(YTE) or Met428Leu, Asn434Ser (LS) which enhance FcRn binding are boxed, in bold text, and shaded in grey. While these examples include a hinge sequence and/or a linker sequence, fusion proteins of the invention can be made using any hinge sequence and/or a linker sequence suitable in length and/or flexibility. Alternatively fusion proteins can be made without using a hinge and/or a linker sequence. For example, the polypeptide components can be directly attached.

~~**[00131]** An exemplary SLPI-Fc fusion protein is the SLPI-hFc. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 2), the WAP domain is underlined, and the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7).~~

~~**SLPI-hFc1 (human IgG1 Fc, long Hinge) (SEQ ID NO:16)**~~
~~**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA**EPKSCDKTHTCPPCP *APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK* **(SEQ ID NO:16)**~~

~~**[00132]** An exemplary SLPI-Fc fusion protein is the SLPI-hFc2 (human IgG2 Fc, long Hinge). As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 2), the WAP domain is underlined, and the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 8).~~

~~**SLPI hFc2 (human IgG2 Fc, long Hinge) (SEQ ID NO:17)**~~
~~**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA**ERKCCVECPPCPAPP *VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ FNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK* (SEQ ID NO:17)~~

~~**[00133]** An exemplary SLPI-Fc fusion protein is the SLPI-ML-hFc1. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO:~~

39), the WAP domain is underlined, the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7), and Met98Leu (ML) mutation in SLPI is boxed.

SLPI-ML-hFc1 (human IgG1 Fc, Met98Leu) (SEQ ID NO:18)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP

GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP

REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP

PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD

KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK **(SEQ ID NO:18)**

[00134] An exemplary SLPI-Fc fusion protein is the SLPI-hFc1-YTE. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 39), the WAP domain is underlined, the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 40), and the Fc mutations Met252Tyr, Ser254Thr, Thr256Glu (YTE) are boxed, in bold text, and shaded in grey.

SLPI-hFc1-YTE (human IgG1 Fc, Met252Tyr, Ser254Thr, Thr256Glu) (SEQ ID NO:19)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP

GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP

APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP

REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP

PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD

KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK **(SEQ ID NO:19)**

[00135] An exemplary SLPI-Fc fusion protein is the SLPI-hFc1-LS. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 39), the WAP domain is underlined, the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 41), and Met428Leu, Asn434Ser (LS) which enhance FcRn binding are boxed, in bold text, and shaded in grey.

SLPI-hFc1-LS (human IgG1 Fc, Met428Leu, Asn434Ser)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP
GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHSHYTQKSLSLSPGK **(SEQ ID NO:20)**

[00136] An exemplary Elafin-Fc fusion protein is the Elafin-hFc1. As shown below, the Elafin polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 5), the WAP domain is underlined, the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 41), and the Asn434Ser (LS) which enhance FcRn binding are boxed, in bold text, and shaded in grey.

Elafin-hFc1 (human IgG1)

AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRC
AMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQEPKSCDKTHTCPPC*PAPELLGGPSVFL*
FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHSHYTQKSLSLSPGK **(SEQ ID NO:21)**

[00137] An exemplary SPLI-Fc fusion protein is the SLPI-hFc1-SLPI. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 39), the WAP domain is underlined, and the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7).

SLPI-hFc1-SLPI (human IgG1)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP
GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
*KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYK**

KPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMD GQCKRDLKCCMGLCGKSCVSPVKA (SEQ ID NO:22)

[00138] An exemplary Elafin-Fc fusion protein is the Elafin-hFc1-Elafin. As shown below, the Elafin polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 5), the WAP domain is underlined, and the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7).

Elafin-hFc1-Elafin (human IgG1)

AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRC AMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ*EPKSCDKTHTCPPCPAPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK***ASTGSAVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQ DKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ** (SEQ ID NO:23)

[00139] An exemplary Elafin-Fc fusion protein is the Elafin-hFc1-SLPI. As shown below, the SLPI polypeptide (SEQ ID NO: 39) portion of the fusion protein is shown in bold, with the WAP domain underlined, the Elafin (SEQ ID NO: 5) polypeptide portion of the fusion protein is shown in bold and italics, the WAP domain is underlined, the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7).

Elafin-hFc1-SLPI (human IgG1)

AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRC AMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQEPKSCDKTHTCPPCP*APELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPG KKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMG LCGKSCVSPVKA** (SEQ ID NO:24)

~~[00140] An exemplary SLPI-Fc fusion protein is the SLPI-hFc1-Elafin. As shown below, the SLPI (SEQ ID NO: 39) portion of the fusion protein is shown in bold, with the WAP domain underlined, the Elafin (SEQ ID NO: 5) polypeptide portion of the fusion protein is shown in bold and italics, the WAP domain is underlined, and the IgG Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7).~~

~~**SLPI-hFc1-Elafin (human IgG1)**~~

~~**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGLCGKSCVSPVKA***EPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKASTGS**AVTGVPVKGQDTVKGRVPFNGQ DPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCC EGSCGMACFVPQ*~~ ~~(SEQ ID NO:25)~~

[00141] These exemplary SLPI-Fc and Elafin-Fc fusion proteins were made using the following techniques.

[00142] The genes encoding human SLPI and Elafin were PCR amplified from human spleen cDNA (Zyagen). Specific point mutations within the gene encoding SLPI, Elafin or the Fc region were generated by overlapping PCR. The SLPI or Elafin encoding gene was cloned in frame with a gene encoding the hinge region, followed by a CH2 domain, and a CH3 domain of human IgG1, IgG2, IgG3, IgG4, or IgM into a mammalian expression vector, containing a mammalian secretion signal sequence up stream of the SLPI or Elafin gene insertion site. In some cases, these vectors were further modified, wherein the gene encoding a linker sequence and either SLPI or Elafin was cloned in frame to the 3' end of the CH3 domain, to generate SLPI-Fc-SLPI, Elafin-Fc-Elafin, SLPI-Fc-Elafin, or Elafin-Fc-SLPI. These expression vectors were transfected into mammalian cells (specifically HEK293 or CHO cells) and grown for several days in 8% CO_2 at 37° C. The recombinant SLPI-Fc and Elafin-Fc fusion proteins were purified from the expression cell supernatant by protein A chromatography. Figure 1B shows a reducing SDS-PAGE gel of the Elafin-Fc (SEQ ID NO:21, lane 1) and SLPI-Fc (SEQ ID NO:16, lane 2) fusion

*VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQC PGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCC MGMCGKSCVSPVKA** (SEQ ID NO: 29)

~~[00151] An exemplary SLPI-TNFα Targeting Molecule fusion protein is TNFR2-ECD-Fc1-SLPI$(G_3S)_2$ Linker. As shown below, the SLPI polypeptide portion of the fusion protein is in bold text, (SEQ ID NO: 2), the WAP domain is underlined, the Fc polypeptide portion is italicized (SEQ ID NO: 47), and the TNFR2-ECD is shaded in grey and in bold text (SEQ ID NO: 46).~~

~~**TNFR2-ECD-Fc1-SLPI$(G_3S)_2$ Linker**~~

~~**LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTY TQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSP TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD**EPKSCDKTH ~~TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVH NAKTKPREQQYNSTYRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK~~GGGSGGGS**~~SGKSFKAGVCPPK KSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLML NPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA~~** ~~(SEQ ID NO: 30)~~

~~[00152] An exemplary SLPI-TNFα Targeting Molecule fusion protein is TNFR2-ECD-Fc1-SLPI ASTGS Linker. As shown below, the SLPI polypeptide portion of the fusion protein is in bold text (SEQ ID NO: 2), the WAP domain is underlined, the Fc polypeptide portion is italicized (SEQ ID NO: 47), and the TNFR2-ECD is shaded in grey and in bold text (SEQ ID NO: 46).~~

~~**TNFR2-ECD-Fc1-SLPI ASTGS Linker**~~

~~**LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTY TQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSP TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD**EPKSCDKTH

~~TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVH~~
~~NAKTKPREQQYNSTYRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKAKGQPREP~~
~~QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY~~
~~SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK~~**~~ASTGSSGKSFKAGVCPPKKSA~~**
~~QCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNP~~~~TRRKPGKCPVTYGQCLMLNPP~~
~~NFCEMDGQCKRDLKCCMGMCGKSCVSPVKA~~ ~~(SEQ ID NO: 31)~~

[00153] These exemplary SLPI-TNFα targeting molecule fusion proteins were made using the following techniques.

[00154] The genes encoding the variable heavy (VH) and variable kappa (VK) regions of the anti-TNFα antibody, D2E7, were generated by gene synthesis. The D2E7-VH gene was cloned in frame with a gene encoding a human IgG1 antibody heavy chain constant region, consisting of a CH1 domain, a hinge domain, a CH2 domain, and a CH3 domain, into a mammalian expression vector, containing a mammalian secretion signal sequence up stream of the VH domain insertion site (D2E7-HC). The D2E7-VK gene was cloned in frame with a human antibody kappa light chain constant (CL) domain, into a mammalian expression vector, containing a mammalian secretion signal sequence up stream of the VK domain insertion site (D2E7-LC). The SLPI encoding gene and the adjacent 5' linker sequence were cloned in frame into the 3' end of either, the CH3 domain of the D2E7 heavy chain gene (D2E7-HC-SLPI), or the CL domain of the D2E7 light chain gene (D2E7-LC-SLPI) coding sequences in the above described mammalian expression vectors. The extracellular domain of the TNFα Receptor 2 (TNFR2-ECD) was generated by gene synthesis and cloned in frame with a gene encoding the hinge region, followed by a CH2 domain and a CH3 domain of human IgG1 (hFc1) into a mammalian expression, containing a mammalian secretion signal sequence up stream of the TNFR2-ECD insertion site. The SLPI encoding gene and the adjacent 5' linker sequence were cloned in frame into the 3' end of the gene encoding TNFR2-ECD-hFc1 into a mammalian expression vector (TNFR2-ECD-hFc1-SLPI).

[00155] The D2E7-HC-SLPI expression vector was co-transfected with either the D2E7-LC or the D2E7-LC-SLPI expression vector into mammalian cells (specifically HEK293 or CHO cells) to generate the D2E7 antibody with SLPI fused to the C-terminus of the heavy chain or to the C-terminus of both the heavy chain and light chain, respectively.

[00159] An exemplary AAT-Fc-SLPI fusion protein is AAT-hFc1-SLPI (human IgG1 Fc). As shown below, the AAT polypeptide portion of the fusion protein is shown in bold text and shaded in grey (SEQ ID NO: 13), the Fc portion is italicized (SEQ ID NO: 7), the SLPI portion is in bold text (SEQ ID NO: 2), and the WAP domain containing polypeptide is underlined (SEQ ID NO: 3).

AAT-hFc1-SLPI (human IgG1 Fc)

EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAF
AMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSE
GLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDTVFA
LVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKY
LGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQ
LGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKF
NKPFVFLMIEQNTKSPLFMGKVVNPTQKEPKSCDKTHTCPPC*PAPELLGGPSVFLFPPKPK*
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
*LHNHYTQKSLSLSPGK**ASTGSS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCP*
DTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSC
VSPVKA (SEQ ID NO: 32)

[00160] An exemplary AAT-Fc-Elafin fusion protein is AAT-hFc1-Elafin. As shown below, the AAT polypeptide portion of the fusion protein is shown in bold text and shaded in grey (SEQ ID NO: 13), the Fc portion is italicized (SEQ ID NO: 7), the Elafin portion are in bold text (SEQ ID NO: 5), and the WAP domain containing polypeptide is underlined (SEQ ID NO: 6).

AAT-hFc1-Elafin (human IgG1 Fc)

EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAF
AMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSE
GLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDTVFA
LVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKY
LGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQ

~~LGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKF NKPFVFLMIEQNTKSPLFMGKVVNPTQK~~EPKSCDKTHTCPPC*PAPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK***ASTGS***AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQ EPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ~~ (SEQ ID NO: 33)

[00161] The genes encoding the SLPI and Elafin were PCR amplified from human spleen cDNA (Zyagen). These genes and flanking linker sequences were cloned in frame into mammalian expression vectors containing the genes encoding AAT and an Ig Fc region, wherein a mammalian secretion precedes the AAT gene. These expression vectors were transfected into mammalian cells (specifically HEK293 or CHO cells) and grown for several days in 8% CO_2 at 37° C. The recombinant AAT-Fc-WAP domain fusion proteins were purified from the expression cell supernatant by protein A chromatography. A near neutral pH buffer was used (Gentle Ag/Ab Elution Buffer, Thermo Scientific) to elute the AAT-Fc-WAP domain fusion protein from the protein A resin. Figure 3B shows a reducing SDS-PAGE gel of the purified fusion proteins: AAT-Fc-Elafin (SEQ ID NO: 33, lane 1) and AAT-Fc-SLPI (SEQ ID NO: 32, lane 2).

[00162] The purified AAT-Fc-WAP domain fusion proteins were tested for activity by determining their ability to inhibit neutrophil elastase. Human serum derived AAT (sdAAT) was used as a positive control in these assays. (Figure 3C). Relative to serum derived AAT, the AAT-Fc-WAP targeting molecule fusion proteins display enhanced potency of NE inhibition of neutrophil elastase. NE inhibition assays were conducted as described above.

Example 4 SLPI-Albumin and Elafin-Albumin

[00163] The studies presented herein describe several, non-limiting examples of recombinant AAT derivatives comprising human SLPI fused an albumin polypeptide. These examples are provided below to further illustrate different features of the present invention. The examples also illustrate useful methodology for practicing the invention. These examples do not and are not intended to limit the claimed invention. The AAT portion is in

What is claimed is:

1. An isolated fusion protein comprising at least one human whey acidic protein (WAP) domain-containing polypeptide operably linked to a second polypeptide, wherein the second polypeptide comprises at least one the following:

an immunoglobulin Fc polypeptide or an amino acid sequence that is derived from an immunoglobulin Fc polypeptide;

a cytokine targeting polypeptide or a sequence derived from a cytokine targeting polypeptide;

a serpin polypeptide or a sequence derived from a serpin polypeptide; or

an albumin polypeptide or an amino acid sequence that is derived from a serum albumin polypeptide.

2. An isolated fusion protein comprising at least one human secretory leukocyte proteinase inhibitor (SLPI) polypeptide operably linked to a second polypeptide, wherein the second polypeptide comprises at least one of the following:

an immunoglobulin Fc polypeptide;

a cytokine targeting polypeptide;

an alpha-1 antitrypsin (AAT) polypeptide;

an alpha-1 antitrypsin (AAT) polypeptide and an immunoglobulin Fc polypeptide; and

a human albumin (HSA) polypeptide.

3. An isolated fusion protein comprising human at least one human Elafin polypeptide operably linked to a second polypeptide, wherein the second polypeptide comprises at least one of the following:

an immunoglobulin Fc polypeptide;

a cytokine targeting polypeptide;

an alpha-1 antitrypsin (AAT) polypeptide;

an alpha-1 antitrypsin (AAT) polypeptide and an immunoglobulin Fc polypeptide; and

an human albumin (HSA) polypeptide.

4. The isolated fusion protein of claim 2, wherein the human SLPI polypeptide is a full-length SLPI polypeptide or derived from a human SLPI polypeptide.

5. The isolated fusion protein of any one of claims 2-4, wherein SLPI polypeptide comprises an amino acid sequence selected the group consisting of SEQ ID NO: 1, 2, and 3.

6. The isolated fusion protein of claim 3, wherein the human Elafin polypeptide is a full-length Elafin polypeptide or derived from a human Elafin polypeptide.

7. The isolated fusion protein of any one of claims 3 and 6, wherein Elafin polypeptide comprises an amino acid sequence selected the group consisting of SEQ ID NO: 4, 5, and 6.

8. The isolated fusion protein of any one of claims 1-6, wherein the immunoglobulin Fc polypeptide is a human Fc polypeptide.

9. The isolated fusion protein of claim 8, wherein human Fc polypeptide is a human IgM polypeptide or a human IgG polypeptide.

10. The isolated fusion protein of claim 9, wherein the human IgG Fc polypeptide is a human IgG1 polypeptide, a human IgG2 Fc polypeptide, human IgG3 Fc polypeptide, or human IgG4 Fc polypeptide.

11. The isolated fusion protein of any one of claims 1-3, wherein the immunoglobulin Fc polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, and 11.

12. The isolated fusion protein of claim 1, wherein the WAP domain containing polypeptide and the immunoglobulin Fc polypeptide are operably linked via a hinge region, a linker region, or both a hinge region and linker region.

13. The isolated fusion protein of any one of claims 2-4, wherein the SLPI polypeptide and the immunoglobulin Fc polypeptide are operably linked via a hinge region, a linker region, or both a hinge region and linker region.

14. The isolated fusion protein of any one of claims 3 or 6, wherein the Elafin polypeptide and the immunoglobulin Fc polypeptide are operably linked via a hinge region, a linker region, or both a hinge region and linker region.

15. The isolated fusion protein of any one of claims 12-14, wherein the hinge region, the linker region or both the hinge region and the linker region comprise a peptide sequence.

16. The isolated fusion protein of claim 1, wherein the albumin polypeptide is a human serum albumin (HSA) polypeptide or is derived from a HSA polypeptide.

17. The isolated fusion protein of any one of claims 2, 3 or 16, wherein the HSA polypeptide comprises the amino acid sequence of SEQ ID NO: 14 or the amino acid sequence of SEQ ID NO: 15.

18. The isolated fusion protein of any one of claims 2, 3 or 16, wherein the HSA polypeptide comprises domain 3 of HSA.

19. The isolated fusion protein of claim 1, wherein the WAP-domain containing polypeptide is operably linked to HSA via an albumin binding polypeptide.

20. The isolated fusion protein of claim 19, wherein the albumin binding polypeptide is an antibody or antibody fragment or derived from an antibody or antibody fragment.

21. The isolated fusion protein of claims 20, wherein the antibody or antibody fragment or chimeric, humanized, or fully human.

22. The isolated fusion protein of claims 19, wherein the albumin binding polypeptide is a peptide.

23. The isolated fusion protein of claim 19, wherein the albumin binding polypeptide is Domain 3 of *Streptococcal* Protein G or a sequence derived from Domain 3 of *Streptococcal* Protein G.

24. The isolated fusion protein of claim 1, wherein the WAP-domain containing polypeptide is covalently linked to a HSA polypeptide.

25. The isolated fusion protein of claim 1, wherein the WAP-domain containing polypeptide is non-covalently linked to a HSA polypeptide.

26. The isolated fusion protein of claim 1, claim 2, or claim 3, wherein the cytokine targeting polypeptide is a cytokine receptor polypeptide or a derivative of a cytokine receptor polypeptide, a cytokine targeting polypeptide that binds a cytokine receptor, or a cytokine targeting polypeptide binds a human cytokine.

27. The isolated fusion protein of claim 26, wherein the cytokine receptor is a human cytokine receptor polypeptide.

28. The isolated fusion protein of claim 27, wherein the human cytokine receptor polypeptide comprises of multiple subunits.

29. The isolated fusion protein of claim 27, wherein the human cytokine receptor is a receptor for TNFα, IgE, IL-12, IL-23, IL-6, IL-1α, IL-1β, IL-17, IL-13, the p40 subunit of IL-12 and IL-23, IL-4, IL-10, IL-2, IL-18, IL-27, or IL-32.

30. The isolated fusion protein of claim 26, wherein the cytokine targeting polypeptide is an antibody or an antibody fragment.

31. The isolated fusion protein of claim 30, wherein the antibody is chimeric, humanized, or fully human.

32. The isolated fusion protein of claim 26, wherein the human cytokine is TNFα, IgE, IL-12, IL-23, IL-6, IL-1α, IL-1β, IL-17, IL-13, the p40 subunit of IL-12 and IL-23, IL-4, IL-10, IL-2, IL-18, IL-27, or IL-32.

33. The isolated fusion protein of claim 32, wherein the cytokine is human TNFα.

34. The isolated fusion protein of claim 2 or claim 3, wherein AAT polypeptide comprises the amino acid sequence of SEQ ID NO: 13 or SEQ ID NO: 38.

35. The isolated fusion protein of claim 1, wherein the fusion protein comprises a serpin polypeptide, a WAP domain-containing polypeptide and an immunoglobulin Fc polypeptide such that at least two of the serpin polypeptide, the WAP domain-containing polypeptide and the immunoglobulin Fc polypeptide are operably linked via a hinge region, a linker region, or both a hinge region and linker region.

36. The isolated fusion protein of claim 2, wherein the fusion protein comprises an AAT polypeptide, a SLPI polypeptide and an immunoglobulin Fc polypeptide such that at least two of the AAT polypeptide, the SLPI polypeptide and the immunoglobulin Fc polypeptide are operably linked via a hinge region, a linker region, or both a hinge region and linker region.

37. The isolated fusion protein of claim 35 or claim 36, wherein the hinge region, the linker region or both the hinge region and the linker region comprise a peptide sequence.

38. The isolated fusion protein of any one of claim 1, claim 2 or claim 3, wherein the Fc polypeptide is modified to enhance FcRn binding.

39. The isolated fusion protein of any one of claims 1-3, wherein the immunoglobulin Fc polypeptide comprising at least one of the following mutations: Met252Tyr, Ser254Thr, Thr256Glu or Met428Leu and Asn434Ser.

40. The isolated fusion protein of any one of claims 1-3, where the fusion protein comprises an amino acid sequence selected from SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28,

and SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, and SEQ ID NO: 37.

41. A method of treating or alleviating a symptom of a disease or disorder associated with aberrant serine protease expression or activity in a subject in need thereof, the method comprising administering a fusion protein according to any one of the previous claims.

42. A method of treating or alleviating a symptom of an inflammatory disease or disorder in a subject in need thereof, the method comprising administering a fusion protein according to any one of the previous claims.

43. A method of treating or alleviating a symptom of an infectious disease or disorder in a subject in need thereof, the method comprising administering a fusion protein according to any one of the previous claims.

44. The method of any one of claims 41-43, wherein the subject is a human.

[00131] An exemplary SLPI-Fc fusion protein is the SLPI-hFc. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 2), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 48), and the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7).

SLPI-hFc1 (human IgG1 Fc, long Hinge) (SEQ ID NO:16)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCE
MDGQCKRDLKCCMGMCGKSCVSPVKAEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED*
PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
*HNHYTQKSLSLSPGK***(SEQ ID NO:16)**

[00132] An exemplary SLPI-Fc fusion protein is the SLPI-hFc2 (human IgG2 Fc, long Hinge). As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 2), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 49), and the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 8).

SLPI-hFc2 (human IgG2 Fc, long Hinge) (SEQ ID NO:17)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCE
MDGQCKRDLKCCMGMCGKSCVSPVKAERKCCVECPPCP*APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQ*
FNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK (SEQ ID NO:17)

[00133] An exemplary SLPI-Fc fusion protein is the SLPI-ML-hFc1. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 39), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 48), the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7), and Met98Leu (ML) mutation in SLPI is boxed.

SLPI-ML-hFc1 (human IgG1 Fc, Met98Leu) (SEQ ID NO:18)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCE
MDGQCKRDLKCCMG[L]CGKSCVSPVKAEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED*
PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK **(SEQ ID NO:18)**

[00134] An exemplary SLPI-Fc fusion protein is the SLPI-hFc1-YTE. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 39), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 48), the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 40), and the Fc mutations Met252Tyr, Ser254Thr, Thr256Glu (YTE) are boxed, in bold text, and shaded in grey.

SLPI-hFc1-YTE (human IgG1 Fc, Met252Tyr, Ser254Thr, Thr256Glu) (SEQ ID NO:19)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCE
MDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHE*
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK **(SEQ ID NO:19)**

[00135] An exemplary SLPI-Fc fusion protein is the SLPI-hFc1-LS. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 39), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 48), the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 41), and Met428Leu, Asn434Ser (LS) which enhance FcRn binding are boxed, in bold text, and shaded in grey.

SLPI-hFc1-LS (human IgG1 Fc, Met428Leu, Asn434Ser)
SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCE
MDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED*
PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEAL
HSHYTQKSLSLSPGK **(SEQ ID NO:20)**

[00136] An exemplary Elafin-Fc fusion protein is the Elafin-hFc1. As shown below, the Elafin polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 5), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 48), the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 41), and the Asn434Ser (LS) which enhance FcRn binding are boxed, in bold text, and shaded in grey.

Elafin-hFc1 (human IgG1)
AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKK
CCEGSCGMACFVPQEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV*
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSL
SPGK **(SEQ ID NO:21)**

[00137] An exemplary SLPI-Fc fusion protein is the SLPI-hFc1-SLPI. As shown below, the SLPI polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 39), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 48), the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7), and the ASTGS linker is shown in normal text (SEQ ID NO: 50).

SLPI-hFc1-SLPI (human IgG1)
SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCE
MDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED*
PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
*HNHYTQKSLSLSPGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKP**
GKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGLCGKSCVSPVKA(SEQ ID NO:22)

[00138] An exemplary Elafin-Fc fusion protein is the Elafin-hFc1-Elafin. As shown below, the Elafin polypeptide portion of the fusion protein is shown in bold (SEQ ID NO: 5), the WAP domain is underlined, the hinge region is shown in normal text (SEQ ID NO: 48), the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7), and the ASTGS linker is shown in normal text (SEQ ID NO: 50).

Elafin-hFc1-Elafin (human IgG1)

AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKK
CCEGSCGMACFVPQEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV*
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
*PGK*ASTGS**AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKD**
TDCPGIKKCCEGSCGMACFVPQ(SEQ ID NO:23)

[00139] An exemplary Elafin-Fc fusion protein is the Elafin-hFc1-SLPI. As shown below, the SLPI polypeptide (SEQ ID NO: 39) portion of the fusion protein is shown in bold, with the WAP domain underlined, the Elafin (SEQ ID NO: 5) polypeptide portion of the fusion protein is shown in bold and italics, the WAP domain is underlined, the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7), the hinge region is shown in normal text (SEQ ID NO: 48), and the ASTGS linker is shown in normal text (SEQ ID NO: 50).

Elafin-hFc1-SLPI (human IgG1)

AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKK
CCEGSCGMACFVPQEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV*
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
*PGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLM**
LNPPNFCEMDGQCKRDLKCCMGLCGKSCVSPVKA(SEQ ID NO:24)

[00140] An exemplary SLPI-Fc fusion protein is the SLPI-hFc1-Elafin. As shown below, the SLPI (SEQ ID NO: 39) portion of the fusion protein is shown in bold, with the WAP domain underlined, the Elafin (SEQ ID NO: 5) polypeptide portion of the fusion protein is shown in bold and italics, the WAP domain is underlined, and the IgG-Fc polypeptide portion of the fusion protein is italicized (SEQ ID NO: 7), the hinge region is shown in normal text (SEQ ID NO: 48), and the ASTGS linker is shown in normal text (SEQ ID NO: 50).

SLPI-hFc1-Elafin (human IgG1)

SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCE
MDGQCKRDLKCCMGLCGKSCVSPVKAEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED*
PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
*HNHYTQKSLSLSPGK*ASTGS***AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRC***
AMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ(SEQ ID NO:25)

VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF

*SCSVMHEALHNHYTQKSLSLSPGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQC**

PGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCC

MGMCGKSCVSPVKA (SEQ ID NO: 29)

[00151] An exemplary SLPI-TNFα Targeting Molecule fusion protein is TNFR2-ECD-Fc1-SLPI$(G_3S)_2$ Linker. As shown below, the SLPI polypeptide portion of the fusion protein is in bold text (SEQ ID NO: 2), the WAP domain is underlined, the Fc polypeptide portion is italicized (SEQ ID NO: 47), the TNFR2-ECD is shaded in grey and in bold text (SEQ ID NO: 46), the hinge region is shown in normal text (SEQ ID NO: 48), and the $(G_3S)_2$ linker is shown in normal text (SEQ ID NO: 51).

TNFR2-ECD-Fc1-SLPI$(G_3S)_2$ Linker

LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR

CSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSST

DICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG

STGDEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVHNAK*

TKPREQQYNSTYRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL

TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS

*LSPGK*GGGSGGGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKC**

PVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA (SEQ ID NO: 30)

[00152] An exemplary SLPI-TNFα Targeting Molecule fusion protein is TNFR2-ECD-Fc1-SLPI ASTGS Linker. As shown below, the SLPI polypeptide portion of the fusion protein is in bold text (SEQ ID NO: 2), the WAP domain is underlined, the Fc polypeptide portion is italicized (SEQ ID NO: 47), the TNFR2-ECD is shaded in grey and in bold text (SEQ ID NO: 46), the hinge region is shown in normal text (SEQ ID NO: 48), and the ASTGS linker is shown in normal text (SEQ ID NO: 50).

TNFR2-ECD-Fc1-SLPI ASTGS Linker

LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR

CSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSST

DICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG

STGDEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVHNAK*

TKPREQQYNSTYRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL

TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS

*LSPGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVT**

YGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA (SEQ ID NO: 31)

[00159] An exemplary AAT-Fc-SLPI fusion protein is AAT-hFc1-SLPI (human IgG1 Fc). As shown below, the AAT polypeptide portion of the fusion protein is shown in bold text and shaded in grey (SEQ ID NO: 13), the Fc portion is italicized (SEQ ID NO: 7), the SLPI portion is in bold text (SEQ ID NO: 2), the WAP domain containing polypeptide is underlined (SEQ ID NO: 3), the hinge region is shown in normal text (SEQ ID NO: 48), and the ASTGS linker is shown in normal text (SEQ ID NO: 50).

AAT-hFc1-SLPI (human IgG1 Fc)

EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEIL
EGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAK
KQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQH
CKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGI
TKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFM
GKVVNPTQKEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE*
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
*QKSLSLSPGK*ASTGS**SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPG**
KCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA(SEQ ID NO: 32)

[00160] An exemplary AAT-Fc-Elafin fusion protein is AAT-hFc1-Elafin. As shown below, the AAT polypeptide portion of the fusion protein is shown in bold text and shaded in grey (SEQ ID NO: 13), the Fc portion is italicized (SEQ ID NO: 7), the Elafin portion is in bold text (SEQ ID NO: 5), the WAP domain containing polypeptide is underlined (SEQ ID NO: 6), the hinge region is shown in normal text (SEQ ID NO: 48), and the ASTGS linker is shown in normal text (SEQ ID NO: 50).

AAT-hFc1-Elafin (human IgG1 Fc)

EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEIL
EGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAK
KQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQH
CKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGI
TKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFM
GKVVNPTQKEPKSCDKTHTCPPCP*APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE*
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
*QKSLSLSPGK*ASTGS**AVTGVPVKGQDTVKGRVPFNGQDPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCA**
MLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ(SEQ ID NO: 33)

SEQUENCE LISTING

<110> INHIBRX LLC
Timmer, John C.
Eckelman, Brendan P.
Guenther, Grant B.
Nguy, Peter L.
Chan, Henry
Deveraux, Quinn

<120> WAP DOMAIN FUSION POLYPEPTIDES AND METHODS OF USE THEREOF

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Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys
            100                 105                 110

Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser
        115                 120                 125

Pro Val Lys Ala
    130
```

<210> 2
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 2

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

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala
```

100 105

<210> 3
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 3

Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys Leu
1 5 10 15

Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys Arg
20 25 30

Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser Pro
35 40 45

Val Lys Ala
50

<210> 4
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 4

Met Arg Ala Ser Ser Phe Leu Ile Val Val Val Phe Leu Ile Ala Gly
1 5 10 15

Thr Leu Val Leu Glu Ala Ala Val Thr Gly Val Pro Val Lys Gly Gln
20 25 30

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

Gly Gln Val Ser Val Lys Gly Gln Asp Lys Val Lys Ala Gln Glu Pro
50 55 60

Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu
65 70 75 80

```
Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys Leu Lys Asp Thr
                85                  90                  95

Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser Cys Gly Met Ala
            100                 105                 110

Cys Phe Val Pro Gln
        115
```

<210> 5
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 5

```
Ala Val Thr Gly Val Pro Val Lys Gly Gln Asp Thr Val Lys Gly Arg
1               5                   10                  15

Val Pro Phe Asn Gly Gln Asp Pro Val Lys Gly Gln Val Ser Val Lys
            20                  25                  30

Gly Gln Asp Lys Val Lys Ala Gln Glu Pro Val Lys Gly Pro Val Ser
        35                  40                  45

Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala Met Leu
    50                  55                  60

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

Lys Cys Cys Glu Gly Ser Cys Gly Met Ala Cys Phe Val Pro Gln
                85                  90                  95
```

<210> 6
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 6

```
Val Ser Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala
1               5                  10                  15

Met Leu Asn Pro Pro Asn Arg Cys Leu Lys Asp Thr Asp Cys Pro Gly
            20                  25                  30

Ile Lys Lys Cys Cys Glu Gly Ser Cys Gly Met Ala Cys Phe Val Pro
        35                  40                  45

Gln
```

<210> 7
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 7

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35                  40                  45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115                 120                 125
```

```
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 8
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 8

```
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
1               5                   10                  15

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            20                  25                  30

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
        35                  40                  45

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    50                  55                  60

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
65                  70                  75                  80

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
```

```
                85                  90                  95

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
            100                 105                 110

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
        115                 120                 125

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    130                 135                 140

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145                 150                 155                 160

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            180                 185                 190

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205

Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 9
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 9

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        35                  40                  45
```

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
                165                 170                 175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 10
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 10

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

```
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20                  25                  30

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        35                  40                  45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50                  55                  60

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
145                 150                 155                 160

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

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
            180                 185                 190

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        195                 200                 205

Ser Leu Ser Leu Ser Leu Gly Lys
    210                 215
```

<210> 11
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 11

```
Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp
1               5                  10                  15

Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr
            20                  25                  30

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

Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys
    50                  55                  60

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

Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys Arg Val Asp His
                85                  90                  95

Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro Asp
            100                 105                 110

Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala Ser
        115                 120                 125

Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp Leu
    130                 135                 140

Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu
145                 150                 155                 160

Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala Thr
                165                 170                 175

Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser
            180                 185                 190

Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser Pro
        195                 200                 205
```

Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly
210 215

<210> 12
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 12

Gly Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser
1 5 10 15

Ile Pro Pro Glu Val Lys Phe Asn Lys
20 25

<210> 13
<211> 394
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 13

Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser His His
1 5 10 15

Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu
20 25 30

Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr
35 40 45

Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu
50 55 60

Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu Gly Leu
65 70 75 80

Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu Gly Phe
85 90 95

```
Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu Gln Leu
            100                 105                 110

Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val Asp
        115                 120                 125

Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr
    130                 135                 140

Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr
145                 150                 155                 160

Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu
                165                 170                 175

Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly
            180                 185                 190

Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu Asp Phe
        195                 200                 205

His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys Arg Leu
    210                 215                 220

Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp Val Leu
225                 230                 235                 240

Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro Asp
                245                 250                 255

Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile
            260                 265                 270

Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu
        275                 280                 285

Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly
    290                 295                 300

Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu Ser Gly
305                 310                 315                 320

Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His Lys Ala
```

325 330 335

Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe
340 345 350

Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys
355 360 365

Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe
370 375 380

Met Gly Lys Val Val Asn Pro Thr Gln Lys
385 390

<210> 14
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 14

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

```
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
        115                 120                 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
    130                 135                 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145                 150                 155                 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
                165                 170                 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180                 185                 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
        195                 200                 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210                 215                 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225                 230                 235                 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
                245                 250                 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260                 265                 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275                 280                 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290                 295                 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305                 310                 315                 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
                325                 330                 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
```

```
            340                 345                 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355                 360                 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370                 375                 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385                 390                 395                 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
                405                 410                 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420                 425                 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435                 440                 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450                 455                 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465                 470                 475                 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
                485                 490                 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500                 505                 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515                 520                 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530                 535                 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545                 550                 555                 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
                565                 570                 575
```

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 15
<211> 196
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 15

Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln
1 5 10 15

Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys
20 25 30

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

Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg
50 55 60

Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys
65 70 75 80

Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys
85 90 95

Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val
100 105 110

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

His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys
130 135 140

Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys
145 150 155 160

Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys

165 170 175

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys
180 185 190

Lys Leu Val Ala
195

<210> 16
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 16

Ser Gly Lys Ser Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala
1 5 10 15

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
20 25 30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
35 40 45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
50 55 60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65 70 75 80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met
85 90 95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Glu Pro Lys Ser Cys
100 105 110

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
115 120 125

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
130 135 140

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
145                 150                 155                 160

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                165                 170                 175

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            180                 185                 190

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        195                 200                 205

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
    210                 215                 220

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
225                 230                 235                 240

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                245                 250                 255

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            260                 265                 270

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
        275                 280                 285

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
305                 310                 315                 320

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                325                 330                 335

Pro Gly Lys
```

<210> 17
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 17

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

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Glu Arg Lys Cys Cys
            100                 105                 110

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
            180                 185                 190

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
        195                 200                 205
```

```
Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
    210                 215                 220

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
                245                 250                 255

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
            260                 265                 270

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
    290                 295                 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305                 310                 315                 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330                 335
```

<210> 18
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 18

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

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60
```

```
Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Leu
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Glu Pro Lys Ser Cys
            100                 105                 110

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
        115                 120                 125

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
    130                 135                 140

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
145                 150                 155                 160

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                165                 170                 175

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            180                 185                 190

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        195                 200                 205

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
    210                 215                 220

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
225                 230                 235                 240

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                245                 250                 255

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            260                 265                 270

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
        275                 280                 285
```

```
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
    290                 295                 300

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
305                 310                 315                 320

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                325                 330                 335

Pro Gly Lys
```

<210> 19
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 19

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

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Leu
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Glu Pro Lys Ser Cys
            100                 105                 110

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
        115                 120                 125
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr
    130                 135                 140

Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
145                 150                 155                 160

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                165                 170                 175

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            180                 185                 190

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        195                 200                 205

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
    210                 215                 220

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
225                 230                 235                 240

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                245                 250                 255

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            260                 265                 270

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
        275                 280                 285

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
305                 310                 315                 320

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                325                 330                 335

Pro Gly Lys
```

<210> 20
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 20

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

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Leu
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Glu Pro Lys Ser Cys
            100                 105                 110

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
        115                 120                 125

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
    130                 135                 140

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
145                 150                 155                 160

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                165                 170                 175

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            180                 185                 190
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        195                 200                 205

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
    210                 215                 220

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
225                 230                 235                 240

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                245                 250                 255

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            260                 265                 270

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
        275                 280                 285

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu
305                 310                 315                 320

His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                325                 330                 335

Pro Gly Lys
```

<210> 21
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 21

```
Ala Val Thr Gly Val Pro Val Lys Gly Gln Asp Thr Val Lys Gly Arg
1               5                   10                  15

Val Pro Phe Asn Gly Gln Asp Pro Val Lys Gly Gln Val Ser Val Lys
            20                  25                  30
```

```
Gly Gln Asp Lys Val Lys Ala Gln Glu Pro Val Lys Gly Pro Val Ser
        35                  40                  45

Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala Met Leu
    50                  55                  60

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
        195                 200                 205

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255
```

```
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Ser Leu Ser Pro Gly Lys
                325
```

<210> 22
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 22

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

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Leu
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Glu Pro Lys Ser Cys
            100                 105                 110
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
        115                 120                 125

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
    130                 135                 140

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
145                 150                 155                 160

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                165                 170                 175

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            180                 185                 190

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        195                 200                 205

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
    210                 215                 220

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
225                 230                 235                 240

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                245                 250                 255

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            260                 265                 270

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
        275                 280                 285

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
305                 310                 315                 320

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                325                 330                 335
```

```
Pro Gly Lys Ala Ser Thr Gly Ser Ser Gly Lys Ser Phe Lys Ala Gly
            340                 345                 350

Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys Pro
        355                 360                 365

Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys Pro
    370                 375                 380

Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn Pro
385                 390                 395                 400

Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys Leu
                405                 410                 415

Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys Arg
            420                 425                 430

Asp Leu Lys Cys Cys Met Gly Leu Cys Gly Lys Ser Cys Val Ser Pro
        435                 440                 445

Val Lys Ala
    450
```

<210> 23
<211> 427
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 23

```
Ala Val Thr Gly Val Pro Val Lys Gly Gln Asp Thr Val Lys Gly Arg
1               5                   10                  15

Val Pro Phe Asn Gly Gln Asp Pro Val Lys Gly Gln Val Ser Val Lys
            20                  25                  30

Gly Gln Asp Lys Val Lys Ala Gln Glu Pro Val Lys Gly Pro Val Ser
        35                  40                  45

Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala Met Leu
    50                  55                  60
```

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
        195                 200                 205

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285
```

```
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Ser Leu Ser Pro Gly Lys Ala Ser Thr Gly Ser Ala Val Thr Gly
                325                 330                 335

Val Pro Val Lys Gly Gln Asp Thr Val Lys Gly Arg Val Pro Phe Asn
            340                 345                 350

Gly Gln Asp Pro Val Lys Gly Gln Val Ser Val Lys Gly Gln Asp Lys
        355                 360                 365

Val Lys Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly
    370                 375                 380

Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn
385                 390                 395                 400

Arg Cys Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu
                405                 410                 415

Gly Ser Cys Gly Met Ala Cys Phe Val Pro Gln
            420                 425
```

<210> 24
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 24

```
Ala Val Thr Gly Val Pro Val Lys Gly Gln Asp Thr Val Lys Gly Arg
1               5                   10                  15

Val Pro Phe Asn Gly Gln Asp Pro Val Lys Gly Gln Val Ser Val Lys
            20                  25                  30

Gly Gln Asp Lys Val Lys Ala Gln Glu Pro Val Lys Gly Pro Val Ser
        35                  40                  45
```

```
Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala Met Leu
    50                  55                  60

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

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

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
        195                 200                 205

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
```

```
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        275                 280                 285

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    290                 295                 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305                 310                 315                 320

Leu Ser Leu Ser Pro Gly Lys Ala Ser Thr Gly Ser Ser Gly Lys Ser
                325                 330                 335

Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg
            340                 345                 350

Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys
        355                 360                 365

Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp
    370                 375                 380

Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr
385                 390                 395                 400

Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly
                405                 410                 415

Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Leu Cys Gly Lys Ser
            420                 425                 430

Cys Val Ser Pro Val Lys Ala
        435
```

<210> 25
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 25

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

```
Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Leu
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Glu Pro Lys Ser Cys
            100                 105                 110

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
        115                 120                 125

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
    130                 135                 140

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
145                 150                 155                 160

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
                165                 170                 175

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
            180                 185                 190

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
        195                 200                 205

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
    210                 215                 220

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
225                 230                 235                 240
```

```
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
                245                 250                 255

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            260                 265                 270

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
        275                 280                 285

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
305                 310                 315                 320

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
                325                 330                 335

Pro Gly Lys Ala Ser Thr Gly Ser Ala Val Thr Gly Val Pro Val Lys
            340                 345                 350

Gly Gln Asp Thr Val Lys Gly Arg Val Pro Phe Asn Gly Gln Asp Pro
        355                 360                 365

Val Lys Gly Gln Val Ser Val Lys Gly Gln Asp Lys Val Lys Ala Gln
    370                 375                 380

Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys Pro Ile
385                 390                 395                 400

Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys Leu Lys
                405                 410                 415

Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser Cys Gly
            420                 425                 430

Met Ala Cys Phe Val Pro Gln
        435
```

<210> 26
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 26

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
```

```
Phe Asn Arg Gly Glu Cys Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly
    210                 215                 220

Lys Ser Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys
225                 230                 235                 240

Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly
                245                 250                 255

Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro
            260                 265                 270

Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val
        275                 280                 285

Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met
    290                 295                 300

Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly
305                 310                 315                 320

Lys Ser Cys Val Ser Pro Val Lys Ala
                325
```

<210> 27
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 27

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys Ala Ser Thr Gly Ser Ser Gly Lys Ser Phe
    210                 215                 220

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

Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg
                245                 250                 255

Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr
            260                 265                 270

Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly
        275                 280                 285
```

Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln
290 295 300

Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys
305 310 315 320

Val Ser Pro Val Lys Ala
325

<210> 28
<211> 566
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 28

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

```
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365
```

```
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly Lys Ser Phe
    450                 455                 460

Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr
465                 470                 475                 480

Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg
                485                 490                 495

Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr
            500                 505                 510

Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly
        515                 520                 525

Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln
    530                 535                 540

Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys
545                 550                 555                 560

Val Ser Pro Val Lys Ala
                565
```

<210> 29
<211> 563
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 29

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

```
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys Ala Ser Thr Gly Ser Ser Gly Lys Ser Phe Lys Ala Gly
    450                 455                 460

Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys Pro
465                 470                 475                 480

Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys Pro
                485                 490                 495

Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn Pro
            500                 505                 510

Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys Leu
        515                 520                 525

Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys Arg
    530                 535                 540

Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser Pro
545                 550                 555                 560

Val Lys Ala
```

<210> 30
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 30

```
Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
1               5                   10                  15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
            20                  25                  30

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

```
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
    50                  55                  60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65                  70                  75                  80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
                85                  90                  95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
            100                 105                 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
        115                 120                 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
    130                 135                 140

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

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
                165                 170                 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
            180                 185                 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
        195                 200                 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
    210                 215                 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270
```

```
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Gln Val Lys Phe Asn Trp Tyr Val Asp Gly Val Gln Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Gln Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asn Trp Leu Asp Gly
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys Gly Gly Gly Ser Gly Gly Gly Ser Ser Gly Lys Ser Phe
465                 470                 475                 480

Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr
                485                 490                 495

Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg
```

```
            500                 505                 510

Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr
        515                 520                 525

Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly
    530                 535                 540

Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln
545                 550                 555                 560

Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys
                565                 570                 575

Val Ser Pro Val Lys Ala
            580
```

<210> 31
<211> 579
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 31

```
Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
1               5                   10                  15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
            20                  25                  30

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

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
    50                  55                  60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65                  70                  75                  80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
                85                  90                  95
```

```
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
            100                 105                 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
        115                 120                 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
    130                 135                 140

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

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
                165                 170                 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
            180                 185                 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
        195                 200                 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
    210                 215                 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Glu Pro Lys Ser Cys
225                 230                 235                 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

Glu Asp Pro Gln Val Lys Phe Asn Trp Tyr Val Asp Gly Val Gln Val
    290                 295                 300

His Asn Ala Lys Thr Lys Pro Arg Glu Gln Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asn Trp Leu Asp Gly
```

```
                325                 330                 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

Pro Gly Lys Ala Ser Thr Gly Ser Ser Gly Lys Ser Phe Lys Ala Gly
465                 470                 475                 480

Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys Pro
                485                 490                 495

Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys Pro
            500                 505                 510

Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn Pro
        515                 520                 525

Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys Leu
    530                 535                 540

Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys Arg
545                 550                 555                 560
```

```
Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser Pro
                565                 570                 575

Val Lys Ala
```

<210> 32
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 32

```
Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser His His
1               5                   10                  15

Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu
            20                  25                  30

Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr
        35                  40                  45

Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu
    50                  55                  60

Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu Gly Leu
65                  70                  75                  80

Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu Gly Phe
                85                  90                  95

Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu Gln Leu
            100                 105                 110

Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val Asp
        115                 120                 125

Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr
    130                 135                 140

Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr
```

145 150 155 160

Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu
165 170 175

Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly
180 185 190

Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu Asp Phe
195 200 205

His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys Arg Leu
210 215 220

Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp Val Leu
225 230 235 240

Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro Asp
245 250 255

Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile
260 265 270

Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu
275 280 285

Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly
290 295 300

Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu Ser Gly
305 310 315 320

Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His Lys Ala
325 330 335

Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe
340 345 350

Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys
355 360 365

Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe
370 375 380

```
Met Gly Lys Val Val Asn Pro Thr Gln Lys Glu Pro Lys Ser Cys Asp
385                 390                 395                 400

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                405                 410                 415

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            420                 425                 430

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        435                 440                 445

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    450                 455                 460

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
465                 470                 475                 480

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                485                 490                 495

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            500                 505                 510

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        515                 520                 525

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
    530                 535                 540

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
545                 550                 555                 560

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                565                 570                 575

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            580                 585                 590

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        595                 600                 605
```

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
610 615 620

Gly Lys Ala Ser Thr Gly Ser Ser Gly Lys Ser Phe Lys Ala Gly Val
625 630 635 640

Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys Pro Glu
645 650 655

Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys Pro Asp
660 665 670

Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn Pro Thr
675 680 685

Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys Leu Met
690 695 700

Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys Arg Asp
705 710 715 720

Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser Pro Val
725 730 735

Lys Ala

<210> 33
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 33

Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser His His
1 5 10 15

Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu
20 25 30

Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr
35 40 45

```
Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu
    50                  55                  60

Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu Gly Leu
65                  70                  75                  80

Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu Gly Phe
                85                  90                  95

Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu Gln Leu
            100                 105                 110

Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val Asp
        115                 120                 125

Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr
    130                 135                 140

Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr
145                 150                 155                 160

Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu
                165                 170                 175

Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly
            180                 185                 190

Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu Asp Phe
        195                 200                 205

His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys Arg Leu
    210                 215                 220

Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp Val Leu
225                 230                 235                 240

Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro Asp
                245                 250                 255

Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile
            260                 265                 270
```

```
Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu
        275                 280                 285

Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly
    290                 295                 300

Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu Ser Gly
305                 310                 315                 320

Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His Lys Ala
                325                 330                 335

Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe
            340                 345                 350

Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys
        355                 360                 365

Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe
    370                 375                 380

Met Gly Lys Val Val Asn Pro Thr Gln Lys Glu Pro Lys Ser Cys Asp
385                 390                 395                 400

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                405                 410                 415

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            420                 425                 430

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
        435                 440                 445

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    450                 455                 460

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
465                 470                 475                 480

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                485                 490                 495
```

```
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
            500                 505                 510

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        515                 520                 525

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
    530                 535                 540

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
545                 550                 555                 560

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
                565                 570                 575

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
            580                 585                 590

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
        595                 600                 605

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
    610                 615                 620

Gly Lys Ala Ser Thr Gly Ser Ala Val Thr Gly Val Pro Val Lys Gly
625                 630                 635                 640

Gln Asp Thr Val Lys Gly Arg Val Pro Phe Asn Gly Gln Asp Pro Val
                645                 650                 655

Lys Gly Gln Val Ser Val Lys Gly Gln Asp Lys Val Lys Ala Gln Glu
            660                 665                 670

Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys Pro Ile Ile
        675                 680                 685

Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys Leu Lys Asp
    690                 695                 700

Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser Cys Gly Met
705                 710                 715                 720

Ala Cys Phe Val Pro Gln
```

725

<210> 34
<211> 697
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 34

Ser Gly Lys Ser Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala
1 5 10 15

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
20 25 30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
35 40 45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
50 55 60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65 70 75 80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met
85 90 95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Ala Ser Thr Gly Ser
100 105 110

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

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
130 135 140

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
145 150 155 160

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
165 170 175

```
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
            180                 185                 190

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
        195                 200                 205

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
    210                 215                 220

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
225                 230                 235                 240

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
                245                 250                 255

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
            260                 265                 270

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
        275                 280                 285

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
    290                 295                 300

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
305                 310                 315                 320

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
                325                 330                 335

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
            340                 345                 350

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
        355                 360                 365

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
    370                 375                 380

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
385                 390                 395                 400

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
```

405 410 415

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
420 425 430

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
435 440 445

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
450 455 460

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
465 470 475 480

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
485 490 495

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
500 505 510

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
515 520 525

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
530 535 540

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
545 550 555 560

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
565 570 575

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
580 585 590

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
595 600 605

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
610 615 620

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
625 630 635 640

```
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
                645                 650                 655

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
            660                 665                 670

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
        675                 680                 685

Ala Ala Ser Gln Ala Ala Leu Gly Leu
    690                 695
```

<210> 35
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 35

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

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
            20                  25                  30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
        35                  40                  45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
    50                  55                  60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65                  70                  75                  80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met
                85                  90                  95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala Ala Ser Thr Gly Ser
            100                 105                 110

Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln
```

```
        115                 120                 125

Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys
    130                 135                 140

Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn
145                 150                 155                 160

Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg
                165                 170                 175

Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys
            180                 185                 190

Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys
        195                 200                 205

Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val
    210                 215                 220

Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe
225                 230                 235                 240

His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys
                245                 250                 255

Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys
            260                 265                 270

Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys
        275                 280                 285

Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys
    290                 295                 300

Lys Leu Val Ala
305
```

<210> 36
<211> 685
<212> PRT
<213> Artificial Sequence

<220>

<223> chemically synthesized

<400> 36

```
Ala Val Thr Gly Val Pro Val Lys Gly Gln Asp Thr Val Lys Gly Arg
1               5                  10                  15

Val Pro Phe Asn Gly Gln Asp Pro Val Lys Gly Gln Val Ser Val Lys
            20                  25                  30

Gly Gln Asp Lys Val Lys Ala Gln Glu Pro Val Lys Gly Pro Val Ser
        35                  40                  45

Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala Met Leu
    50                  55                  60

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

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

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

Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala
        115                 120                 125

Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn
    130                 135                 140

Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu
145                 150                 155                 160

Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr
                165                 170                 175

Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala
            180                 185                 190

Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp
        195                 200                 205

Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys
```

```
    210                 215                 220

Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr
225                 230                 235                 240

Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe
                245                 250                 255

Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala
            260                 265                 270

Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu
        275                 280                 285

Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln
    290                 295                 300

Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser
305                 310                 315                 320

Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr
                325                 330                 335

Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu
            340                 345                 350

Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln
        355                 360                 365

Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu
    370                 375                 380

Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala
385                 390                 395                 400

Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys
                405                 410                 415

Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr
            420                 425                 430

Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg
        435                 440                 445
```

```
Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala
    450                 455                 460

Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu
465                 470                 475                 480

Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu
                485                 490                 495

Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr
            500                 505                 510

Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg
        515                 520                 525

Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys
    530                 535                 540

Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu
545                 550                 555                 560

Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys
                565                 570                 575

Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu
            580                 585                 590

Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr
        595                 600                 605

Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys
    610                 615                 620

Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr
625                 630                 635                 640

Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu
                645                 650                 655

Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly
            660                 665                 670
```

```
Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly Leu
        675                 680                 685


<210>  37
<211>  296
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  chemically synthesized

<400>  37

Ala Val Thr Gly Val Pro Val Lys Gly Gln Asp Thr Val Lys Gly Arg
1               5                  10                  15


Val Pro Phe Asn Gly Gln Asp Pro Val Lys Gly Gln Val Ser Val Lys
            20                  25                  30


Gly Gln Asp Lys Val Lys Ala Gln Glu Pro Val Lys Gly Pro Val Ser
        35                  40                  45


Thr Lys Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Ala Met Leu
    50                  55                  60


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


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


Ser Thr Gly Ser Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys Glu
            100                 105                 110


Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu Val
        115                 120                 125


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


Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His Pro
145                 150                 155                 160


Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val Leu
                165                 170                 175
```

```
Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg Val
            180                 185                 190

Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe Ser
        195                 200                 205

Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala Glu
    210                 215                 220

Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu Arg
225                 230                 235                 240

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

Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala Ala
            260                 265                 270

Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe Ala
        275                 280                 285

Glu Glu Gly Lys Lys Leu Val Ala
    290                 295
```

<210> 38
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 38

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Gly Thr Glu Ala Ala Gly Ala Glu Phe Leu Glu Ala Ile Pro Leu Ser
1               5                   10                  15

Ile Pro Pro Glu Val Lys Phe Asn Lys
            20                  25
```

<210> 39
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 39

Ser Gly Lys Ser Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala
1 5 10 15

Gln Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys
20 25 30

Pro Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu
35 40 45

Asp Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys
50 55 60

Pro Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys
65 70 75 80

Glu Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Leu
85 90 95

Cys Gly Lys Ser Cys Val Ser Pro Val Lys Ala
100 105

<210> 40
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 40

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

Pro Lys Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

```
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65                  70                  75                  80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85                  90                  95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            100                 105                 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
        115                 120                 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    130                 135                 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145                 150                 155                 160

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
            180                 185                 190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        195                 200                 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
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<210> 41
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 41

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
```

20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
145 150 155 160

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln
195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 42
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> chemically synthesized

<400> 42

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

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

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 43
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 43

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 44
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 44

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu
115

<210> 45
<211> 335

<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 45

```
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
1               5                  10                  15

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
            20                  25                  30

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
        35                  40                  45

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
    50                  55                  60

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
65                  70                  75                  80

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
                85                  90                  95

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
            100                 105                 110

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
        115                 120                 125

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
    130                 135                 140

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
145                 150                 155                 160

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
                165                 170                 175

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
            180                 185                 190

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
```

195 200 205

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
210 215 220

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

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

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
260 265 270

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
290 295 300

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
305 310 315 320

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330 335

<210> 46
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 46

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

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
20 25 30

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

```
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
    50                  55                  60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65                  70                  75                  80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
                85                  90                  95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
            100                 105                 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
        115                 120                 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
    130                 135                 140

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

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
                165                 170                 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
            180                 185                 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
        195                 200                 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
    210                 215                 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225                 230                 235
```

<210> 47
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> chemically synthesized

<400> 47

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Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
1               5                  10                  15

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            20                  25                  30

Val Val Val Asp Val Ser His Glu Asp Pro Gln Val Lys Phe Asn Trp
        35                  40                  45

Tyr Val Asp Gly Val Gln Val His Asn Ala Lys Thr Lys Pro Arg Glu
    50                  55                  60

Gln Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
65                  70                  75                  80

His Gln Asn Trp Leu Asp Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                85                  90                  95

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            100                 105                 110

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        115                 120                 125

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    130                 135                 140

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145                 150                 155                 160

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            180                 185                 190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        195                 200                 205

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 48
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge region

<400> 48

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge region

<400> 49

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
1 5 10

<210> 50
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 50

Ala Ser Thr Gly Ser
1 5

<210> 51
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 51

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

CLAIMS

1. An isolated fusion protein comprising at least one human whey acidic protein (WAP) domain-containing polypeptide comprising a human secretory leukocyte proteinase inhibitor (SLPI) polypeptide comprising the amino acid sequence of SEQ ID NO: 3 operably linked to an immunoglobulin Fc polypeptide comprising the amino acid sequence of SEQ ID NO: 10.

2. An isolated fusion protein comprising at least one human secretory leukocyte proteinase inhibitor (SLPI) polypeptide comprising the amino acid sequence of SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 39 operably linked to an immunoglobulin Fc polypeptide comprising the amino acid sequence of SEQ ID NO: 10.

3. The isolated fusion protein of claim 1, wherein the WAP domain containing polypeptide and the immunoglobulin Fc polypeptide are operably linked via a hinge region, a linker region, or both a hinge region and linker region.

4. The isolated fusion protein of claim 2, wherein the SLPI polypeptide and the immunoglobulin Fc polypeptide are operably linked via a hinge region, a linker region, or both a hinge region and linker region.

5. The isolated fusion protein of claim 3, wherein the hinge region, the linker region or both the hinge region and the linker region comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, and SEQ ID NO: 51.

6. The isolated fusion protein of claim 4, wherein the peptide sequence comprises the amino acid sequence of SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, or SEQ ID NO: 51.

7. The isolated fusion protein of claim 1, wherein the immunoglobulin Fc polypeptide is modified to enhance FcRn binding.

8. The isolated fusion protein of claim 1, wherein the immunoglobulin Fc polypeptide comprises at least one mutation at a position selected from the group consisting of: Met252, Ser254, Thr256, Met428, and Asn434.

9. The isolated fusion protein of claim 1, wherein the immunoglobulin Fc polypeptide comprises at least one of the following mutations: Met252Tyr, Ser254Thr, Thr256Glu, Met428Leu or Asn434Ser.

10. The isolated fusion protein of claim 2, wherein the immunoglobulin Fc polypeptide is modified to enhance FcRn binding.

11. The isolated fusion protein of claim 2, wherein the immunoglobulin Fc polypeptide comprises at least one mutation at a position selected from the group consisting of: Met252, Ser254, Thr256, Met428, and Asn434.

12. The isolated fusion protein of claim 2, wherein the immunoglobulin Fc polypeptide comprises at least one of the following mutations: Met252Tyr, Ser254Thr, Thr256Glu, Met428Leu or Asn434Ser.

13. The isolated fusion protein of claim 2, wherein the human secretory leukocyte proteinase inhibitor (SLPI) polypeptide comprises of the amino acid sequence of SEQ ID NO: 3 operably linked to an immunoglobulin Fc polypeptide comprising the amino acid sequence of SEQ ID NO: 10.

14. The isolated fusion protein of claim 1, wherein the fusion protein further comprises a serpin polypeptide comprising the amino acid sequence of SEQ ID NO: 13 or SEQ ID NO: 38.

15. The isolated fusion protein of claim 2, wherein the fusion protein comprises an AAT polypeptide comprising the amino acid sequence of SEQ ID NO: 13 or SEQ ID NO: 38.

16. Use of the fusion protein of claim 1 or claim 2 in the manufacture of a medicament for treating or alleviating a symptom of a disease or disorder associated with aberrant serine protease expression or activity in a subject in need thereof.

17. Use of the fusion protein of claim 1 or claim 2 in the manufacture of a medicament for treating or alleviating a symptom of an inflammatory disease or disorder in a subject in need thereof.

18. Use of the fusion protein of claim 1 or claim 2 in the manufacture of a medicament for treating or alleviating a symptom of an infectious disease or disorder in a subject in need thereof.

19. The use of the fusion protein of any one of claims 16-18, in the manufacture of a medicament for treating or alleviating a symptom of a disease or disorder associated with aberrant serine protease expression or activity in a subject in need thereof, wherein the subject is a human.