47, 48, 57
<223> n = A, T, G or C

<400> 170
atg ggt ccg gtt ccg acc tct aaa cca acc mcn act ggt aaa ggt dnn     48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa
1               5                   10                  15

cac atc grn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc     96
His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg     144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg     192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc     240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
```

```
 65                  70                  75                  80

ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg     288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95

gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct     336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg     384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct     432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc     480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cgt gat ctg aaa tac gtt gct gat ggt ray ctg tgc ctg cgt acc tct     528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Cys Leu Arg Thr Ser
                165                 170                 175

acc cat ccg gaa tct acc taa                                         549
Thr His Pro Glu Ser Thr  *
            180
```

<210> 171
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-29 C1 mutant for expression in E. coli

<221> VARIANT
<222> (11)...(11)
<223> Xaa = Thr or Pro

<221> VARIANT
<222> (16)...(16)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<221> VARIANT
<222> (19)...(19)
<223> Xaa = Gly or Asp

<221> VARIANT
<222> (170)...(170)
<223> Xaa = Asn or Asp

<400> 171

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Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Xaa
 1               5                  10                  15
His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
```

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


<210> 172
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-29 C5 mutant for expression in E. coli

<221> CDS
<222> (1)...(549)

<221> variation
<222> 33, 57, 515, 516
<223> n = A, T, G or C

<400> 172
atg ggt ccg gtt ccg acc tct aaa cca acc mcn act ggt aaa ggt tgc      48
Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Cys
 1               5                  10                  15

cac atc grn cgt ttc aaa tct ctg tct ccg cag gaa ctg gct tct ttc      96
His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
            20                  25                  30

aaa aaa gct cgt gac gct ctg gaa gaa tct ctg aaa ctg aaa aac tgg     144
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
        35                  40                  45

tct tgc tct tct ccg gtt ttc ccg ggt aac tgg gat ctg cgt ctg ctg     192
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60

cag gtt cgt gaa cgt ccg gtt gct ctg gaa gct gaa ctg gct ctg acc     240
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
 65                  70                  75                  80

ctg aaa gtt ctg gaa gct gct gca ggt cct gct ctg gaa gat gtt ctg     288
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
                 85                  90                  95
```

```
gat cag ccg ctg cac act ctg cac cac atc ctg tct cag ctg cag gct      336
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
            100                 105                 110

tgc att caa ccg caa ccg acc gct ggt ccg cgt ccg cgt ggt cgt ctg      384
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
        115                 120                 125

cac cac tgg ctg cat cgt ctg cag gaa gct ccg aaa aaa gaa tct gct      432
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
    130                 135                 140

ggt tgc ctg gaa gct tct gtt acc ttc aac ctg ttc cgt ctg ctg acc      480
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145                 150                 155                 160

cgt gat ctg aaa tac gtt gct gat ggt ray ctg dnn ctg cgt acc tct      528
Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Xaa Leu Arg Thr Ser
                165                 170                 175

acc cat ccg gaa tct acc taa                                          549
Thr His Pro Glu Ser Thr  *
            180
```

<210> 173
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-29 C5 mutant for expression in E. coli

<221> VARIANT
<222> (11)...(11)
<223> Xaa = Thr or Pro

<221> VARIANT
<222> (19)...(19)
<223> Xaa = Gly or Asp

<221> VARIANT
<222> (170)...(170)
<223> Xaa = Asp or Asn

<221> VARIANT
<222> (172)...(172)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 173

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Met Gly Pro Val Pro Thr Ser Lys Pro Thr Xaa Thr Gly Lys Gly Cys
 1               5                  10                  15
His Ile Xaa Arg Phe Lys Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe
        20                  25                  30
Lys Lys Ala Arg Asp Ala Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp
    35                  40                  45
Ser Cys Ser Ser Pro Val Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu
    50                  55                  60
Gln Val Arg Glu Arg Pro Val Ala Leu Glu Ala Glu Leu Ala Leu Thr
65                  70                  75                  80
Leu Lys Val Leu Glu Ala Ala Ala Gly Pro Ala Leu Glu Asp Val Leu
```

85 90 95
Asp Gln Pro Leu His Thr Leu His His Ile Leu Ser Gln Leu Gln Ala
100 105 110
Cys Ile Gln Pro Gln Pro Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu
115 120 125
His His Trp Leu His Arg Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala
130 135 140
Gly Cys Leu Glu Ala Ser Val Thr Phe Asn Leu Phe Arg Leu Leu Thr
145 150 155 160
Arg Asp Leu Lys Tyr Val Ala Asp Gly Xaa Leu Xaa Leu Arg Thr Ser
165 170 175
Thr His Pro Glu Ser Thr
180

<210> 174
<211> 531
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-29 d2/7 C5 mutant for expression in E. coli

<221> CDS
<222> (1)...(531)

<221> variation
<222> (497)...(498)
<223> n = A, T, G or C

<400> 174
atg aaa cca acc acc act ggt aaa ggt tgc cac atc ggt cgt ttc aaa 48
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
1 5 10 15

tct ctg tct ccg cag gaa ctg gct tct ttc aaa aaa gct cgt gac gct 96
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
20 25 30

ctg gaa gaa tct ctg aaa ctg aaa aac tgg tct tgc tct tct ccg gtt 144
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
35 40 45

ttc ccg ggt aac tgg gat ctg cgt ctg ctg cag gtt cgt gaa cgt ccg 192
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
50 55 60

gtt gct ctg gaa gct gaa ctg gct ctg acc ctg aaa gtt ctg gaa gct 240
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
65 70 75 80

gct gca ggt cct gct ctg gaa gat gtt ctg gat cag ccg ctg cac act 288
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
85 90 95

ctg cac cac atc ctg tct cag ctg cag gct tgc att caa ccg caa ccg 336
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
100 105 110

acc gct ggt ccg cgt ccg cgt ggt cgt ctg cac cac tgg ctg cat cgt 384

```
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
        115                 120                 125

ctg cag gaa gct ccg aaa aaa gaa tct gct ggt tgc ctg gaa gct tct      432
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
    130                 135                 140

gtt acc ttc aac ctg ttc cgt ctg ctg acc cgt gat ctg aaa tac gtt      480
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
145                 150                 155                 160

gct gat ggt aac ctg dnn ctg cgt acc tct acc cat ccg gaa tct acc      528
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
                165                 170                 175

taa                                                                  531
 *



<210> 175
<211> 176
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-29 d2/7 C5 mutant for expression in E.
      coli

<221> VARIANT
<222> (166)...(166)
<223> Xaa = Ser, Ala, Thr, Val or Asn

<400> 175
Met Lys Pro Thr Thr Thr Gly Lys Gly Cys His Ile Gly Arg Phe Lys
 1               5                  10                  15
Ser Leu Ser Pro Gln Glu Leu Ala Ser Phe Lys Lys Ala Arg Asp Ala
            20                  25                  30
Leu Glu Glu Ser Leu Lys Leu Lys Asn Trp Ser Cys Ser Ser Pro Val
        35                  40                  45
Phe Pro Gly Asn Trp Asp Leu Arg Leu Leu Gln Val Arg Glu Arg Pro
    50                  55                  60
Val Ala Leu Glu Ala Glu Leu Ala Leu Thr Leu Lys Val Leu Glu Ala
65                  70                  75                  80
Ala Ala Gly Pro Ala Leu Glu Asp Val Leu Asp Gln Pro Leu His Thr
                85                  90                  95
Leu His His Ile Leu Ser Gln Leu Gln Ala Cys Ile Gln Pro Gln Pro
            100                 105                 110
Thr Ala Gly Pro Arg Pro Arg Gly Arg Leu His His Trp Leu His Arg
        115                 120                 125
Leu Gln Glu Ala Pro Lys Lys Glu Ser Ala Gly Cys Leu Glu Ala Ser
    130                 135                 140
Val Thr Phe Asn Leu Phe Arg Leu Leu Thr Arg Asp Leu Lys Tyr Val
145                 150                 155                 160
Ala Asp Gly Asn Leu Xaa Leu Arg Thr Ser Thr His Pro Glu Ser Thr
                165                 170                 175
```