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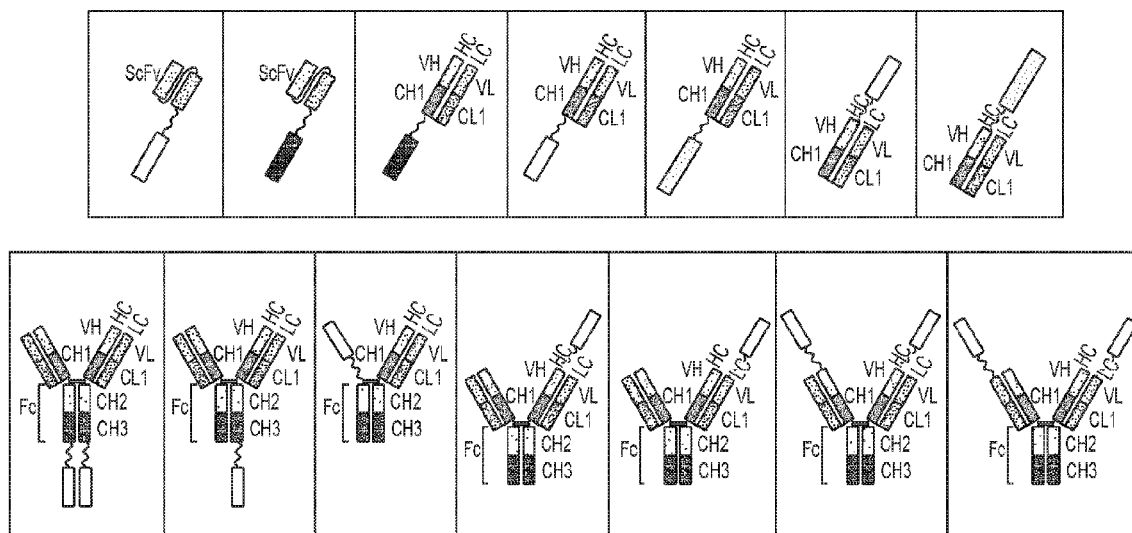


FIG. 14

(57) Abstract: Provided herein are fusion protein constructs that can bind a complement-associated antigen, comprising a targeting moiety and a complement modulator protein, or a fragment thereof or a variant thereof. The targeting moiety is an antibody or an antigen binding fragment thereof, in some examples. Further provided are methods of using the fusion protein constructs, for example, in treating complement mediation conditions.



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FUSION PROTEIN CONSTRUCTS FOR COMPLEMENT ASSOCIATED DISEASE

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Application No. 62/778,014 filed December 11, 2018, which is incorporated by reference herein in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on December 11, 2019, is named 53542_707_601_SL.txt and is 950,242 bytes in size.

SUMMARY

[0003] Provided herein in one embodiment is a monomeric fusion protein construct that binds a complement-associated antigen; the monomeric fusion protein construct comprising: a first polypeptide comprising: a domain A and a domain B arranged from N-terminus to C-terminus in an A-B orientation, a second polypeptide comprising: a domain E and a domain F arranged from N-terminus to C-terminus in an E-F orientation, wherein at least one of domain A, domain B, domain E or domain F can be conjugated to a domain R, and wherein: domain A can comprise a heavy chain variable region amino acid sequence (VH) or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E can comprise a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F can comprise a light chain constant region amino acid sequence (CL1), wherein the domain B of the first polypeptide and domain F of the second polypeptide are linked via one or more disulfide bonds.

[0004] In some embodiments, the first polypeptide comprises the domain A, the domain B, and the domain R, wherein the domains of the first polypeptide can be arranged, from N-terminus to C-terminus, in an R-A-B orientation, and wherein the domain R and the domain A are conjugated. In some embodiments, the first polypeptide comprises the domain A, the domain B, and the domain R, wherein the domains of the first polypeptide are arranged, from N-terminus to C-terminus, in an A-B-R orientation, and wherein the domain B and the domain R can be

conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide are arranged, from N-terminus to C-terminus, in an R-E-F orientation, and wherein the domain E and the domain R can be conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide are arranged, from N-terminus to C-terminus, in an E-F-R orientation, and wherein the domain F and the domain R can be conjugated. In some embodiments, the monomeric fusion protein construct further comprises a second complement modulatory polypeptide, wherein the second complement modulatory polypeptide and domain R are the same or are different.

[0005] One embodiment provides a fusion protein construct that binds a complement-associated antigen, the fusion protein construct can comprise: a first polypeptide and a second polypeptide, wherein the first polypeptide comprises a domain A, a domain B, a domain R, a hinge region, a domain C, and a domain D, wherein the domains A,B, hinge region, C, and D of the first polypeptide are arranged, from N-terminus to C-terminus, in an A-B-hinge region-C-D orientation, wherein domain A can comprise a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B can comprise a heavy chain CH1 constant region amino acid sequence, domain C can comprise a heavy chain CH2 constant region amino acid sequence, domain D can comprise a heavy chain CH3 constant region amino acid sequence, and domain R can comprise a complement modulator polypeptide, and wherein (1) domain A and domain R can be conjugated, or (2) domain D and domain R can be conjugated; the second polypeptide can comprise a domain E and a domain F, wherein the domains E and F of the second polypeptide are arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (i) domain E can comprise a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and (ii) domain F can comprise a light chain constant region amino acid sequence (CL1), and wherein the domain B of the first polypeptide and domain F of the second polypeptide are linked via one or more disulfide bonds.

[0006] In some embodiments, the fusion protein construct can be a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain D and the domain R can be conjugated in at least one of the first polypeptides, and wherein the two first polypeptides are linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct can be a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain A and the domain R can be conjugated in at least one of the first polypeptides, and wherein the two first polypeptides are linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein

construct can further comprise domain R1, wherein domain R1 can comprise a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or are different.

[0007] In some embodiments, domain A and domain R can be conjugated, and domain D and domain R1 can be conjugated. In some embodiments, domain D and domain R can be conjugated, and domain A and domain R1 can be conjugated. In some embodiments, the fusion protein construct can be a tetravalent heterodimeric fusion protein construct comprising c) a third polypeptide that comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide are arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; and d) a fourth polypeptide that comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide are arranged, from N-terminus to C-terminus, in an E-F orientation, wherein the domain B of the third polypeptide and domain F of the fourth polypeptide are linked via one or more disulfide bonds, and wherein the first and third polypeptides are linked together via one or more disulfide bonds at the hinge region. In some embodiments, the domain D and the domain R can be conjugated in the first polypeptide. In some embodiments, the domain A and the domain R can be conjugated in the first polypeptide.

[0008] In some embodiments, the fusion protein construct can further comprise domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or are different. In some embodiments, the domain R1 can be conjugated to the first polypeptide. In some embodiments, the domain R1 can be conjugated to the second polypeptide. In some embodiments, the domain R1 is conjugated to the third polypeptide. In some embodiments, the domain R1 is conjugated to the fourth polypeptide.

[0009] Another embodiment provides a fusion protein construct that binds a complement-associated antigen, the fusion protein construct comprising: a first polypeptide and a second polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a domain R, a hinge region, and a domain C, wherein the domains A,B, hinge region, and C of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region-C orientation, wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence, and domain R comprises a complement modulator polypeptide, and wherein (1) domain A and domain R can be conjugated, or (2) domain C and domain R can be conjugated; the second polypeptide comprises a domain E and a domain F, wherein the domains E and F

can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (i) domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and (ii) domain F comprises a light chain constant region amino acid sequence (CL1), and wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0010] In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain C and the domain R can be conjugated in at least one of the first polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain A and the domain R can be conjugated in at least one of the first polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 can comprise a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, domain A and domain R can be conjugated, and domain C and domain R1 can be conjugated. In some embodiments, domain C and domain R can be conjugated, and domain A and domain R1 can be conjugated.

[0011] In some embodiments, the fusion protein construct is a tetravalent heterodimeric fusion protein construct comprising c) a third polypeptide that comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; and d) a fourth polypeptide that comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein the domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, and wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[0012] In some embodiments, the domain C and the domain R can be conjugated in the first polypeptide. In some embodiments, the domain A and the domain R can be conjugated in the first polypeptide. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, the domain

R1 is conjugated to the first polypeptide. In some embodiments, the domain R1 is conjugated to the second polypeptide. In some embodiments, the domain R1 is conjugated to the third polypeptide. In some embodiments, the domain R1 is conjugated to the fourth polypeptide.

[0013] Another embodiment provides a fusion protein construct that binds a complement-associated antigen, the fusion protein comprising: a first polypeptide and a second polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a domain R, and a hinge region, wherein the domains A,B, and the hinge region of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region orientation, wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, and wherein (1) domain A and domain R can be conjugated, or (2) hinge region and domain R can be conjugated; the second polypeptide comprises a domain E and domain F, wherein the domains E and F can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1), and wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0014] In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain A and the domain R can be conjugated in at least one of the first polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the hinge region and the domain R can be conjugated in at least one of the first polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, domain A and domain R can be conjugated, and hinge domain and domain R1 can be conjugated. In some embodiments, the hinge domain and domain R can be conjugated, and domain A and domain R1 can be conjugated. In some embodiments, the fusion protein construct is a tetravalent heterodimeric fusion protein construct comprising c) a third polypeptide that comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a

domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; and d) a fourth polypeptide that comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein the domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, and wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[0015] In some embodiments, the hinge domain and the domain R can be conjugated in the first polypeptide. In some embodiments, the domain A and the domain R can be conjugated in the first polypeptide. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, the domain R1 is conjugated to the first polypeptide. In some embodiments, the domain R1 is conjugated to the second polypeptide. In some embodiments, the domain R1 is conjugated to the third polypeptide. In some embodiments, the domain R1 is conjugated to the fourth polypeptide.

[0016] Another embodiment provides a trivalent heterodimeric fusion protein construct that binds a complement-associated antigen, the trivalent heterodimeric fusion protein construct comprising: a first polypeptide, a second polypeptide, a third polypeptide and a fourth polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a hinge region, a domain C, a domain D, and a domain R, wherein the domains A, B, hinge region, C, and D of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation, and wherein (1) domain A and domain R can be conjugated, or (2) domain D and the domain R can be conjugated; the second polypeptide comprises: a domain E and a domain F, wherein domains E and F of the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; the third polypeptide comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; the fourth polypeptide comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; wherein domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds and wherein domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region, and wherein domain A comprises a heavy

chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain D comprises a heavy chain CH3 constant region amino acid sequence, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1).

[0017] In some embodiments, the domain A and the domain R of the first polypeptide can be conjugated. In some embodiments, the domain D and the domain R of the first polypeptide can be conjugated.

[0018] Another embodiment provides a trivalent heterodimeric fusion protein construct that binds a complement-associated antigen, the trivalent heterodimeric fusion protein construct comprising: a first polypeptide, a second polypeptide, a third polypeptide and a fourth polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a hinge region, a domain C, and a domain R, wherein the domains A, B, hinge region, and C, of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C orientation, and wherein (1) the domain A and the domain R can be conjugated, or (2) the domain C and the domain R can be conjugated; the second polypeptide comprises: a domain E and a domain F, wherein domains E and F of the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; the third polypeptide comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; the fourth polypeptide comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; wherein domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds and wherein domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region, and wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain E comprises a light chain variable region amino

acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1).

[0019] In some embodiments, the domain A and the domain R of the first polypeptide can be conjugated. In some embodiments, the domain C and the domain R of the first polypeptide can be conjugated.

[0020] Yet another embodiment provides a trivalent heterodimeric fusion protein construct that binds a complement-associated antigen, the trivalent heterodimeric fusion protein construct comprising a first polypeptide, a second polypeptide, a third polypeptide and a fourth polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a hinge region, and a domain R, wherein the domains A, B, and the hinge region of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region orientation, and wherein (1) the domain A and the domain R can be conjugated, or (2) the hinge region and the domain R can be conjugated; the second polypeptide comprises: a domain E and a domain F, wherein domains E and F of the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; the third polypeptide comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; the fourth polypeptide comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; wherein domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds and wherein domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region, and wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1).

[0021] In some embodiments, the domain A and the domain R of the first polypeptide can be conjugated. In some embodiments, the hinge region and the domain R of the first polypeptide can be conjugated.

[0022] Another embodiment provides a fusion protein construct that binds a complement-associated antigen, the fusion protein construct comprising: a first polypeptide and a second

polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a hinge region, a domain C and a domain D, wherein the domains A,B, hinge region, C, and D can be arranged, from N-terminus to C-terminus, in an A-B-hinge region-C-D orientation, wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain D comprises a heavy chain CH3 constant region amino acid sequence; the second polypeptide comprises: a domain E, domain F, and domain R, wherein the domains E and F can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (1) the domain E and the domain R can be conjugated, or (2) the domain F and the domain R can be conjugated, and wherein domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1), and wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0023] In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain E and the domain R can be conjugated in at least one of the second polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain F and the domain R can be conjugated in at least one of the second polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, domain E and domain R can be conjugated, and domain F and domain R1 can be conjugated. In some embodiments, domain F and domain R can be conjugated, and domain E and domain R1 can be conjugated. In some embodiments, the fusion protein construct is a tetravalent heterodimeric fusion protein construct comprising c) a third polypeptide that comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; and d) a fourth polypeptide that comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in

an E-F orientation, wherein the domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, and wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[0024] In some embodiments, the domain E and the domain R can be conjugated in the first polypeptide. In some embodiments, the domain F and the domain R can be conjugated in the first polypeptide. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, the domain R1 is conjugated to the first polypeptide. In some embodiments, the domain R1 is conjugated to the second polypeptide. In some embodiments, the domain R1 is conjugated to the third polypeptide. In some embodiments, the domain R1 is conjugated to the fourth polypeptide.

[0025] Another embodiment provides a fusion protein construct that binds a complement-associated antigen, the fusion protein construct comprising: a first polypeptide and a second polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a hinge region, and a domain C, wherein the domains A,B, hinge region, and C can be arranged, from N-terminus to C-terminus, in an A-B-hinge region-C orientation, wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence; the second polypeptide comprises: a domain E, domain F, and domain R, wherein the domains E and F can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (1) the domain E and the domain R can be conjugated, or (2) the domain F and the domain R can be conjugated, and wherein domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1), and wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0026] In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain E and the domain R can be conjugated in at least one of the second polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain F and the domain R can be conjugated in at least one of the second polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion

protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, domain E and domain R can be conjugated, and domain F and domain R1 can be conjugated. In some embodiments, the fusion protein construct domain F and domain R can be conjugated, and domain E and domain R1 can be conjugated. In some embodiments, the fusion protein construct is a tetravalent heterodimeric fusion protein construct comprising c) a third polypeptide that comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; and d) a fourth polypeptide that comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein the domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, and wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[0027] In some embodiments, the domain E and the domain R can be conjugated in the first polypeptide. In some embodiments, the domain F and the domain R can be conjugated in the first polypeptide. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, the domain R1 is conjugated to the first polypeptide. In some embodiments, the domain R1 is conjugated to the second polypeptide. In some embodiments, the domain R1 is conjugated to the third polypeptide. In some embodiments, the domain R1 is conjugated to the fourth polypeptide.

[0028] Yet another embodiment provides a fusion protein construct that binds a complement-associated antigen, the fusion protein construct comprising: a first polypeptide and a second polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, and a hinge region, wherein the domains A, B, and hinge region can be arranged, from N-terminus to C-terminus, in an A-B-hinge region orientation, wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence; the second polypeptide comprises: a domain E, domain F, and domain R, wherein the domains E and F can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (1) the domain E and the domain R can be conjugated, or (2) the domain F and the domain R can be conjugated, and wherein domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding

fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1), and wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0029] In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain E and the domain R can be conjugated in at least one of the second polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct is a tetravalent homodimeric fusion protein construct comprising two of the first polypeptide and two of the second polypeptide, wherein the domain F and the domain R can be conjugated in at least one of the second polypeptides, and wherein the two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, domain E and domain R can be conjugated, and domain F and domain R1 can be conjugated. In some embodiments, domain F and domain R can be conjugated, and domain E and domain R1 can be conjugated.

[0030] In some embodiments, the fusion protein construct is a tetravalent heterodimeric fusion protein construct comprising c) a third polypeptide that comprises: (i) a domain A, a domain B, a hinge region, a domain C, and a domain D, (ii) a domain A, a domain B, a hinge region, and a domain C, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; and d) a fourth polypeptide that comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein the domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, and wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[0031] In some embodiments, the domain E and the domain R can be conjugated in the first polypeptide. In some embodiments, the domain F and the domain R can be conjugated in the first polypeptide.

[0032] In some embodiments, the fusion protein construct further comprises domain R1, wherein domain R1 comprises a second complement modulatory polypeptide, and wherein domain R1 and domain R can be the same or can be different. In some embodiments, the domain R1 is conjugated to the first polypeptide. In some embodiments, the domain R1 is conjugated to

the second polypeptide. In some embodiments, the domain R1 is conjugated to the third polypeptide. In some embodiments, the domain R1 is conjugated to the fourth polypeptide.

[0033] Another embodiment provides a trivalent heterodimeric fusion protein construct that binds a complement- associated antigen, the trivalent heterodimeric fusion protein construct comprising: a first polypeptide, a second polypeptide, a third polypeptide and a fourth polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a hinge region, a domain C, and a domain D, wherein the domains A, B, the hinge region, C, and D of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region-C-D orientation; the second polypeptide comprises: a domain E, a domain F, and a domain R, wherein the domains E and F can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (1) the domain E and the domain R can be conjugated, or (2) the domain F and the domain R can be conjugated; the third polypeptide comprises: (i) a domain A, a domain B, a domain C, a domain D, and a hinge region, (ii) a domain A, a domain B, a domain C, and a hinge region, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C, and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region-C-D orientation; the fourth polypeptide comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; wherein domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds and wherein domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region, and wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain D comprises a heavy chain CH3 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1).

[0034] In some embodiments, the domain E and the domain R of the second polypeptide can be conjugated. In some embodiments, the domain F and the domain R of the second polypeptide can be conjugated.

[0035] Another embodiment provides a trivalent heterodimeric fusion protein construct that binds a complement- associated antigen, the trivalent heterodimeric fusion protein construct comprising: a first polypeptide, a second polypeptide, a third polypeptide and a fourth

polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, a hinge region, and a domain C, wherein the domains A, B, the hinge region, and C of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region-C orientation; the second polypeptide comprises: a domain E, a domain F, and a domain R, wherein the domains E and F can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (1) the domain E and the domain R can be conjugated, or (2) the domain F and the domain R can be conjugated; the third polypeptide comprises: (i) a domain A, a domain B, a domain C, a domain D, and a hinge region, (ii) a domain A, a domain B, a domain C, and a hinge region, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, hinge region, C and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region-C-D orientation; the fourth polypeptide comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; wherein domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds and wherein domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region, and wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1).

[0036] In some embodiments, the domain E and the domain R of the second polypeptide can be conjugated. In some embodiments, the domain F and the domain R of the second polypeptide can be conjugated.

[0037] Another embodiment provides a trivalent heterodimeric fusion protein construct that binds a complement-associated antigen, the trivalent heterodimeric fusion protein construct comprising: a first polypeptide, a second polypeptide, a third polypeptide and a fourth polypeptide, wherein the first polypeptide comprises: a domain A, a domain B, and a hinge region, wherein the domains A, B, and the hinge region of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region orientation; the second polypeptide comprises: a domain E, a domain F, and a domain R, wherein the domains E and F can be arranged, from N-terminus to C-terminus, in an E-F orientation, wherein (1) the domain E and the domain R can be conjugated, or (2) the domain F and the domain R can be conjugated; the

third polypeptide comprises: (i) a domain A, a domain B, a domain C, a domain D, and a hinge region, (ii) a domain A, a domain B, a domain C, and a hinge region, or (iii) a domain A, a domain B, and a hinge region, wherein the domains A, B, the hinge region, C and D of the third polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge region -C-D orientation; the fourth polypeptide comprises: a domain E and a domain F, wherein domains E and F of the fourth polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation; wherein domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds and wherein domain B of the third polypeptide and domain F of the fourth polypeptide can be linked via one or more disulfide bonds, wherein the first and third polypeptides can be linked together via one or more disulfide bonds at the hinge region, and wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1).

[0038] In some embodiments, the domain E and the domain R of the second polypeptide can be conjugated. In some embodiments, the domain F and the domain R of the second polypeptide can be conjugated.

[0039] Another embodiment provides a fusion protein construct that binds a complement-associated antigen, the fusion protein construct comprising: a first polypeptide, a second polypeptide, and a third polypeptide, wherein the first polypeptide comprises a domain R, a hinge region, a domain C and a domain D, wherein the domains R, hinge region, C, and D can be arranged, from N-terminus to C-terminus, in an R-hinge-C-D orientation, and wherein domain R comprises a complement modulator polypeptide, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain D comprises a heavy chain CH3 constant region amino acid sequence; wherein domain R and the hinge domain can be conjugated, the second polypeptide comprises a domain A, a domain B, a hinge region, a domain C, and a domain D, wherein the domains A, B, hinge region, C, and D can be arranged, from N-terminus to C-terminus arranged, in an A-B-hinge-C-D orientation, and wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, and domain B comprises a heavy chain CH1 constant region amino acid sequence; the third polypeptide comprises a domain E and a domain F, wherein the domains can be arranged, from N-terminus to C-terminus, in an E-F orientation, and wherein domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, domain F

comprises a light chain constant region amino acid sequence (CL1); wherein domain B of the second polypeptide and domain F of the third polypeptide can be linked via one or more disulfide bonds; and wherein the first and second polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[0040] Another embodiment provides a monomeric fusion protein construct that binds a complement-associated antigen, the monomeric fusion protein construct comprising: a first polypeptide comprising: a domain A, a domain B, and a hinge region, , arranged, from N terminus to C terminus in an A-B-hinge orientation; a second polypeptide comprising: a domain E, and a domain F, arranged, from N-terminus to C-terminus in an E-F orientation, wherein at least one of domain A, hinge domain, domain E or domain F is conjugated to a domain R, and wherein: domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1) wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0041] In some embodiments, the first polypeptide comprises the domain A, the domain B, the hinge domain, and the domain R, wherein the domains of the first polypeptide can be arranged, from N-terminus to C-terminus, in an R-A-B-hinge orientation, and wherein the domain R and the domain A can be conjugated. In some embodiments, the first polypeptide comprises the domain A, the domain B, the hinge domain, and the domain R, wherein the domains of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge-R orientation, and wherein the hinge domain and the domain R can be conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide can be arranged, from N-terminus to C-terminus, in an R-E-F orientation, and wherein the domain E and the domain R can be conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F-R orientation, and wherein the domain F and the domain R can be conjugated. In some embodiments, the fusion protein construct further comprises a second complement modulatory polypeptide, wherein the second complement modulatory polypeptide and domain R can be the same or can be different.

[0042] Another embodiment provides a monomeric fusion protein construct that binds a complement-associated antigen, the monomeric fusion protein construct comprising: a first

polypeptide comprising: a domain A, a domain B, a hinge region, and a domain C arranged, from N terminus to C terminus in an A-B-hinge-C region orientation; a second polypeptide comprising: a domain E, and a domain F, arranged, from N-terminus to C-terminus in an E-F orientation, wherein at least one of domain A, domain C, domain E or domain F is conjugated to a domain R, and wherein: domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1) wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0043] In some embodiments, the first polypeptide comprises the domain A, the domain B, the hinge domain, the domain C, and the domain R, wherein the domains of the first polypeptide can be arranged, from N-terminus to C-terminus, in an R-A-B-hinge-C orientation, and wherein the domain R and the domain A can be conjugated. In some embodiments, the first polypeptide comprises the domain A, the domain B, the hinge domain, the domain C, and the domain R, wherein the domains of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge-C-R orientation, and wherein the domain C and the domain R can be conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide can be arranged, from N-terminus to C-terminus, in an R-E-F orientation, and wherein the domain E and the domain R can be conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F-R orientation, and wherein the domain F and the domain R can be conjugated. In some embodiments, the fusion protein construct further comprises a second complement modulatory polypeptide, wherein the second complement modulatory polypeptide and domain R can be the same or can be different.

[0044] Another embodiment provides a monomeric fusion protein construct that binds a complement-associated antigen, the monomeric fusion protein construct comprising: a) a first polypeptide comprising: a domain A, a domain B, a hinge region, a domain C and a domain D arranged, from N terminus to C terminus in an A-B-hinge-C-D region orientation; b) a second polypeptide comprising: a domain E, and a domain F, arranged, from N-terminus to C-terminus in an E-F orientation, wherein at least one of domain A, domain D, domain E or domain F is conjugated to a domain R, and wherein: (i) domain A comprises a heavy chain variable region

amino acid sequence (VH), or an antigen-binding fragment thereof, (ii) domain B comprises a heavy chain CH1 constant region amino acid sequence, (iii) domain C comprises a heavy chain CH2 constant region amino acid sequence, (iv) domain D comprises a heavy chain CH3 constant region amino acid sequence, (v) domain R comprises a complement modulator polypeptide, (vi) domain E comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and (vii) domain F comprises a light chain constant region amino acid sequence (CL1) wherein the domain B of the first polypeptide and domain F of the second polypeptide can be linked via one or more disulfide bonds.

[0045] In some embodiments, the first polypeptide comprises the domain A, the domain B, the hinge domain, the domain C, the domain D and the domain R, wherein the domains of the first polypeptide can be arranged, from N-terminus to C-terminus, in an R-A-B-hinge-C-D orientation, and wherein the domain R and the domain A can be conjugated. In some embodiments, the first polypeptide comprises the domain A, the domain B, the hinge domain, the domain C, the domain D, and the domain R, wherein the domains of the first polypeptide can be arranged, from N-terminus to C-terminus, in an A-B-hinge-C-D-R orientation, and wherein the domain C and the domain R can be conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide can be arranged, from N-terminus to C-terminus, in an R-E-F orientation, and wherein the domain E and the domain R can be conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F-R orientation, and wherein the domain F and the domain R can be conjugated. In some embodiments, the fusion protein construct further comprises a second complement modulatory polypeptide, wherein the second complement modulatory polypeptide and domain R can be the same or can be different.

[0046] In some embodiments, the conjugation comprises linking of two domains with a peptide linker, without a linker, an enzymatic conjugation, a chemical conjugation, or any combination thereof. In some embodiments, the complement-associated antigen is C3d, iC3b, C3dg or fragments thereof, or variants thereof. In some embodiments, the fusion protein construct binds C3 and C3b with lower binding affinity than that toward C3d. In some embodiments, the fusion protein construct binds C3 and C3b with a K_D affinity of about 10^{-3} M or higher. In some embodiments, the fusion protein construct binds iC3b, C3dg, or both, with a K_D affinity of 10^{-8} M or less. In some embodiments, the fusion protein construct modulates alternative complement activity in a subject upon administration of the fusion protein construct or a pharmaceutical composition comprising the fusion protein construct, to the subject. In some embodiments, the

fusion protein construct modulates classical complement activity in a subject upon administration of the fusion protein construct or a pharmaceutical composition comprising the fusion protein construct, to the subject. In some embodiments, the fusion protein construct modulates lectin complement activity in a subject upon administration of the fusion protein construct or a pharmaceutical composition comprising the fusion protein construct, to the subject. In some embodiments, the fusion protein construct binds a domain of a mammalian annexin protein.

[0047] In some embodiments, the fusion protein construct binds the domain of a mammalian annexin protein with a KD affinity of 10^{-8} M or less. In some embodiments, the domain is an annexin core domain. In some embodiments, the annexin core domain comprises an alpha-helical domain. In some embodiments, the annexin core domain comprises a calcium binding site and a membrane binding site. In some embodiments, the annexin core domain comprises at least one annexin repeat. In some embodiments, the fusion protein construct binds an annexin repeat sequence within the domain. In some embodiments, the fusion protein construct binds a phospholipid. In some embodiments, the fusion protein construct binds the phospholipid with a KD affinity of 10^{-8} M or less. In some embodiments, the phospholipid is selected from the group consisting of phosphatidylethanolamine (PE), cardiolipin (CL), phosphatidylcholine (PC), phosphatidylinositol, phosphatidylglycerol, phosphatidylserine, and phosphatidic acid, and malondialdehyde (MDA). In some embodiments, the complement modulator peptide comprises domain A of a complement receptor 1 (CR1) protein or a fragment thereof that retains at least three short consensus repeats (SCRs) of domain A. In some embodiments, the fusion protein construct further comprises domain B of the CR1 protein or a fragment thereof that retains at least three SCRs of domain B.

[0048] In some embodiments, the fusion protein construct further comprises domain C of the CR1 protein or a fragment thereof that retains at least three SCRs of domain C. In some embodiments, the fusion protein construct further comprises domain D of the CR1 or a fragment thereof that retains at least three SCRs of domain D. In some embodiments, the complement modulator polypeptide comprises the first three SCRs of domain A, the first three SCRs of domain B, and the first three SCRs of domain C of the CR1 protein. In some embodiments, the complement modulator polypeptide is CR1 (1-10). In some embodiments, the complement modulator polypeptide is CR1 (1-17). In some embodiments, the complement modulator peptide comprises the amino acid sequence of SEQ ID No. 41 or SEQ ID No. 91, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator polypeptide comprises the amino acid sequence of SEQ ID No. 42 or SEQ ID No. 92, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments,

the complement modulator peptide is decay-accelerating factor (DAF) or a biologically active fragment thereof. In some embodiments, the DAF is a human DAF. In some embodiments, the biologically active fragment of human DAF comprises at least one of a short consensus repeat (SCR) domain and an O-glycosylated serine/threonine-rich domain of a full-length human DAF.

[0049] In some embodiments, the biologically active fragment of DAF comprises SCR 1 to 4, or SCR 2 to 4 of a full-length human DAF. In some embodiments, the biologically active fragment of DAF comprises the amino acid sequence of SEQ ID No. 184, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is factor H or a biologically active fragment thereof. In some embodiments, the factor H is a human factor H. In some embodiments, the biologically active fragment of human factor H comprises one or more groups of short consensus repeats (SCRs) comprising SCRs 1 to 20, SCRs 1 to 2, SCRs 2 to 3, SCRs 3 to 4, SCRs 4 to 5, SCRs 5 to 6, SCRs 6 to 7, SCRs 7 to 8, SCRs 8 to 9, SCRs 9 to 10, SCRs 10 to 11, SCRs 11 to 12, SCRs 12 to 13, SCRs 13 to 14, SCRs 14 to 15, SCRs 15 to 16, SCRs 16 to 17, SCRs 17 to 18, SCRs 19 to 20 of a full-length human factor H, or any combination of SCRs 1 to 20. In some embodiments, the biologically active fragment of human factor H comprises SCRs 1 to 4 or SCRs 1 to 5 of a full-length human factor H. In some embodiments, the biologically active fragment of human factor H comprises a stretch of amino acids selected from the group consisting of: amino acids 21-266, amino acids 21-320, amino acids 21-509 or amino acids 19-1106 of SEQ ID No. 9, or a variant thereof with an amino acid sequence at least 85% identical to the stretch of amino acids.

[0050] In some embodiments, the factor H or biologically active fragment thereof comprises the amino acid sequence of SEQ ID NO: 72 or SEQ ID NO: 108, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is MCP or a biologically active fragment thereof. In some embodiments, the MCP is human MCP. In some embodiments, the biologically active fragment of human MCP comprises at least one of a short consensus repeat (SCR) domain of a full-length human MCP. In some embodiments, the biologically active fragment of human MCP comprises SCRs 3 to 4 of the full-length human MCP. In some embodiments, the MCP comprises the amino acid sequence of SEQ ID NO: 187, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is Map44 or a biologically active fragment thereof. In some embodiments, the Map44 is human Map44. In some embodiments, the Map44 comprises the amino acid sequence of SEQ ID NO: 186, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is CD59 or a biologically active fragment thereof.

[0051] In some embodiments, the CD59 is human CD59.

[0052] In some embodiments, the CD59 comprises the amino acid sequence of SEQ ID NO: 185, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the fusion protein construct comprises a human antibody or an antigen-binding fragment thereof. In some embodiments, the fusion protein construct comprises a humanized antibody or an antigen-binding fragment thereof. In some embodiments, the first and third polypeptides each comprise at least one orthogonal modification that favors formation of a heterodimer as compared to a homodimer. In some embodiments, the first polypeptide comprises a knob modification, and the third polypeptide comprises a hole modification; or wherein the third polypeptide comprises a knob modification and the first polypeptide comprises a hole modification. In some embodiments, the first and third polypeptides comprise modifications resulting in charge or surface complementarity.

[0053] In some embodiments, (a) the first polypeptide comprises (i) three heavy chain complementarity determining regions (CDRs) having the amino acid sequences of SEQ ID NOs: 11, 12 and 13; 17, 18 and 19; 23, 24 and 25; 29, 30 and 31; 35, 36 and 37; 147, 148, and 149; 188, 189, and 190; 196, 197, and 198; 204 or 343, 205, and 206; 212, 213, and 214; 220, 221, and 222; 228, 229, and 230; 29, 259 and 31; or 29, 260 and 31; or (ii) three heavy chain CDRs having amino acid sequences that differ by a single conservative amino acid substitution within one of SEQ ID NOs: 11, 12 and 13; 17, 18 and 19; 23, 24 and 25; 29, 30 and 31; 35, 36 and 37; 147, 148, and 149; 188, 189, and 190; 196, 197, and 198; 204 or 343, 205, and 206; 212, 213, and 214; 220, 221, and 222; 228, 229, and 230; 29, 259 and 31; or 29, 260 and 31; and (b) the second polypeptide comprises (i) three light chain complementarity determining regions (CDRs) having the amino acid sequences of SEQ ID NOs: 14, 15 and 16; 20, 21 and 22; 26, 27 and 28; 32, 33 and 34; 38, 39, and 40; 150, 151, and 152; 191, 192, and 193; 199, 200, and 201; 207, 208, and 209; 215, 216, and 217; 223, 224 and 225; or 231, 232, and 233, or (ii) three light chain CDRs having amino acid sequences that differ by a single conservative amino acid substitution within one of SEQ ID NOs 14, 15 and 16; 20, 21 and 22; 26, 27 and 28; 32, 33 and 34; 38, 39, and 40; 150, 151, and 152; 191, 192, and 193; 199, 200, and 201; 207, 208, and 209; 215, 216, and 217; 223, 224 and 225; or 231, 232, and 233.

[0054] In some embodiments, the second polypeptide (the light chain comprising domains E and F) comprises at least three CDRs, wherein the light chain CDRs are defined as CDR-L1, CDR-L2, CDR-L3, respectively: for SEQ ID Nos. 279, 68, 287, and 59, the CDRs comprise residues 27-37 (CDR-L1), 55-57 (CDR-L2), and 94-102 (CDR-L3); for SEQ ID No. 289 the CDRs comprise residues 27-38 (CDR-L1), 56-58 (CDR-L2), 95-102 (CDR-L3). In some embodiments, the first polypeptide (the heavy chain comprising at least domains A and B) comprises at least three CDRs, wherein the heavy chain CDRs are defined as CDR-H1, CDR-H2, CDR-H3,

respectively: for SEQ ID Nos. 280, 281, 282, 284, 285, 286, 73, and 288 the CDRs comprise residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-100 (CDR-H3); for SEQ ID No. 244, the CDRs comprise residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-102 (CDR-H3); for SEQ ID No. 290, the CDRs comprise residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-110 (CDR-H3). In some embodiments, the first polypeptide (the heavy chain comprising at least domains A and B) comprises at least three CDRs, wherein the heavy chain CDRs are defined as CDR-H1, CDR-H2, CDR-H3, respectively, for SEQ ID No. 342, comprise SEQ ID No. 23, SEQ ID No. 24, and SEQ ID No. 25. In some embodiments, the second polypeptide (the light chain comprising at least domains E and F) comprises at least three CDRs, wherein the light chain CDRs are defined as CDR-L1, CDR-L2, CDR-L3, respectively, for the light chain, comprise SEQ ID No. 26, SEQ ID No. 27, and SEQ ID No. 28.

[0055] In some embodiments, the fusion protein construct further comprises at least one amino acid linker, wherein the at least one linker comprises the amino acid sequence of any of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, SEQ ID NO: 241, or SEQ ID NO: 242.

[0056] In some embodiments, the fusion protein construct can comprise the amino acid sequence of at least one of SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO:

140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, and SEQ ID NO: 144. In some embodiments, the first polypeptide comprises the sequence of SEQ ID No. 282 (domain A, domain B, domain C, and domain D) conjugated to a complement modulator polypeptide comprising a sequence selected from the group consisting of SEQ ID Nos. 41, 42, and 72 (domain R); and wherein the second polypeptide comprises the sequence of SEQ ID No. 279 (domain E and domain F). In some embodiments, the first polypeptide comprises the sequence of SEQ ID No. 282 (domain A, domain B, domain C, and domain D); and wherein the second polypeptide comprises the sequence of SEQ ID No. 279 (domain E and domain F) conjugated to a complement modulator polypeptide comprising a sequence selected from the group consisting of SEQ ID No. 72 (domain R).

[0057] Another embodiment provides a pharmaceutical composition comprising a fusion protein construct according to any one of the above embodiments. Yet another embodiment provides a polynucleotide that encodes a fusion protein. Another embodiment provides a method of treatment comprising providing to a subject a therapeutically effective amount of a pharmaceutical composition.

[0058] In some embodiments, the subject suffers from a complement-mediated disease or a complement-mediated inflammation. In some embodiments, the fusion protein construct specifically binds to C3d with a KD affinity of 10^{-8} M or less, and the subject suffers from the complement-mediated disease, wherein the complement-mediated disease is characterized by an increased deposition of C3d. In some embodiments, the fusion protein construct specifically binds to C2 antibody-reactive phospholipid with a KD affinity of 10^{-8} M or less, and the subject suffers from a complement-mediated disease, wherein the complement-mediated disease is characterized by an increased deposition of C2 antibody-reactive phospholipid. In some embodiments, the subject suffers from the complement-mediated inflammation, wherein the complement mediated inflammation comprises an inflammatory fibrotic disease, and wherein the inflammatory fibrotic disease comprises focal segmental glomerulosclerosis, primary sclerosing cholangitis, or membranoproliferative glomerulonephritis. In some embodiments, the subject suffers from a complement-mediated auto-immune disease, comprising rheumatoid arthritis, systemic lupus erythematosus, lupus nephritis, or pemphigus vulgaris. In some embodiments, the subject suffers from a complement-mediated kidney disease, comprising membranoproliferative glomerulonephritis, or complement 3 glomerulopathy. In some embodiments, the subject suffers from a complement-mediated cardiovascular disease. In some embodiments, the cardiovascular disease comprises atherosclerosis or thrombosis. In some embodiments, the subject suffers from a complement-mediated dermatological disease.

[0059] In some embodiments, the dermatological disease comprises psoriasis, acne inversa, lupus erythematosus, cutaneous small vessel vasculitis, urticaria, urticarial vasculitis, or bullous pemphigoid. In some embodiments, the subject suffers from the complement-mediated inflammation, and wherein the complement-mediated inflammation is associated with a condition or disease selected from the group consisting of ischemia/reperfusion injury, burn injury, endotoxemia and septic shock, adult respiratory distress syndrome, cardiopulmonary bypass, hemodialysis, anaphylactic shock, asthma, angioedema, Crohn's disease, sickle cell anemia, glomerulonephritis, membranous nephritis, pancreatitis, transplant rejection, hyperacute xenograft rejection, recurrent fetal loss, preeclampsia, drug allergy, IL-2 induced vascular leakage syndrome, radiographic contrast media allergy, myasthenia gravis, Alzheimer's disease, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, acute disseminated encephalomyelitis, Addison's disease, antiphospholipid antibody syndrome, autoimmune hepatitis, Goodpasture's syndrome, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, idiopathic thrombocytopenic purpura, pemphigus, Sjogren's syndrome, Takayasu's arteritis, myocardial infarction, stroke, acute respiratory distress syndrome, sepsis, plasmapheresis, plateletpheresis, leukopheresis, extracorporeal membrane oxygenation, heparin-induced extracorporeal LDL precipitation, bowel inflammation, urticarial, vasculitis, and lupus nephritis.

[0060] In some embodiments, the subject suffers from a condition or disease selected from the group consisting of ischemia-reperfusion injury, rheumatoid arthritis (RA), lupus nephritis, ischemia-reperfusion injury, atypical hemolytic uremic syndrome (aHUS), typical or infectious hemolytic uremic syndrome (tHUS), dense deposit disease (DDD), paroxysmal nocturnal hemoglobinuria (PNH), multiple sclerosis (MS), macular degeneration, hemolysis, elevated liver enzymes, and low platelets (HELLP) syndrome, sepsis, dermatomyositis, diabetic retinopathy, thrombotic thrombocytopenic purpura (TTP), spontaneous fetal loss, Pauci-immune vasculitis, epidermolysis bullosa, recurrent fetal loss, multiple sclerosis (MS), traumatic brain injury, a cardiovascular disorder, myocarditis, a cerebrovascular disorder, a peripheral vascular disorder, a renovascular disorder, a mesenteric/enteric vascular disorder, revascularization to transplants and/or replants, vasculitis, Henoch-Schönlein purpura nephritis, systemic lupus erythematosus-associated vasculitis, vasculitis associated with rheumatoid arthritis, immune complex vasculitis, Takayasu's disease, capillary leak syndrome, dilated cardiomyopathy, diabetic angiopathy, thoracic-abdominal aortic aneurysm, Kawasaki's disease (arteritis), venous gas embolus (VGE), and restenosis following stent placement, rotational atherectomy, percutaneous transluminal coronary angioplasty (PTCA), myasthenia gravis, cold-agglutinin disease (CAD), paroxysmal cold hemoglobinuria (PCH), dermatomyositis, scleroderma, warm autoimmune hemolytic

anemia, Graves' disease, Hashimoto's thyroiditis, type I diabetes, psoriasis, pemphigus, autoimmune hemolytic anemia (AIHA), idiopathic thrombocytopenic purpura (ITP), Goodpasture's syndrome, antiphospholipid syndrome (APS), Degos disease, and catastrophic APS (CAPS).

[0061] In some embodiments, the subject suffers from a condition or disease selected from the group consisting of age-related macular degeneration (AMD), type II membranoproliferative glomerulonephritis (MPGN II), hemolytic uremic syndrome (HUS), asthma, amyloidosis, and thrombotic thrombocytopenic purpura. In some embodiments, the hemolytic uremic syndrome (HUS) is an atypical hemolytic uremic syndrome (aHUS). In some embodiments, the subject suffers from a drusen-associated disease or a drusen-related disease. In some embodiments, the drusen-related disease is amyloidosis, elastosis, dense deposit disease, glomerulonephritis, atherosclerosis or an ocular drusen-related disease.

[0062] Another embodiment provides a pharmaceutical composition comprising a tetravalent fusion protein construct for modulating complement activity, the tetravalent fusion protein construct comprising: (i) an antibody or an antigen binding fragment thereof that binds a complement-associated antigen; and (ii) a first complement modulator peptide and a second complement modulator peptide, wherein the first and second complement modulator polypeptides can be the same or different.

[0063] In some embodiments, the at least one of the first and second complement modulator peptides is conjugated to the antibody or antigen binding fragment by a linker.

[0064] Another embodiment provides a pharmaceutical composition comprising a trivalent fusion protein construct for modulating complement activity, the trivalent fusion protein construct comprising: (i) an antibody or an antigen binding fragment thereof that binds a complement-associated antigen; and (ii) one complement modulator peptide.

[0065] In some embodiments, the antibody or an antigen binding fragment thereof and the complement modulator peptide can be conjugated by a linker.

[0066] Another embodiment provides a pharmaceutical composition comprising a trivalent fusion protein construct for modulating complement activity, the trivalent fusion protein construct comprising: (i) a Fab that binds a complement-associated antigen; (ii) an antibody Fc domain; and (iii) a complement modulator peptide conjugated to the Fab or the Fc domain.

[0067] In some embodiments, the Fab or the Fc domain and the complement modulator peptide can be conjugated by a linker.

[0068] Another embodiment provides a pharmaceutical composition comprising a trivalent fusion protein construct comprising: a) a first polypeptide monomer comprising an antibody CH2 or CH3 domain, wherein the domain has at least one orthogonal modification that favors

formation of a heterodimer as compared to a homodimer; b) a second polypeptide monomer comprising an antibody CH2 or CH3 domain, wherein the domain has at least one orthogonal modification that favors formation of a heterodimer with the first polypeptide monomer as compared to a homodimer; and wherein one of the first and second polypeptide further comprises a complement modulator peptide, and wherein the trivalent fusion protein construct binds a complement-associated antigen.

[0069] In some embodiments, the first polypeptide comprises a knob modification, and wherein the second polypeptide comprises a hole modification. In some embodiments, the first and second polypeptides comprise modifications resulting in charge or surface complementarity. In some embodiments, the complement modulator peptide is connected to one of the first and second polypeptide by an amino acid linker.

[0070] Another embodiment provides a pharmaceutical composition comprising a fusion protein construct that comprises: an antibody or an antigen-binding fragment thereof comprising (i) three heavy chain complementarity determining regions (CDRs) having the amino acid sequences of SEQ ID NOs: 11, 12 and 13; 17, 18 and 19; 23, 24 and 25; 29, 30 and 31; 35, 36 and 37; 147, 148, and 149; 188, 189, and 190; 196, 197, and 198; 204 or 343, 205, and 206; 212, 213, and 214; 220, 221, and 222; 228, 229, and 230; 29, 259 and 31; 29, 260 and 31; residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-100 (CDR-H3) of SEQ ID Nos. 280, 281, 282, 284, 285, 286, 73, or 288; residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-102 (CDR-H3) of SEQ ID No. 244; or residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-110 (CDR-H3) of SEQ ID No. 290 or (ii) three heavy chain CDRs having amino acid sequences that differ by a single conservative amino acid substitution within one of SEQ ID NOs: 11, 12 and 13; 17, 18 and 19; 23, 24 and 25; 29, 30 and 31; 35, 36 and 37; 147, 148, and 149; 188, 189, and 190; 196, 197, and 198; 204 or 343, 205, and 206; 212, 213, and 214; 220, 221, and 222; 228, 229, and 230; 29, 259 and 31; or 29, 260 and 31; residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-100 (CDR-H3) of SEQ ID Nos. 280, 281, 282, 284, 285, 286, 73, or 288; residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-102 (CDR-H3) of SEQ ID No. 244; or residues 26-33 (CDR-H1), 51-58 (CDR-H2), and 97-110 (CDR-H3) of SEQ ID No. 290 and (ii) three light chain complementarity determining regions (CDRs) having the amino acid sequences of SEQ ID NOs: 14, 15 and 16; 20, 21 and 22; 26, 27 and 28; 32, 33 and 34; 38, 39, and 40; 150, 151, and 152; 191, 192, and 193; 199, 200, and 201; 207, 208, and 209; 215, 216, and 217; 223, 224 and 225; or 231, 232, and 233; residues 27-37 (CDR-L1), 55-57 (CDR-L2), and 94-102 (CDR-L3) of SEQ ID Nos. 279, 68, 287, or 59; or residues 27-38 (CDR-L1), 56-58 (CDR-L2), 95-102 (CDR-L3) of SEQ ID No. 289 or (ii) three light chain CDRs having amino acid sequences that differ by a single conservative amino acid substitution within one of SEQ ID NOs 14, 15 and 16; 20,

21 and 22; 26, 27 and 28; 32, 33 and 34; 38, 39, and 40; 150, 151, and 152; 191, 192, and 193; 199, 200, and 201; 207, 208, and 209; 215, 216, and 217; 223, 224 and 225; or 231, 232, and 233; residues 27-37 (CDR-L1), 55-57 (CDR-L2), and 94-102 (CDR-L3) of SEQ ID Nos. 279, 68, 287, or 59; or residues 27-38 (CDR-L1), 56-58 (CDR-L2), 95-102 (CDR-L3) of SEQ ID No. 289 and a complement modulator peptide.

[0071] Another embodiment provides a pharmaceutical composition comprising a fusion protein construct that comprises: an antibody or an antigen-binding fragment thereof comprising (a) a heavy chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 54, 58, 67, 73, 74, 81, 88, 89, 98, 99, 112, 145, 153, 194, 202, 210, 218, 226, 234, 238, 243, 244, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, 274, 280, 281, 282, 283, 284, 285, 286, 288, 290, and 342; and (b) a light chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 45, 59, 68, 195, 203, 211, 219, 227, 235, 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, and 278, 279, 287, and 289, or (c) a heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos: 54, 58, 67, 73, 74, 81, 88, 89, 98, 99, 112, 145, 153, 194, 202, 210, 218, 226, 234, 238, 243, 244, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, 274, 280, 281, 282, 283, 284, 285, 286, 288, 290, and 342; and (d) a light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within at least one of SEQ ID Nos: 45, 59, 68, 195, 203, 211, 219, 227, 235, 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, and 278, 279, 287, and 289.

[0072] Another embodiment provides a pharmaceutical composition comprising a fusion protein construct that comprises a sequence selected from the group consisting of: SEQ ID NOs: 45, 51, 54, 58, 59, 62, 64, 67, 68, 73, 74, 79, 75, 81, 88, 89, 98, 99, 112, 121, 194, 195, 202, 203, 210, 211, 218, 219, 237, 226, 226, 227, 234, 235, 238, 239, 240, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, and 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, and 342; and a complement modulator peptide.

[0073] In some embodiments, the complement modulator peptide is connected to the antibody or an antigen binding fragment thereof by an amino acid linker. In some embodiments, the amino acid linker comprises the amino acid sequence of any of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181,

SEQ ID NO: 182, SEQ ID NO: 183, SEQ ID NO: 241, or SEQ ID NO: 242. In some embodiments, the pharmaceutical composition comprises the antigen-binding fragment, wherein the antigen-binding fragment comprises an Fv fragment, Fab, Fab', F(ab')₂, or an scFv. In some embodiments, the fusion protein construct modulates alternative complement activity in a subject upon administration of the pharmaceutical composition to the subject. In some embodiments, the antibody or an antigen-binding fragment thereof or the Fab binds a domain of a mammalian annexin protein. In some embodiments, the antibody or an antigen-binding fragment thereof or the Fab binds a domain of a mammalian annexin protein with a KD affinity of 10⁻⁸M or less. In some embodiments, the domain is an annexin core domain. In some embodiments, the annexin core domain comprises an alpha-helical domain. In some embodiments, the annexin core domain comprises a calcium binding site and a membrane binding site. In some embodiments, the annexin core domain comprises at least one annexin repeat sequence. In some embodiments, the antibody or antigen-binding fragment thereof or the Fab binds the at least one annexin repeat sequence.

[0074] In some embodiments, the complement-associated antigen comprises a phospholipid, and wherein the antibody or an antigen-binding fragment thereof or the Fab binds the phospholipid. In some embodiments, the antibody or an antigen-binding fragment thereof or the Fab binds the phospholipid with a KD affinity of 10⁻⁸M or less. In some embodiments, the phospholipid is selected from the group consisting of phosphatidylethanolamine (PE), cardiolipin (CL), phosphatidylcholine (PC) and malondialdehyde (MDA). In some embodiments, the complement-associated antigen comprises a C3 complement protein or a fragment thereof, and wherein the antibody or antigen binding fragment thereof or the Fab binds the C3 complement protein or a fragment thereof. In some embodiments, the antibody or an antigen-binding fragment thereof or the Fab binds the C3 complement protein or a fragment thereof KD affinity of 10⁻⁸M or less. In some embodiments, the C3 complement protein fragment is C3d. In some embodiments, the complement modulator peptide comprises complement receptor 1 (CR1) protein. In some embodiments, the complement modulator peptide comprises domain A of the CR1 protein or a fragment thereof that retains at least three short consensus repeats (SCRs) of domain A. In some embodiments, the complement modulator peptide comprises domain B of the CR1 protein or a fragment thereof that retains at least three SCRs of domain B.

[0075] In some embodiments, the complement modulator peptide comprises domain C of the CR1 protein or a fragment thereof that retains at least three SCRs of domain C. In some embodiments, the pharmaceutical composition further comprises domain D of the CR1 protein or a fragment thereof that retains at least three SCRs of domain D. In some embodiments, the complement modulator peptide comprises first three SCRs of domain A, first three SCRs of

domain B, and first three SCRs of domain C of the CR1 protein. In some embodiments, the CR1 protein is a human CR1 protein. In some embodiments, the complement modulator polypeptide is CR1 (1-10). In some embodiments, the complement modulator polypeptide is CR1 (1-17). In some embodiments, the CR1 (1-10) comprises the amino acid sequence of SEQ ID NO: 41 or SEQ ID NO: 91, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the CR1 (1-17) comprises the amino acid sequence of SEQ ID NO: 42 or SEQ ID NO: 92, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is a decay-accelerating factor (DAF) or a biologically active fragment thereof. In some embodiments, the DAF is a human DAF.

[0076] In some embodiments, the biologically active fragment of human DAF comprises at least one of a short consensus repeat (SCR) domain and an O-glycosylated serine/threonine-rich domain of a full-length human DAF. In some embodiments, the biologically active fragment of human DAF comprises SCR 1 to 4, or SCR 2 to 4 of a full-length human DAF. In some embodiments, the biologically active fragment of human DAF comprises the amino acid sequence of SEQ ID NO: 184, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is factor H or a biologically active fragment thereof. In some embodiments, the factor H is a human factor H. In some embodiments, the biologically active fragment of human factor H comprises a stretch of amino acids selected from the group consisting of: amino acids 21-266, amino acids 21-320, amino acids 21-509 or amino acids 19-1106 of SEQ ID NO: 9, or a variant thereof with an amino acid sequence at least 85% identical to the stretch of amino acids. In some embodiments, the biologically active fragment of human factor H comprises one or more groups of short consensus repeats (SCRs) comprising SCRs 1 to 20, SCRs 1 to 2, SCRs 2 to 3, SCRs 3 to 4, SCRs 4 to 5, SCRs 5 to 6, SCRs 6 to 7, SCRs 7 to 8, SCRs 8 to 9, SCRs 9 to 10, SCRs 10 to 11, SCRs 11 to 12, SCRs 12 to 13, SCRs 13 to 14, SCRs 14 to 15, SCRs 15 to 16, SCRs 16 to 17, SCRs 17 to 18, SCRs 19 to 20 of a full-length human factor H, or any combination of SCRs 1 to 20.

[0077] In some embodiments, the biologically active fragment of human factor H comprises SCRs 1 to 4 of a full-length human factor H. In some embodiments, the biologically active fragment of human factor H comprises SCRs 1 to 5 of a full-length human factor H. In some embodiments, the biologically active fragment of human factor H comprises the amino acid sequence of SEQ ID NO: 72 or SEQ ID NO: 108, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is MCP or a biologically active fragment thereof. In some embodiments, the MCP is a human MCP. In some embodiments, the biologically active fragment of human MCP comprises at least

one of a short consensus repeat (SCR) domain of a full-length human MCP. In some embodiments, the biologically active fragment of human MCP comprises SCRs 3 to 4 of the full-length human MCP. In some embodiments, the biologically active fragment of human MCP comprises the amino acid sequence of SEQ ID NO: 187, or a variant thereof with an amino acid sequence at least 85% identical.

[0078] In some embodiments, the complement modulator peptide is Map44 or a biologically active fragment thereof. In some embodiments, the Map44 is a human Map44. In some embodiments, the Map44 comprises the amino acid sequence of SEQ ID NO: 186, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the complement modulator peptide is CD59 or a biologically active fragment thereof. In some embodiments, the CD59 is a human CD59. In some embodiments, the CD59 comprises the amino acid sequence of SEQ ID NO: 185, or a variant thereof with an amino acid sequence at least 85% identical. In some embodiments, the antibody or an antigen-binding fragment thereof is a human antibody or an antigen-binding fragment thereof. In some embodiments, the antibody or an antigen-binding fragment thereof is a humanized antibody or an antigen-binding fragment thereof.

[0079] Another embodiment provides a polynucleotide that encodes a fusion protein. Another embodiment provides a method of treatment comprising providing to a subject a therapeutically effective amount of a pharmaceutical composition. In some embodiments, the subject suffers from complement-mediated inflammation. In some embodiments, the complement-mediated inflammation comprises an inflammatory fibrotic disease, and wherein the inflammatory fibrotic disease comprises focal segmental glomerulosclerosis, primary sclerosing cholangitis, or membranoproliferative glomerulonephritis. In some embodiments, the subject suffers from a complement-mediated auto-immune disease, comprising rheumatoid arthritis, systemic lupus erythematosus, lupus nephritis, or pemphigus vulgaris. In some embodiments, the subject suffers from a complement-mediated kidney disease, comprising membranoproliferative glomerulonephritis, or complement 3 glomerulopathy. In some embodiments, the subject suffers from a complement-mediated cardiovascular disease. In some embodiments, the cardiovascular disease comprises atherosclerosis or thrombosis. In some embodiments, the subject suffers from a complement-mediated dermatological disease. In some embodiments, the dermatological disease comprises psoriasis, acne inversa, lupus erythematosus, cutaneous small vessel vasculitis, urticaria, urticarial vasculitis, and bullous pemphigoid.

[0080] In some embodiments, the complement-mediated inflammation is associated with a condition or disease selected from the group consisting of ischemia/reperfusion injury, burn injury, endotoxemia and septic shock, adult respiratory distress syndrome, cardiopulmonary

bypass, hemodialysis, anaphylactic shock, asthma, angioedema, Crohn's disease, sickle cell anemia, glomerulonephritis, membranous nephritis, pancreatitis, transplant rejection, hyperacute xenograft rejection, recurrent fetal loss, preeclampsia, drug allergy, IL-2 induced vascular leakage syndrome, radiographic contrast media allergy, myasthenia gravis, Alzheimer's disease, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, acute disseminated encephalomyelitis, Addison's disease, antiphospholipid antibody syndrome, autoimmune hepatitis, Goodpasture's syndrome, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, idiopathic thrombocytopenic purpura, pemphigus, Sjogren's syndrome, Takayasu's arteritis, myocardial infarction, stroke, acute respiratory distress syndrome, sepsis, plasmapheresis, plateletpheresis, leukopheresis, extracorporeal membrane oxygenation, heparin-induced extracorporeal LDL precipitation, bowel inflammation, urticarial, and vasculitis and lupus nephritis.

[0081] In some embodiments, the subject suffers from a condition or disease selected from the group consisting of ischemia-reperfusion injury, rheumatoid arthritis (RA), lupus nephritis, ischemia-reperfusion injury, atypical hemolytic uremic syndrome (aHUS), typical or infectious hemolytic uremic syndrome (tHUS), dense deposit disease (DDD), paroxysmal nocturnal hemoglobinuria (PNH), multiple sclerosis (MS), macular degeneration, hemolysis, elevated liver enzymes, and low platelets (HELLP) syndrome, sepsis, dermatomyositis, diabetic retinopathy, thrombotic thrombocytopenic purpura (TTP), spontaneous fetal loss, Pauci-immune vasculitis, epidermolysis bullosa, recurrent fetal loss, multiple sclerosis (MS), traumatic brain injury, a cardiovascular disorder, myocarditis, a cerebrovascular disorder, a peripheral vascular disorder, a renovascular disorder, a mesenteric/enteric vascular disorder, revascularization to transplants and/or replants, vasculitis, Henoch-Schönlein purpura nephritis, systemic lupus erythematosus-associated vasculitis, vasculitis associated with rheumatoid arthritis, immune complex vasculitis, Takayasu's disease, capillary leak syndrome, dilated cardiomyopathy, diabetic angiopathy, thoracic-abdominal aortic aneurysm, Kawasaki's disease (arteritis), venous gas embolus (VGE), and restenosis following stent placement, rotational atherectomy, percutaneous transluminal coronary angioplasty (PTCA), myasthenia gravis, cold-agglutinin disease (CAD), paroxysmal cold hemoglobinuria (PCH), dermatomyositis, scleroderma, warm autoimmune hemolytic anemia, Graves' disease, Hashimoto's thyroiditis, type I diabetes, psoriasis, pemphigus, autoimmune hemolytic anemia (AIHA), idiopathic thrombocytopenic purpura (ITP), Goodpasture's syndrome, antiphospholipid syndrome (APS), Degos disease, and catastrophic APS (CAPS).

[0082] In some embodiments, the subject can suffer from a condition or disease selected from the group consisting of age-related macular degeneration (AMD), type II membranoproliferative

glomerulonephritis (MPGN II), hemolytic uremic syndrome (HUS), asthma, amyloidosis, and thrombotic thrombocytopenic purpura. In some embodiments, the hemolytic uremic syndrome (HUS) is an atypical hemolytic uremic syndrome (aHUS). In some embodiments, the subject can suffer from a drusen-associated disease or a drusen-related disease. In some embodiments, the drusen-related disease can be amyloidosis, elastosis, dense deposit disease, glomerulonephritis, atherosclerosis or an ocular drusen-related disease.

[0083] An additional embodiment provides a fusion protein construct that binds a complement-associated antigen, the monomeric fusion protein construct comprising: a first polypeptide comprising: a domain A, and a domain B, arranged, from N- terminus to C-terminus in an A-B orientation, a second polypeptide comprising: a domain E, and a domain F, arranged, from N-terminus to C-terminus in an E-F orientation, wherein at least one of domain A and domain E can be conjugated to a domain R, and wherein: domain A can comprise a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain R comprises a complement modulator polypeptide, domain E can comprise a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and domain F can comprise a light chain constant region amino acid sequence (CL1). In some embodiments, the first polypeptide comprises the domain A, the domain B, and the domain R, wherein the domains of the first polypeptide are arranged, from N-terminus to C-terminus, in an R-A-B orientation, and wherein the domain R and the domain A are conjugated. In some embodiments, the second polypeptide comprises the domain E, the domain F, and the domain R, wherein the domains of the second polypeptide are arranged, from N-terminus to C-terminus, in an R-E-F orientation, and wherein the domain E and the domain R are conjugated.

[0084] Another embodiment provides a fusion protein construct comprising: an antibody or an antigen binding fragment thereof that specifically binds to complement protein 3d (c3d), and two molecules of a complement modulator polypeptide, wherein each molecule of the complement modulator polypeptide comprises a biologically active fragment of a complement protein selected from the group consisting of: CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, and factor H, wherein the fusion protein construct has a lower half-maximal inhibitory concentration, in a complement assay, compared to that of a comparator protein construct that does not comprise the antibody but is otherwise identical.

[0085] In some embodiments, the each molecule of the complement modulator polypeptide can be conjugated to a heavy chain of the antibody or the antigen binding fragment thereof. In some embodiments, the each molecule of the complement modulator polypeptide can be conjugated to the C terminus of the heavy chain.

[0086] In some embodiments, the antibody or the antigen binding fragment thereof can comprise a first polypeptide and a second polypeptide, wherein the first polypeptide can comprise a heavy chain sequence comprising the amino acid sequence of at least one of: SEQ ID NO: 54, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 243, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 285, and SEQ ID NO: 286; and the second polypeptide can comprise a light chain sequence comprising the amino acid sequence of at least one of: SEQ ID NO: 59, SEQ ID NO: 68, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 135, and SEQ ID NO: 27.

[0087] In some embodiments, the first polypeptide can comprise at least two amino acid sequences selected from the group consisting of SEQ ID NO: 54, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 243, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 285, and SEQ ID NO: 286; and the second polypeptide can comprise at least two amino acid sequences selected from the group consisting of SEQ ID NO: 59, SEQ ID NO: 68, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 135, and SEQ ID NO: 279.

[0088] In some embodiments, the at least two amino acid sequences of the first polypeptide can be the same amino acid sequence, and the at least two amino acid sequences of the second polypeptide can be the same amino acid sequence. In some embodiments, the at least two amino acid sequences of the first polypeptide can be SEQ ID NO: 282 or SEQ ID NO: 285, and the at least two amino acid sequences of the second polypeptide can be SEQ ID NO: 279.

[0089] In some embodiments, the fusion protein construct further comprises a linker. In some embodiments the linker can comprise the amino acid sequence of any of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, SEQ ID NO: 241, or SEQ ID NO: 242.

[0090] In some embodiments, the complement protein is factor H or a biologically active fragment thereof. In some embodiments, the factor H or biologically active fragment thereof can

comprise the amino acid sequence of SEQ ID NO: 72 or SEQ ID NO: 108, or a variant thereof with an amino acid sequence at least 85% identical.

[0091] In some embodiments, the complement protein is CR1 or a fragment thereof. In some embodiments, the complement protein can comprise the amino acid sequence of SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, or SEQ ID NO: 92, or a variant thereof with an amino acid sequence at least 85% identical.

[0092] In some embodiments, the fusion protein construct can comprise the amino acid sequence of at least one of SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 83, SEQ ID NO: 84, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 279, SEQ ID NO: 282, and SEQ ID NO: 285.

[0093] Another embodiment provides, a fusion protein construct comprising: an antibody or an antigen binding fragment thereof that specifically binds to a complement-associated antigen, wherein the antibody comprises a first polypeptide and a second polypeptide, wherein the first polypeptide and the second polypeptide each comprises a heavy chain, and a light chain; and a first molecule and a second molecule of a complement modulator polypeptide, wherein the first molecule and the second molecule each comprises a biologically active fragment of a complement protein selected from the group consisting of: CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, and factor H, wherein upon administration of the fusion protein construct to a subject having a disease, an albumin to creatinine ratio in a urine sample from the subject having the disease is lower than an albumin to creatine ratio in a urine sample from a subject

administered with a comparable fusion protein construct, wherein the comparable fusion protein construct does not comprise the antibody or the antigen binding fragment thereof but is otherwise identical

[0094] In some embodiments, the disease is a complement-mediated kidney disease. In some embodiments, the complement-mediated kidney disease is a membranoproliferative glomerulonephritis or complement 3 glomerulopathy.

[0095] In some embodiments, the albumin to creatinine ratio in the urine sample from the subject having the disease can be at least about 1%, 2%, 3%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85% lower (e.g., than in a subject administered with a comparable fusion protein construct).

[0096] Another embodiment provides a fusion protein construct that comprises: an antibody or an antigen-binding fragment thereof comprising: a heavy chain comprising the amino acid sequence of at least one of SEQ ID Nos: 54, 58, 60, 61, 64, 65, 67, 69, 70, 71, 73, 74, 75, 76, 78, 80, 81, 82, 85, 87, 88, 89, 98, 99, 112, 132, 133, 134, 145, 153, 194, 202, 210, 218, 226, 234, 238, 243, 244, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, 274, 280, 281, 282, 283, 284, 285, 286, 288, 290, and 342; and a light chain comprising the amino acid sequence of at least one of SEQ ID Nos: 45, 59, 68, 77, 79, 84, 86, 135, 195, 203, 211, 219, 227, 235, 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, 278, 279, 287, and 289; or a heavy chain comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos: 54, 58, 60, 61, 64, 65, 67, 69, 70, 71, 73, 74, 75, 76, 78, 80, 81, 82, 85, 87, 88, 89, 98, 99, 112, 132, 133, 134, 145, 153, 194, 202, 210, 218, 226, 234, 238, 243, 244, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, 274, 280, 281, 282, 283, 284, 285, 286, 288, 290, and 342; and a light chain comprising an amino acid sequence that differs by one or more conservative amino acid substitution within at least one of SEQ ID Nos: 45, 59, 68, 77, 79, 84, 86, 135, 195, 203, 211, 219, 227, 235, 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, 278, 279, 287, and 289.

[0097] In some embodiments, the fusion protein construct can further comprise a complement modulator polypeptide, wherein the complement modulator polypeptide comprises at least one of complement receptor 1 (CR1) protein, DAF, MCP, Crry, MAp44, MAp19, CD59, factor H, and biologically active fragments thereof

The present invention as claimed herein is described in the following items 1 to 57:

1. A fusion protein construct comprising:

- (1) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
 - (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
- (2) a complement modulator polypeptide, wherein the complement modulator polypeptide comprises factor H, or a biologically active fragment thereof.

2. A fusion protein construct comprising:

- (1) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
 - (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino

- acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
- (2) a complement modulator polypeptide, wherein the complement modulator polypeptide comprises CR1 or a biologically active fragment thereof.
3. The fusion protein construct of item 1 or 2, wherein the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258.
 4. The fusion protein construct of item 3, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
 5. The fusion protein construct of any one of items 1 to 4, wherein the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254.
 6. The fusion protein construct of item 5, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
 7. The fusion protein construct of item 6, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 282.
 8. The fusion protein construct of item 6, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 285.
 9. The fusion protein construct of any one of items 1 to 8, wherein:
 - (a) the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258; and,
 - (b) the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254.
 10. The fusion protein construct of item 9, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
 11. The fusion protein construct of item 10, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
 12. The fusion protein construct of item 11, wherein the fusion protein construct further comprises a linker linking the antibody or antigen binding fragment thereof to the

- complement modulator polypeptide.
13. The fusion protein construct of item 12, wherein the linker comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, and SEQ ID NO: 241.
 14. The fusion protein construct of item 12, wherein the linker is bound to the C-terminus of the heavy chain and comprises the amino acid sequence of SEQ ID NO: 138.
 15. The fusion protein construct of any one of items 1 or 3 to 14, wherein the complement modulator polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108.
 16. The fusion protein construct of any one of items 2 to 14, wherein the complement modulator polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
 17. The fusion protein construct of item 15, wherein the complement modulator polypeptide comprises an amino acid sequence of SEQ ID NO: 72.
 18. The fusion protein construct of item 16, wherein the complement modulator polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 41 and SEQ ID NO: 42.
 19. The fusion protein construct of any one of items 1 to 18, wherein the antibody or antigen binding fragment thereof comprises:
 - (a) a first heavy chain and a second heavy chain, wherein each of the first and the second heavy chain comprises three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ

- ID NO: 31, and
- (b) a first light chain and a second light chain, wherein each of the first and the second light chain comprises three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34.
20. The fusion protein construct of item 19, wherein each of the first and the second heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254, and wherein each of the first and the second light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258.
 21. The fusion protein construct of item 20, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 284, and wherein the first and the second light chain each comprises the amino acid sequence of SEQ ID NO: 279.
 22. The fusion protein construct of item 21, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 282.
 23. The fusion protein construct of item 21, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 285.
 24. The fusion protein construct of item 21, wherein the fusion protein further comprises a linker linking the antibody or antigen binding fragment thereof to one of the complement modulator polypeptides.
 25. The fusion protein construct of item 24, wherein the linker comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, and SEQ ID NO: 241.

26. The fusion protein construct of item 24, comprising:
 - (c) a first linker bound to the C-terminus of the first heavy chain and comprising the amino acid sequence of SEQ ID NO: 138; and
 - (d) a second linker bound to the C-terminus of the second heavy chain and comprising the amino acid sequence of SEQ ID NO: 138.
27. The fusion protein construct of item 26, wherein the complement modulator polypeptide that comprises Factor H or a biologically active fragment thereof comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108.
28. The fusion protein construct of item 26, wherein the complement modulator polypeptide that comprises CR1 or a biologically active fragment thereof comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
29. The fusion protein construct of any one of items 1 to 28, wherein the fusion protein construct is selected from the group consisting of:
 - (1) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (2) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (3) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41;

- (4) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279;
 - (5) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (6) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (7) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and,
 - (8) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279.
30. An antibody or antigen-binding fragment thereof comprising:
- a heavy chain comprising: three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3) comprising the following set of amino acid sequences: SEQ ID NOs: 29, 260, and 31, and
 - a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3) comprising the following set of amino acid sequences: SEQ

- ID NOs: 32, 33, and 34.
31. The antibody or antigen-binding fragment thereof of item 30, wherein:
 - (a) the heavy chain comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 254; and
 - (b) the light chain comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 258.
 32. The antibody or antigen-binding fragment thereof of item 31, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
 33. The antibody or antigen-binding fragment thereof of item 32, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
 34. The antibody or antigen-binding fragment thereof of item 33, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 282.
 35. The antibody or antigen-binding fragment thereof of item 33, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 285.
 36. A pharmaceutical composition comprising the fusion protein of any one of items 1 to 29 or the antibody or antigen-binding fragment thereof of any one of items 30 to 35.
 37. A method of treating a complement mediated disease characterized by an increased deposition of C3d, the method comprising administering to a subject a fusion protein construct comprising:
 - (i) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
 - (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the

- amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
- (ii) a complement modulator polypeptide comprising a complement protein selected from the group consisting of: CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, factor H, and a biologically active fragment thereof.
38. Use of a fusion protein construct in the manufacture of a medicament for treating a complement mediated disease characterized by an increased deposition of C3d, wherein the fusion protein construct comprises:
- (1) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
- (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
- (b) a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
- (2) a complement modulator polypeptide comprising a complement protein selected from the group consisting of: CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, factor H, and a biologically active fragment thereof.
39. The method of item 37, or use of item 38, wherein the complement mediated disease is a complement mediated kidney disease.
40. The method or use of item 39, wherein the complement mediated kidney disease is selected from the group consisting of: focal segmental glomerulosclerosis, glomerulonephritis, complement 3 glomerulopathy (C3G), membranoproliferative

glomerulonephritis, C3 glomerulonephritis, type II membranoproliferative glomerulonephritis (MPGN II), membranous nephropathy (MN), IgA nephropathy (IgAN), lupus nephritis (LN), hemolytic uremic syndrome (HUS), atypical hemolytic uremic syndrome (aHUS), and diabetic retinopathy.

41. The method of item 37, or the use of item 38, wherein the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258, or wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
42. The method of item 37, or the use of item 38, wherein the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254, or wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 282, 284, or 285.
43. The method of item 37, or the use of item 38, wherein:
 - (a) the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258; and,
 - (b) the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254.
44. The method or use of item 43, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279, and wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
45. The method or use of item 44, wherein the fusion protein construct further comprises a linker linking the antibody or antigen binding fragment thereof to the complement modulator polypeptide, wherein the linker is bound to the C-terminus of the heavy chain and comprises the amino acid sequence of and one of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, and SEQ ID NO: 241.
46. The method of item 37, or the use of item 38, wherein the complement modulator

polypeptide comprises:

- (a) an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108, or,
 - (b) an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
47. The method or use of item 46, wherein the complement modulator polypeptide comprises:
- (a) an amino acid sequence of SEQ ID NO: 72, or,
 - (b) an amino acid sequence selected from the group consisting of: SEQ ID NO: 41 and SEQ ID NO: 42.
48. The method of item 37, or the use of item 38, wherein the antibody or antigen binding fragment thereof comprises:
- (a) a first heavy chain and a second heavy chain, wherein each of the first and the second heavy chain comprises three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a first light chain and a second light chain, wherein each of the first and the second light chain comprises three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34.
49. The method or use of item 48, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 282.
50. The method or use of item 49, comprising:
- (c) a first linker bound to the C-terminus of the first heavy chain and comprising the amino acid sequence of SEQ ID NO: 138; and
 - (d) a second linker bound to the C-terminus of the second heavy chain and comprising the amino acid sequence of SEQ ID NO: 138.

51. The method or use of item 50, wherein the complement modulator polypeptide comprises:
- (a) an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108, or,
 - (b) an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
52. The method of item 37, or the use of item 38, wherein the fusion protein construct is selected from the group consisting of:
- (1) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (2) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (3) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41;
 - (4) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279;
 - (5) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light

- chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
- (6) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (7) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and,
 - (8) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279.
53. The method of item 37, or the use of item 38, wherein the fusion protein construct comprises:
- (i) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72; and,
 - (ii) two light chain-containing polypeptides, each comprising the amino acid sequence of SEQ ID NO: 279.
54. The method of item 37, or the use of item 38, wherein the fusion protein construct comprises:
- (i) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 41; and,
 - (ii) two light chain-containing polypeptides, each comprising the amino acid sequence

of SEQ ID NO: 279.

55. The method or use of item 53, wherein the complement mediated disease is a complement mediated kidney disease.
56. The method or use of item 55, wherein the complement mediated kidney disease is selected from the group consisting of: focal segmental glomerulosclerosis, glomerulonephritis, complement 3 glomerulopathy (C3G), membranoproliferative glomerulonephritis, C3 glomerulonephritis, type II membranoproliferative glomerulonephritis (MPGN II), membranous nephropathy (MN), IgA nephropathy (IgAN), lupus nephritis (LN), hemolytic uremic syndrome (HUS), atypical hemolytic uremic syndrome (aHUS), and diabetic retinopathy.
57. The method or use of item 55, wherein the complement mediated kidney disease is IgA nephropathy (IgAN), complement 3 glomerulopathy (C3G), or lupus nephritis (LN).

INCORPORATION BY REFERENCE

[0098] All publications, patents, patent applications, and NCBI accession numbers mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference, and as if set forth in their entireties. In the event of a conflict between a term as used herein and the term as defined in the incorporated reference, the definition of this disclosure controls.

BRIEF DESCRIPTION OF THE DRAWINGS

[0099] The novel features of the disclosure are set forth with particularity in the appended claims. A better understanding of the features and advantages of this disclosure will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of this disclosure are utilized, and the accompanying drawings of which.

[00100] FIG. 1 illustrates an exemplary monomeric fusion protein construct of this disclosure, comprising a linkage between the light chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the N-terminus of the light chain via a linker.

[00101] FIG. 2 illustrates an exemplary monomeric fusion protein construct of this disclosure, comprising a linkage between the heavy chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the N-terminus of the heavy chain via a linker.

[00102] FIG. 3 illustrates an exemplary monomeric fusion protein construct of this disclosure, comprising a linkage between the heavy chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the C-terminus of the heavy chain via a linker.

[00103] FIG. 4 illustrates an exemplary monomeric fusion protein construct of this disclosure, comprising a linkage between the light chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the C-terminus of the light chain via a linker.

[00104] FIG. 5 illustrates an exemplary tetravalent homodimeric fusion protein construct of this disclosure, comprising a linkage between the heavy chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the C-terminus of the heavy chain via a linker.

[00105] FIG. 6 illustrates an exemplary tetravalent homodimeric fusion protein construct of this disclosure, comprising a linkage between the heavy chain of a targeting moiety and a

complement modulator polypeptide. The complement modulator polypeptide is connected to the N-terminus of the heavy chain via a linker.

[00106] FIG. 7 illustrates an exemplary trivalent heterodimeric fusion protein construct of this disclosure, comprising a linkage between the heavy chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the C-terminus of the heavy chain via a linker.

[00107] FIG. 8 illustrates an exemplary trivalent heterodimeric fusion protein construct of this disclosure, comprising a linkage between the heavy chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the N-terminus of the heavy chain via a linker.

[00108] FIG. 9 illustrates an exemplary tetravalent homodimeric fusion protein construct of this disclosure, comprising a linkage between the light chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the C-terminus of the light chain via a linker.

[00109] FIG. 10 illustrates an exemplary tetravalent homodimeric fusion protein construct of this disclosure, comprising a linkage between the light chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the N-terminus of the light chain via a linker.

[00110] FIG. 11 illustrates an exemplary trivalent heterodimeric fusion protein construct of this disclosure, comprising a linkage between the light chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the N-terminus of the light chain via a linker.

[00111] FIG. 12 illustrates an exemplary trivalent heterodimeric fusion protein construct of this disclosure, comprising a linkage between the light chain of a targeting moiety and a complement modulator polypeptide. The complement modulator polypeptide is connected to the C-terminus of the light chain via a linker.

[00112] FIG. 13 illustrates an exemplary fusion protein construct of this disclosure, comprising a linkage between the N-terminus of the Fc region of a targeting moiety and a complement modulator polypeptide.

[00113] FIG. 14 illustrates exemplary designs for C2-complement modulator fusion protein constructs of this disclosure.

[00114] FIG. 15 illustrates exemplary designs for anti-C3d-complement modulator fusion protein constructs of this disclosure.

[00115] FIG. 16 illustrates exemplary designs for anti-C3d complement modulator fusion protein constructs of this disclosure.

[00116] **FIG. 17** illustrates exemplary designs for anti-C3d complement modulator fusion protein constructs of this disclosure.

[00117] **FIG. 18** illustrates exemplary designs for anti-C3d complement modulator fusion protein constructs of this disclosure.

[00118] **FIG. 19** illustrates an exemplary fusion protein construct of this disclosure, a tetravalent heterodimer, comprising two different complement modulator polypeptides connected to the C-terminus of a heavy chain via a polypeptide linker.

[00119] **FIG. 20** illustrates PEPperMAP® Linear Epitope Mappings and the results from five mouse IgG1 antibodies against C3dg extended. The linear C3d epitopes were determined using PEPperPRINT technology (PEPperPRINT GmbH, Heidelberg, Germany). 15 amino acid long peptides derived from C3dg primary sequence offset by one amino acid were synthesized, in duplicates, on a PEPperPRINT microarray. The array was then sequentially incubated with antibodies (*e.g.*, 3d8b, 3d9a, 3d29) and stained with secondary DyLight680 dye labeled Goat anti-mouse IgG (H+L) antibody. The microarray was read using the LI-COR Odyssey Imaging System and analyzed by PEPperPRINT.

[00120] **FIG. 21** illustrates recognition of an epitope on the C-terminus of C3dg by exemplary anti-C3d antibody 3d29. FIG. 21 discloses SEQ ID NOS 301-341 on the x-axis of the graph, respectively, in order of appearance and the sequence "NLDVSLQLPS" as SEQ ID NO: 299.

[00121] **FIG. 22** illustrates recognition of an epitope on the C-terminus of C3dg by exemplary anti-C3d antibody 3d8b. FIG. 22 discloses SEQ ID NOS 301-341 on the x-axis of the graph, respectively, in order of appearance and the sequence "NLDVSLQLPS" as SEQ ID NO: 299.

[00122] **FIG. 23** illustrates recognition of an epitope on the C-terminus of C3dg by exemplary anti-C3d antibody 3d9a. FIG. 23 discloses SEQ ID NOS 301-341 on the x-axis of the graph, respectively, in order of appearance and the sequence "NLDVSLQLPS" as SEQ ID NO: 299.

[00123] **FIG. 24** illustrates epitope mapping using negative control anti-C3d antibody, that did not bind a linear epitope, tested at various concentrations. FIG. 24 discloses SEQ ID NOS 301-341 on the x-axis of the graph, respectively, in order of appearance.

[00124] **FIG. 25** illustrates epitope mapping using a negative control anti-C4d antibody, tested at various concentrations. FIG. 25 discloses SEQ ID NOS 301-341 on the x-axis of the graph, respectively, in order of appearance

[00125] **FIGs. 26A-26L** illustrates exemplary designs for C2-complement modulator (CR1) fusion protein constructs of this disclosure. **FIG. 26A** shows a fusion protein construct comprising a CR1 (1-10) polypeptide and an exemplary C2-scFv, wherein the CR1 (1-10) polypeptide is connected to the C-terminus of the light chain variable domain of the exemplary C2-scFv. **FIG. 26B** shows a fusion protein construct comprising a Crry polypeptide and an

exemplary C2-scFv, wherein the Crry polypeptide is connected to the C-terminus of the light chain variable domain of the exemplary C2-scFv. **FIG. 26C** shows a fusion protein construct comprising a Crry polypeptide and an exemplary C2-Fab, wherein the Crry polypeptide is connected to the C-terminus of the heavy chain of the exemplary C2-Fab. **FIG. 26D** shows a fusion protein construct comprising a CR1 (1-10) polypeptide and an exemplary C2-Fab, wherein the CR1 (1-10) polypeptide is connected to the N-terminus of the heavy chain of the exemplary C2-Fab. **FIG. 26E** shows a fusion protein construct comprising a CR1 (1-10) polypeptide and an exemplary C2-Fab, wherein the CR1 (1-10) is connected to the C-terminus of the heavy chain of the exemplary C2-Fab. **FIG. 26F** shows a fusion protein construct comprising a CR1 (1-17) polypeptide and an exemplary C2-Fab, wherein the CR1 (1-17) polypeptide is connected to the N-terminus of the heavy chain of the exemplary C2-Fab. **FIG. 26G** shows a fusion protein construct comprising a CR1 (1-17) polypeptide and an exemplary C2-Fab, wherein the CR1 (1-17) polypeptide is connected to the C-terminus of the heavy chain of the exemplary C2-Fab. **FIG. 26H** shows a fusion protein construct comprising a single CR1 (1-10) polypeptide and an exemplary full-length C2-antibody, wherein the CR1 (1-10) is connected to the C-terminus of one of the heavy chains of the exemplary full-length C2-antibody, wherein the fusion protein construct comprises a knob-into-hole heterodimeric antibody construct. **FIG. 26I** shows a fusion protein construct comprising two CR1 (1-10) polypeptides and an exemplary full length C2-antibody, wherein each the C-terminus of each heavy chain of the exemplary full-length C2-antibody is connected to a single CR1 (10) polypeptide, wherein the fusion protein construct comprises a knob-into-hole heterodimeric antibody construct. **FIG. 26J** shows a fusion protein construct comprising a single CR1 (1-10) polypeptide and an exemplary C2-antibody fragment comprising a variable heavy region, a variable light region, and a constant region, wherein the single CR1 (10) polypeptide is connected to the N-terminus of the CH2-CH3 constant region of the exemplary C2-antibody fragment. **FIG. 26K** shows a fusion protein construct comprising a single CR1 (1-10) polypeptide and an exemplary full-length C2-antibody, wherein the single CR1 (10) polypeptide is connected to the N-terminus of one of the light chains of the exemplary full-length C2-antibody. **FIG. 26L** shows a fusion protein construct comprising a single CR1 (1-10) polypeptide and an exemplary full-length C2-antibody, wherein the single CR1 (10) polypeptide is connected to the N-terminus of one of the heavy chains of the exemplary full-length C2-antibody.

[00126] FIGs. 27A-27E illustrates exemplary designs for anti-C3d (3d29)-complement modulator (CR1 or factor H) fusion protein constructs of this disclosure. **FIG. 27A** shows a fusion protein construct comprising a Crry polypeptide and an exemplary antiC3d-Fab, wherein

the Crry polypeptide is connected to the C-terminus of the heavy chain of the exemplary anti-C3d-Fab. **FIG. 27B** shows a fusion protein construct comprising a CR1 (1-10) polypeptide and an exemplary anti-C3d Fab, wherein the CR1 (1-10) polypeptide is connected to the C-terminus of the heavy chain of the exemplary anti-C3d Fab. **FIG. 27C** shows a fusion protein construct comprising factor H and an exemplary anti-C3d Fab, wherein the Factor H is connected to the C-terminus of the heavy chain of the exemplary anti-C3d Fab. **FIG. 27D** shows a fusion protein construct comprising a single factor H polypeptide and an exemplary full-length anti-C3d antibody, wherein the single factor H polypeptide is connected to the C-terminus of the heavy chain of the exemplary full-length anti-C3d antibody. **FIG. 27E** shows a fusion protein construct comprising two single factor H polypeptides and an exemplary full-length anti-C3d antibody, wherein the C-terminus of each heavy chain of the exemplary full-length anti-C3d antibody is connected to a single factor H polypeptide.

[00127] FIGs. 28A-28H illustrates exemplary designs for anti-C3d (3d8b)-complement modulator (CR1 or factor H) fusion protein constructs of this disclosure. **FIG. 28A** shows a fusion protein construct comprising a Crry polypeptide and an exemplary anti-C3d Fab, wherein the Crry is connected to the C-terminus of the heavy chain of the exemplary anti-C3d Fab. **FIG. 28B** shows a fusion protein construct comprising a CR1 (1-10) polypeptide and an exemplary anti-C3d Fab, wherein the CR1 (1-10) polypeptide is connected to the C-terminus of the heavy chain of the exemplary anti-C3d Fab. **FIG. 28C** shows a fusion protein construct comprising a factor H polypeptide and an exemplary anti-C3d Fab, wherein the factor H polypeptide is connected to the C-terminus of the heavy chain of the exemplary anti-C3d Fab. **FIG. 28D** shows a fusion protein construct comprising a single CR1 (1-10) polypeptide and an exemplary full-length anti-C3d antibody, wherein the single CR1 (1-10) polypeptide is connected to the C-terminus of one of the light chains of the exemplary full-length anti-C3d antibody. **FIG. 28E** shows a fusion protein construct comprising a single CR1 (1-10) polypeptide and an exemplary full-length anti-C3d antibody, wherein the single CR1 (1-10) polypeptide is connected to the C-terminus of one of the heavy chains of the exemplary full-length antibody. **FIG. 28F** shows a fusion protein construct comprising two CR1 (1-10) polypeptides and an exemplary full-length anti-C3d antibody, wherein the C-terminus of each heavy chain of the exemplary full-length anti-C3d antibody is connected to a single CR1 (1-10) polypeptide. **FIG. 28G** shows a fusion protein construct comprising a single factor H polypeptide and an exemplary full-length anti-C3d antibody, wherein the single factor H polypeptide is connected to the C-terminus of one of the heavy chains of the exemplary full-length anti-C3d antibody. **FIG. 28H** shows a fusion protein construct comprising two factor H polypeptides and an exemplary full-length anti-C3d

antibody, wherein the C-terminus of each heavy chain of the exemplary full-length anti-C3d antibody is connected to a single factor H polypeptide.

[00128] FIGs. 29A-29C illustrates exemplary designs for anti-C3d (3d8b)-complement modulator (factor H) fusion protein constructs of this disclosure. **FIG. 29A** illustrates fH 1-5 - 3d8b heavy chain murine IgG1 (the complement modulator is connected to the N-terminus of the heavy chain via a linker). **FIG. 29B** illustrates 3d8b kappa light chain – fH 1-5 (the complement modulator is connected to the C-terminus of the light chain via a linker). **FIG. 29C** illustrates fH 1-5 - 3d8b kappa light chain (the complement modulator is connected to the N-terminus of the light chain via a linker).

[00129] FIG. 30 illustrates an exemplary design for IgG1-complement modulator (factor H) fusion protein constructs of this disclosure, where the complement modulator (factor H) is connected to the hinge region of the IgG1 via a linker.

[00130] FIGs. 31A-31F illustrates exemplary designs for anti-C3d (3d8b)-complement modulator (CR1 1-17) fusion protein constructs of this disclosure. **FIG. 31A** shows a fusion protein construct comprising one CR1 (1-17) polypeptide and an exemplary Fab fragment of the anti-C3d antibody 3d8b, wherein the C-terminus of the heavy chain of the exemplary Fab fragment is connected to the single CR1 (1-17) polypeptide. **FIG. 31B** shows a fusion protein construct comprising one CR1 (1-17) polypeptide and an exemplary full length anti-C3d 3d8b antibody, wherein the C-terminus of one of the heavy chains of the exemplary full-length anti-C3d 3d8b antibody is connected to the single CR1 (1-17) polypeptide. **FIG. 31C** shows a fusion protein construct comprising two CR1 (1-17) polypeptides and an exemplary full-length anti-C3d 3d8b antibody, wherein the C-terminus of each of the heavy chains of the exemplary full-length anti-C3d 3d8b antibody is connected to a single CR1 (1-17) polypeptide. **FIG. 31D** shows a fusion protein construct comprising two CR1 (1-17) polypeptides and an exemplary full-length anti-C3d 3d8b antibody, wherein the C-terminus of each of the light chains of the exemplary full-length anti-C3d 3d8b antibody is connected to a single CR1 (1-17) polypeptide. **FIG. 31E** shows a fusion protein construct comprising two CR1 (1-17) polypeptides and an exemplary full length anti-C3d 3d8b antibody, wherein the N-terminus of each of the heavy chains of the exemplary full-length anti-C3d 3d8b antibody is connected to a single CR1 (1-17) polypeptide. **FIG. 31F** shows a fusion protein construct comprising two CR1 (1-17) polypeptides and an exemplary full-length anti-C3d 3d8b antibody, wherein the N-terminus of each of the light chains of the exemplary full-length anti-C3d 3d8b antibody is connected to a single CR1 (1-17) polypeptide.

[00131] FIGs. 32A - 32B show quantification of C3 positive staining is expressed as percentage of total glomerular area (ImageJ software analyses) or semi-quantitative scoring. **FIG. 32A** shows the

staining of glomerular C3 deposits in harvested kidneys measured by immunofluorescence (IF). **FIG. 32 B** shows the C3 deposits of harvested livers using IF.

[00132] FIGs. 33A – 33B show quantification of C3 positive staining is expressed as percentage of total glomerular area (ImageJ software analyses) or semi-quantitative scoring. **FIG. 33A** shows the staining of glomerular C3 deposits in harvested kidneys measured by IF. **FIG. 33B** shows the C3 deposits of harvested livers using IF.

[00133] FIG. 34 shows the percent of infarct volume in Balb/c mice.

[00134] FIG. 35 shows the delta in urine albumin: creatinine ratios (uACR) in adriamycin-injured mice between days 8 and 22 of the study. Day 8 is prior to treatment and day 22 represents 12 days after dosing with complement inhibitors (after treatment).

DETAILED DESCRIPTION

[00135] This disclosure provides fusion protein constructs comprising an antibody or an antigen binding fragment thereof and two molecules of a complement modulator polypeptide. The antibody or antigen binding fragment thereof can specifically bind to a complement protein. The complement protein can be, for example, complement protein 3d (c3d). In some cases, a molecule of the complement modulator polypeptide can comprise at least a biologically active fragment of a complement protein. The complement protein can be, for example, CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, or factor H. In some cases, the fusion protein construct has a lower half-maximal inhibitory concentration (based on for example a complement assay) compared to that of a comparator protein construct that does not comprise the antibody but is otherwise identical. In some cases, a molecule of the complement modulator polypeptide can be conjugated to a heavy chain of the antibody or the antigen binding fragment thereof. In some cases, a molecule of the complement modulator polypeptide can be conjugated to a light chain of the antibody or the antigen binding fragment thereof. In some cases, a molecule of the complement modulator polypeptide is conjugated to the C terminus of the heavy chain and/or the light chain. In some cases, a molecule of the complement modulator polypeptide is conjugated to the N terminus of the heavy chain and/or the light chain.

[00136] This disclosure provides a fusion protein construct comprising an antibody or an antigen binding fragment thereof that specifically binds to a complement-associated antigen, and a first molecule and a second molecule of a complement modulator polypeptide. In some case, the antibody can comprise a first polypeptide and a second polypeptide. In some cases, the first polypeptide and the second polypeptide can each comprise a heavy chain, and a light chain. In some cases, the first molecule and the second molecule can each comprise a biologically active fragment of a complement protein. The complement protein can be CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, or factor H. In some cases, an albumin to creatine ratio can be measured in a biological

sample from a subject. In some cases, the albumin to creatine ratio is determined at some point after administration of the fusion protein construct of this disclosure or after the administration of a comparable fusion protein construct. In some cases, the albumin to creatine ratio is compared between two or more biological samples from the same subject or from another subject. In some cases, the biological sample is a urine sample. In some cases, the subject has a disease disclosed in this disclosure. In some cases, the subject does not have a disease. In some cases, the albumin to creatinine ratio in a urine sample, after the administration of a fusion protein construct of this disclosure, from a subject having a disease (e.g., renal disease) is lower than an albumin to creatine ratio in a urine sample from a subject administered with a comparable fusion protein construct. In some cases, the comparable fusion protein construct does not comprise the antibody or the antigen binding fragment thereof but is otherwise identical to the fusion protein constructs of this disclosure.

[00137] This disclosure provides fusion protein constructs comprising at least two components that are fused to each other: (i) a targeting moiety that binds to a complement-associated antigen, and (ii) a complement modulator. The components of the construct can be fused to each other through covalent or non-covalent interactions. The fusion construct proteins can be engineered to optimize and tailor their target binding valency depending on the target, the condition and the amount of complement modulator desired. For example, the fusion protein constructs can be designed as bivalent, trivalent, or tetravalent, and each valency can relate to the target binding component or the complement modulator. When valency is used to describe the fusion protein construct, it is the sum of the valencies of each component. In some cases, the targeting moiety can be bivalent while the complement modulator is monovalent, providing a trivalent fusion protein construct. In certain other cases, the targeting moiety can be mono or bivalent while the complement modulator is bivalent, providing a trivalent or tetravalent fusion construct, respectively.

[00138] In addition, the targeting moiety within the fusion protein constructs can specifically bind to more than one antigen, thereby making the fusion protein construct a bispecific, trispecific, or multispecific molecule. The fusion protein constructs of the disclosure, armed with their increased specificity and increased valency, can bind to a plurality of targets. In certain examples, the fusion protein construct may have additional advantageous properties, such as suitability for production and pharmaceutical formulation due to their improved stability, low aggregation, pharmacokinetic and biological properties, or any combination thereof.

[00139] The targeting moiety can be an antibody or an antigen-binding fragment thereof that is capable of specifically binding one or more complement-associated antigens, such as, an antigen that is displayed locally on or near a site associated with complement activation. Examples of the

targeting moiety can include an antibody or an antigen binding fragment thereof specific for a domain of a mammalian annexin protein. Alternately, the targeting moiety can include an antibody or an antigen-binding fragment thereof specific for a phospholipid. The targeting moiety can include an antibody or an antigen-binding fragment thereof specific for a complement protein, such as a fragment of C3 associated with complement activation, *e.g.*, C3b, iC3b, C3d and C3dg. It is also possible that targeting moiety is a bispecific or a trispecific antibody or antigen binding fragment thereof that is specific for any combinations of the following targets: a domain of a mammalian annexin protein, a phospholipid, and a complement protein, such as a fragment of C3, *e.g.*, C3d, iC3b, C3d, C3dg, C3a, C3b, C3c or C3f. In addition, targeting moieties that are multivalent, such as trivalent, tetravalent, are also contemplated to be part of the fusion protein constructs described here.

[00140] Some examples of the fusion protein constructs can be trivalent, bispecific and comprise (i) a bivalent antibody or an antigen binding fragment thereof (*e.g.*, an antibody Fab region); (ii) an antibody Fc domain; and (iii) a complement modulator fused to said antibody or antigen binding fragment thereof, or to said Fc domain. The bivalent antibody or an antigen-binding fragment thereof can be the targeting moiety of the trivalent, bispecific fusion protein construct and can bind to two molecules of a target, such as, a domain of a mammalian annexin protein (*e.g.*, annexin IV, annexin-2), a phospholipid, a complement protein or a fragment of a complement protein (*e.g.*, iC3b, C3d, C3dg, C3a, C3b, C3c or C3f). The complement modulator of the trivalent, bispecific fusion protein construct can be an inhibitor of complement activation. A further variant of a trivalent, bispecific fusion protein construct can comprise a bispecific trivalent heterodimeric polypeptide construct comprising a) a first polypeptide monomer comprising an antibody CH2 or CH3 domain, wherein said domain has at least one amino acid modification resulting in a cavity (also referred to as a “hole”); b) a second polypeptide monomer comprising an antibody CH2 or CH3 domain, wherein said domain has at least one amino acid modification resulting in a protuberance (also referred to as a “knob”); such that, upon heterodimerization of said first and second polypeptide monomers, said knob interacts with said hole; and wherein one of said first and second polypeptide is further fused to a complement modulator.

[00141] In another example, the fusion protein construct comprises a tetravalent construct for modulating complement activity, said tetravalent construct comprising: (i) a bivalent antibody or an antigen binding fragment thereof; and (ii) two complement modulators. The bivalent antibodies of the tetravalent fusion construct may be full length bivalent antibodies or antigen binding fragments thereof, *e.g.*, variable region fragments, or a bivalent single chain variable fragment. The two complement modulators can be the same proteins or different, to form a

bispecific tetravalent or a trispecific tetravalent fusion protein construct. In other examples, the fusion protein construct is monomeric and comprises one or more amino acid modifications that eliminate disulfide bonding that occurs in forming a homodimeric construct.

[00142] An antibody is composed of four polypeptides: two heavy chains and two light chains. The antigen binding portion of an antibody is formed by the light chain variable domain (VL) and the heavy chain variable domain (VH). At one extremity of these domains six loops form the antigen binding site, also referred to as the complementarity determining regions (CDR). Three CDRs are located on the VH domain (H1, H2 and H3) and the three others are on the VL domain (L1, L2 and L3). During B cell development a unique immunoglobulin region is formed by somatic recombination known as V(D)J recombination. The variable region of the immunoglobulin heavy or light chain is encoded by different gene segments. The heavy chain is encoded by three segments called variable (V), diversity (D) and joining (J) segments whereas the light chain variable is formed by the recombination of only two segments V and J. A large number of antibody paratopes (also referred to herein as antigen binding sites) can be generated by recombination between one of the multiple copies of the V, D and J segments that are present in the genome. The V segment encodes the CDR1 and CDR2 whereas the CDR3 is generated by the recombination events. During the course of the immune response further diversity is introduced into the antigen binding site by a process called somatic hypermutation (SHM). During this process, point mutations are introduced in the variable genes of the heavy and light chains and in particular into the regions encoding the CDRs. This additional variability allows for the selection and expansion of B cells expressing antibody variants with improved affinity for their cognate antigen. The vast majority of immunoglobulins are bivalent and monospecific molecules carrying the same specificity on both arms as they are composed of two identical heavy chain polypeptides and two identical light chain polypeptides. However, it was recognized very early during the development of hybridoma technology that hybrid hybridomas can be created by a fusion event between two hybridomas (See, *e.g.*, M.R. Suresh et al., *Methods Enzymol* 1986; 121: 210-228). These 'quadromas' express two different heavy and two different light chains and therefore produce a variety of different antibody species resulting from the random pairing of the heavy and light chains. Amongst these different species, bispecific antibodies (bsAbs) are generated, carrying a different specificity on each arm. Another naturally occurring exception is the immunoglobulin of the IgG4 isotype that can undergo heavy chain exchange due to a less stable dimerization mediated by the hinge region of that isotype (See, *e.g.*, van der Neut Kolfshoten M et al., *Science*. 2007 317(5844):1554-7). Although this exchange seems to happen *in vivo*, its biological significance remains unclear. Monoclonal antibodies have emerged as a successful and attractive class of molecules for therapeutic

intervention in several areas of human disease. However, targeting or neutralizing a single protein is not always sufficient to achieve efficacy in certain diseases which limits the therapeutic use of monoclonal antibodies. It is increasingly clear that in a number of indications neutralizing one component of a biological system is not sufficient to achieve efficacy. One solution to this problem is the co-administration of several monoclonal antibodies. This approach is however complicated by regulatory aspects if the antibodies to be combined have not been previously approved individually. Moreover, combination approaches are also costly from a manufacturing perspective. Accordingly, there exists a need for antibodies and therapeutics that enable targeting of multiple antigens with a single molecule.

[00143] This disclosure, which at least includes bi, tri, and tetravalent fusion protein constructs, provides molecules that have an improved therapeutic capability of addressing diseases, disorders, or conditions associated with the complement system.

Complement Modulator

[00144] The complement system is a major effector of humoral immunity and natural immunity. The complement system has three independent pathways of complement activation: a classical pathway, an alternative pathway, and a lectin pathway. While all three pathways differ with regard to initiating events, all three pathways converge with the cleavage of complement component C3. Key to the activity of the complement system is the covalent attachment of processed protein fragments derived from a serum protein, complement C3 and/or C4, to tissue sites of complement activation. This unusual property is due to the presence of a thioester bond in C3 that, when cleaved during C3 activation, converts C3 to a form designated C3b which can then utilize ester or amide bonds to link to cell and tissue-attached molecules. Once C3b is covalently attached, it is rapidly processed to the iC3b, C3dg and C3d forms, each of which remain covalently attached to the target tissue site. This process results in the “marking” of the tissue as one in which an inflammatory injury or other complement-related process is underway.

[00145] Complement can be activated by any of three pathways: the classical, lectin and alternative pathways. The classical pathway is activated through the binding of the complement system protein C1q to antigen-antibody complexes, pentraxins or apoptotic cells. The pentraxins include C-reactive protein and serum amyloid P component. The lectin pathway is initiated by binding of carbohydrates to mannose-binding lectin or by the binding of ficolins or collectins to carbohydrates or acetylated molecules.

[00146] The alternative pathway is activated on surfaces of pathogens that do not express or contain complement inhibitors. This results from the process termed ‘tickover’ of C3 that occurs

spontaneously, involving the interaction of conformationally altered C3 with factor B, and results in the fixation of active C3b on pathogens or other surfaces. The alternative pathway can also be initiated when certain antibodies block endogenous regulatory mechanisms, by IgA-containing immune complexes, or when expression of complement regulatory proteins is decreased. In addition, the alternative pathway is activated by a mechanism called the 'amplification loop' when C3b that is deposited onto targets via the classical or lectin pathway, or indeed through the tickover process itself, binds factor B. See Muller-Eberhard (1988) *Ann. Rev. Biochem.* 57:321. For example, Holers and colleagues have shown that the alternative pathway is amplified at sites of local injury when inflammatory cells are recruited following initial complement activation. See Girardi et al., *J. Clin. Invest.* 2003, 112:1644. Dramatic complement amplification through the alternative pathway then occurs through a mechanism that involves either the additional generation of injured cells that fix complement, local synthesis of alternative pathway components, or more likely because infiltrating inflammatory cells that carry preformed C3 and properdin greatly increase activation specifically at that site.

[00147] Alternative pathway amplification is initiated when circulating factor B binds to activated C3b. This complex is then cleaved by circulating factor D to yield an enzymatically active C3 convertase complex, C3bBb. C3bBb cleaves additional C3 generating C3b, which drives inflammation and also further amplifies the activation process, generating a positive feedback loop. Factor H is a key regulator (inhibitor) of the alternative complement pathway activation and initiation mechanisms that competes with factor B for binding to conformationally altered C3 in the tickover mechanism and to C3b in the amplification loop. Binding of C3b to Factor H also leads to degradation of C3b by factor I to the inactive form iC3b (also designated C3bi), thus exerting a further check on complement activation. Factor H regulates complement in the fluid phase, circulating at a plasma concentration of approximately >400-600 µg/ml, but its binding to cells is a regulated phenomenon enhanced by the presence of a negatively charged surface as well as fixed C3b, iC3b, C3dg or C3d. See Jozsi et al., *Histopathol.* (2004) 19:251-258.

[00148] Complement activation, C3 fragment fixation and complement-mediated inflammation are involved in the etiology and progression of numerous diseases. The down-regulation of complement activation has been shown to be effective in treating several diseases in animal models and in ex vivo studies, including, for example, systemic lupus erythematosus and glomerulonephritis (Y. Wang et al., *Proc. Nat'l Acad. Sci. USA* (1996) 93:8563-8568), rheumatoid arthritis (Y. Wang et al., *Proc. Nat'l Acad. Sci. USA* (1995) 92:8955-8959), cardiopulmonary bypass and hemodialysis (C. S. Rinder, *J. Clin. Invest.* (1995) 96:1564-1572), hyperacute rejection in organ transplantation (T. J. Kroshus et al., *Transplantation* (1995)

60:1194-1202), myocardial infarction (J. W. Homeister et al., *J. Immunol.* (1993) 150:1055-1064; H. F. Weisman et al., *Science* (1990) 249:146-151), ischemia/reperfusion injury (E. A. Amsterdam et al., *Am. J. Physiol.* (1995) 268:H448-H457), antibody-mediated allograft rejection, for example, in the kidneys (J. B. Colvin, *J. Am. Soc. Nephrol.* (2007) 18(4):1046-56), and adult respiratory distress syndrome (R. Rabinovici et al., *J. Immunol.* (1992) 149:1744-1750). Moreover, other inflammatory conditions and autoimmune/immune complex diseases are also closely associated with complement activation (B. P. Morgan. *Eur. J. Clin. Invest.* (1994) 24:219-228), including, but not limited to, thermal injury, severe asthma, anaphylactic shock, bowel inflammation, urticaria, angioedema, vasculitis, multiple sclerosis, myasthenia gravis, myocarditis, membranoproliferative glomerulonephritis, atypical hemolytic uremic syndrome, Sjögren's syndrome, renal and pulmonary ischemia/reperfusion, and other organ-specific inflammatory disorders. It is currently uncertain whether complement activation is essential to the pathogenesis and injury of all diseases in which local tissue C3 activation and inflammatory injury occurs; nevertheless, C3 fragment fixation is frequently found as an associated event.

[00149] The endogenous membrane-bound proteins that control alternative pathway activation are decay-accelerating factor (DAF/CD55), membrane cofactor protein (MCP/CD46), and complement receptor 1 (CRI). Other endogenous proteins that control alternative pathway activation include Factor H, a circulating -155 kDa glycoprotein that regulates alternative pathway activation in the fluid phase as well as on tissue surfaces. See J.J. Alexander et al., *Mol. Immunol.* (2006) 44: 123-132. Uncontrolled alternative pathway activation has been implicated in the pathogenesis of a diverse group of diseases, including age-related macular degeneration (AMD), atypical hemolytic uremic syndrome (aHUS), type II membranoproliferative glomerulonephritis (MPGN II), asthma, and renal ischemia/reperfusion (I/R) injury. See J.M. Thurman et al., *J. Immunol.* (2006) 176:1305- 1310. Injury to host tissues by the alternative pathway indicates insufficient local control of the alternative pathway by the target tissue. Indeed, recent studies have demonstrated that mutations in CRPs are strong risk factors for aHUS (M.C. Pickering et al., *J. Exp. Med.* (2007) 204: 1249-1256) and MPGN II (R.J. Smith et al., *J. Am. Soc. Nephrol.* (2007) 18:2447- 2456), and functional polymorphisms in factor H, a circulating regulator of the alternative pathway, are associated with the development of AMD (R.J. Klein *et al.*, *Science* (2005) 308:385-389; A.O. Edwards *et al.*, *Science* (2005) 308:421-424; J.L. Haines *et al.*, *Science* (2005) 308:419-421; G.S. Hageman *et al.*, *Proc. Nat'l Acad. Sci USA* (2005) 102:7227- 7232).

[00150] Ischemic acute kidney injury (AKI) in rodents (J.M. Thurman *et al.*, *J. Immunol.* (2003) 170:1517-1523; J.M. Thurman *et al.*, *Am. Soc. Nephrol.* (2006) 17:707-715) and in humans (J.M. Thurman *et al.*, *Kidney Int.* (2005) 67:524-530) is associated with activation of

the alternative pathway on the basolateral surface of injured tubular cells. It has been found that Complement receptor 1-related gene/protein y (Crry, a rodent analog of human MCP and CR1) is the only C-reactive protein (CRP) expressed by proximal tubular epithelial cells in mice, and that ischemia/reperfusion causes reduced surface expression of this protein. See J.M. Thurman et al., *J. Clin. Invest.* (2006) 116:357-368. Mice with congenital deficiency of Crry (Crry^{+/-}) are more sensitive than wild-type controls to ischemic acute renal failure (Id.), highlighting the importance of basolateral Crry for controlling the alternative pathway on this surface. It is not yet known whether polymorphisms or mutations in the CRPs may confer increased risk of developing AKI in humans. Nevertheless, uncontrolled activation of the alternative pathway in the setting of reduced surface Crry indicates that circulating factor H has a limited ability to protect the surface of hypoxic tubular epithelial cells.

[00151] Factor H circulates in high concentrations (>400-600 µg/ml) and is a potent inhibitor of the alternative complement pathway. See J.J. Alexander *et al.*, *Mol. Immunol.* (2006) 44: 123-132. Alternative pathway inhibition on cell surfaces by factor H, however, requires that it properly bind to that surface. Several regions within the factor H protein bind to anionic surfaces, such as membranes rich in heparin sulfate or sialic acid, as well as to C3b on the surface. See S. Meri *et al.*, *Proc. Nat'l Acad. Sci USA* (1990) 87:3982-3986; M.K. Pangburn *et al.*, *Immunol.* (2000) 164:4742-4751. Activation of the alternative pathway on a particular surface is strongly influenced by the affinity of factor H for that surface. The polymorphisms and mutations associated with AMD and aHUS, respectively, most frequently involve the region of factor H required for binding anionic surfaces and not the complement regulatory region. See M.C. Pickering *et al.*, *J. Exp. Med.* (2007) 204:1249-1256; A.P. Sjöberg et al., *J. Biol. Chem.* (2007) 282: 10894-10900. Thus, certain tissues or cell types require factor H to regulate alternative pathway activation on their surface. Different binding regions of the factor H protein may be necessary for complement regulation on those tissues or cell types. In some cases, the binding of factor H to surfaces in particular tissues may be affected by other proteins. Identification of putative tissue-specific binding partners of factor H may provide potential mechanisms for modulating, i.e., stimulating or inhibiting, activity of the alternative complement pathway in different tissues.

[00152] Accordingly, the complement modulator of this disclosure can be a complement modulator protein or a complement modulator polypeptide (*e.g.*, a complement inhibitor polypeptide) such as, *e.g.*, a membrane cofactor protein (MCP) (SEQ ID NO: 1) (UniProtKB/Swiss-Prot. Accession No. P15529), a decay accelerating factor (DAF), a CD59, a Crry, a CR1, a CR2, a factor H, or variants thereof, or fragments thereof. Additional complement modulators may include an anti-C5 antibody, eculizumab, pexelizumab, an anti-

C3b antibody, an anti-C6 antibody, an anti-C7 antibody, an anti-C8 antibody, an anti-C9 antibody, an anti-factor B antibody, an anti-MASP antibody, an anti-factor D antibody, and an anti-properdin antibody, an anti-MBL antibody, Factor I, a linear peptide, a cyclic peptide, a compstatin or its analogs, N-acetylaspartylglutamic acid (NAAGA), and a biologically active fragment of any the preceding. In certain instances, the complement inhibitor can be a human complement inhibitor (*e.g.*, a human MCP, a human DAF, a human CD59, a human CR1, a human Factor H, human Map44, human Map19, or another complement inhibitor derived from humans). In additional instances, the complement inhibitor can be a mammalian complement inhibitor (*e.g.*, a mouse DAF, a mouse CD59 (also known as isoform A), a mouse CD59 isoform B, a mouse Crry, a mouse Factor H, a mouse Map44, a mouse Map19, or another complement inhibitor derived from mouse. Thus, the polypeptides can be human polypeptides or polypeptides of a non-human species. For example, the complement modulator polypeptides can be from a non-human primate (*e.g.*, orangutan, chimpanzee, macaque, gorilla, lemur, or gibbon), horse, cow, pig, sheep, goat, dog, cat, or rodent (*e.g.*, mouse, rabbit, hamster, gerbil, Guinea pig, or rat).

[00153] The complement modulator of the fusion protein construct can be a variant complement modulator. Variant complement modulator polypeptides, may contain one or more amino acid substitutions as compared to the corresponding wild-type sequence (*e.g.*, no more than 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, nine, eight, seven, six, five, four, three, two, or one amino acid substitution compared to the wild type sequence). The amino acid substitutions can be conservative, non-conservative, or a mixture of both. Variant polypeptides may, in some embodiments, contain one or more deletions or additions, or a combination of one or more deletions, additions, and substitutions. In some examples, the variant complement modulator polypeptides can contain one or more amino acid deletions, additions, or substitutions per 100 amino acids of the polypeptide. In some examples where the complement modulator polypeptide comprises short consensus repeats (SCRs), variant polypeptides may contain no amino acid substitutions, deletions, or additions in the complement modulator polypeptide SCRs.

[00154] A variant complement modulator polypeptide can comprise an amino acid sequence that is at least 70 (*e.g.*, at least 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99) % identical to the corresponding wild-type amino acid sequence. Functional fragments of a complement modulator polypeptide or variant polypeptide described herein are shorter than the full-length polypeptides. A variant complement modulator polypeptide can comprise an amino acid sequence that is at least 90%, 95%, or 98% identical to

one or more functional (biologically active) fragments or domains of a complement modulator polypeptide identified herein. Variant polypeptides, and functional fragments of wild-type proteins or variants, retain at least 50 (*e.g.*, at least 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 or greater) % of a complement modulatory activity of the corresponding wild-type polypeptide.

[00155] A variant complement modulator polypeptide, or functional fragment of the complement modulator polypeptide, can have greater than 100% of the ability of the corresponding wild-type protein to modulate complement activity. Methods for detecting and/or quantifying complement activity are known in the art and described herein.

[00156] Other examples of sequences useful as complement modulators in this disclosure include one or more short consensus repeat (SCR) domains from one or more of the following complement-related proteins: Factor H; complement receptor 1; complement receptor 2; Factor B; DAF; and others. In some cases, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 SCR regions are incorporated in complement modulators described herein. In some cases, where the complement modulator polypeptide comprises a “membrane cofactor protein,” “MCP,” or “CD46,” it can refer to a widely distributed C3b/C4b-binding cell surface glycoprotein which may inhibit complement activation on host cells and can serve as a cofactor for the factor I-mediated cleavage of C3b and C4b, including homologs thereof. MCP may belong to a family known as the regulators of complement activation (“RCA”). Family members may share certain structural features, comprising varying numbers of short consensus repeat (SCR) domains, which are typically between 60 and 70 amino acids in length. Beginning at its amino-terminus, MCP may comprise four SCRs, a serine/threonine/proline-enriched region, an area of undefined function, a transmembrane hydrophobic domain, a cytoplasmic anchor and a cytoplasmic tail. It is understood that species and strain variations exist for the disclosed peptides, polypeptides, and proteins, and that human MCP or biologically active fragments thereof can encompass all species and strain variations.

[00157] SEQ ID No. 1 represents an exemplary sequence for the full-length human MCP (*see, e.g.*, UniProtKB/Swiss-Prot. Accession No. P15529). Amino acids 1-34 may correspond to the signal peptide, amino acids 35-343 may correspond to the extracellular domain, amino acids 344-366 may correspond to the transmembrane domain, and amino acids 367-392 may correspond to the cytoplasmic domain. In the extracellular domain, amino acids 35-96 may correspond to SCR 1, amino acids 97-159 may correspond to SCR 2, amino acids 160-225 may correspond to SCR 3, amino acids 226-285 may correspond to SCR 4, and amino acids 302-326 may correspond to the serine/threonine-rich domain. It is understood that species and strain

variations exist for the disclosed peptides, polypeptides, and proteins, and that MCP or biologically active fragments thereof can encompass all species and strain variations. As used herein, the term “biologically active” fragment of MCP may refer to any soluble fragment lacking both the cytoplasmic domain and the transmembrane domain, including fragments comprising, consisting essentially of or consisting of 1, 2, 3, or 4 SCR domains, with or without the serine/threonine-rich domain, having some or all of the complement inhibitory activity of the full-length human MCP protein. In some embodiments, the complement inhibitor portion comprises full-length human MCP (amino acids 35-392 of SEQ ID NO: 1), the extracellular domain of human MCP (amino acids 35-343 of SEQ ID NO: 1), or SCRs 1-4 of human MCP (amino acids 35-285 of SEQ ID NO: 1).

[00158] In some cases, where the complement modulator polypeptide comprises a Decay accelerating factor, also referred to as CD55 (DAF/CD55) (SEQ ID NO: 2 and SEQ ID NO: 3), is membrane-bound glycoprotein, having a molecular weight of about 70 kiloDalton (kDa), which inhibits complement activation on host cells. Like several other complement regulatory proteins, DAF comprises several approximately 60 amino acid repeating motifs termed short consensus repeat (SCR).

[00159] As used herein, the term “decay accelerating factor,” “DAF,” or “CD55” refers to a seventy kilodalton (“kDa”) membrane glycoprotein comprising four short consensus repeat (SCR) domains followed by a heavily O-glycosylated serine/threonine-rich domain at the C-terminus that elevates the molecule from the membrane surface, followed by a glycosylphosphatidylinositol (“GPI”) anchor. DAF protects the cell surface from complement activation by dissociating membrane-bound C3 convertases that are required to cleave complement protein C3 and to amplify the complement cascade. DAF prevents assembly or accelerates decay of both the C3- and C5-convertases of the alternative and classical complement pathways.

[00160] SEQ ID No. 2 represents an exemplary sequence for the full-length human DAF (*see, e.g.,* UniProtKB/Swiss-Prot. Accession No. P08173); SEQ ID NO: 3 represents an exemplary sequence for the full-length mouse DAF (*see, e.g.,* UniProtKB/Swiss-Prot. Accession No. Q61475). In the human DAF sequence, amino acids 1-34 may correspond to the signal peptide, amino acids 35-353 may appear in the mature protein, and amino acids 354-381 may be removed from the polypeptide after translation. Within the mature protein, amino acids 35-96 may correspond to SCR 1, amino acids 96-160 may correspond to SCR 2, amino acids 161-222 may correspond to SCR 3, amino acids 223-285 may correspond to SCR 4, and amino acids 287-353 may correspond to the O-glycosylated serine/threonine-rich domain. The GPI anchor may be attached to human DAF at a serine at position 353. In the mouse DAF sequence, amino

acids 1-34 may correspond to the signal peptide, amino acids 35-362 may appear in the mature protein, and amino acids 363-390 may be removed from the polypeptide after translation. Within the mature protein, amino acids 35-96 may correspond to SCR 1, amino acids 97-160 may correspond to SCR 2, amino acids 161-222 may correspond to SCR 3, amino acids 223-286 may correspond to SCR 4, and amino acids 288-362 may correspond to the O-glycosylated serine/threonine-rich domain. The GPI anchor may be attached to mouse DAF at a serine at position 362. It is understood that species and strain variations exist for the disclosed peptides, polypeptides, and proteins, and that DAF or biologically active fragments thereof can encompass all species and strain variations. As used herein, the term “biologically active” fragment of DAF may refer to any fragment of DAF lacking a GPI anchor, the amino acid to which it is attached (*e.g.*, Ser-353), or both, including any fragments of the full-length DAF protein comprising, consisting essentially of or consisting of 1, 2, 3, or 4 SCR domains, with or without the O-glycosylated serine/threonine-rich domain, having some or all the complement inhibitory activity of the full-length DAF protein.

[00161] SEQ ID No. 4 represents an exemplary sequence for the full-length human CD59 (*see, e.g.*, UniProtKB/Swiss-Prot. Accession No. P13987); SEQ ID NO: 5 represents an exemplary sequence for the full-length mouse CD59, isoform A (*see, e.g.*, UniProtKB/Swiss-Prot. Accession No. O55186); SEQ ID NO: 6 represents an exemplary sequence for the full-length mouse CD59, isoform B (*see, e.g.*, UniProtKB/Swiss-Prot. Accession No. P58019). In the human CD59 sequence, amino acids 1-25 of SEQ ID NO: 4 may correspond to the leader peptide, amino acids 26-102 of SEQ ID NO: 4 may correspond to the mature protein, and amino acids 103-128 of SEQ ID NO: 4 may be removed after translation. The GPI anchor may be attached to CD59 at an asparagine at position 102 of SEQ ID NO: 4. In isoform A of the mouse CD59 sequence, amino acids 1-23 of SEQ ID NO: 5 may correspond to the leader peptide, amino acids 24-96 of SEQ ID NO: 5 may correspond to the mature protein, and amino acids 97-123 of SEQ ID NO: 5 may be removed after translation. The GPI anchor may be attached to CD59 at a serine at position 96 of SEQ ID NO: 5. In isoform B of the mouse CD59 sequence, amino acids 1-23 of SEQ ID NO: 6 may correspond to the leader peptide, amino acids 24-104 of SEQ ID NO: 6 may correspond to the mature protein, and amino acids 105-129 of SEQ ID NO: 6 may be removed after translation. The GPI anchor may be attached to CD59 at an asparagine at position 104 of SEQ ID NO: 6. It is understood that species and strain variations exist for the disclosed peptides, polypeptides, and proteins, and that CD59 or biologically active fragments thereof can encompass all species and strain variations. As used herein, the term “biologically active” fragment of human CD59 can refer to any fragment of human CD59 lacking a GPI anchor, the amino acid to which it is attached (*e.g.*, Asn-102), or both, including any fragments

of the full-length human CD59 protein having some or all the complement inhibitory activity of the full-length CD59 protein; and the term “biologically active” fragment of mouse CD59 can refer to any fragment of mouse CD59 isoform A or isoform B lacking a GPI anchor and/or the amino acid to which it is attached (*e.g.*, Ser-96 of isoform A, or Asp-104 of isoform B), including any fragments of either full-length mouse CD59 protein isoform having some or all the complement inhibitory activity of the full-length CD59 protein.

[00162] SEQ ID No. 7 represents an exemplary sequence for the full-length mouse Crry protein. Amino acids 1-40 may correspond to the leader peptide, amino acids 41-483 of SEQ ID NO: 7 may correspond to the mature protein, comprising amino acids 41-405 of SEQ ID NO: 7, that may correspond to the extracellular domain, amino acids 406-426 of SEQ ID NO: 7, that may correspond to the transmembrane domain, and amino acids 427-483 of SEQ ID NO: 7, that may correspond to the cytoplasmic domain. In the extracellular domain, amino acids 83-143 of SEQ ID NO: 7 may correspond to SCR 1, amino acids 144-205 of SEQ ID NO: 7 may correspond to SCR 2, amino acids 206-276 of SEQ ID NO: 7 may correspond to SCR 3, amino acids 277-338 of SEQ ID NO: 7 may correspond to SCR 4, and amino acids 339-400 of SEQ ID NO: 7 may correspond to SCR 5. It is understood that species and strain variations exist for the disclosed peptides, polypeptides, and proteins, and that mouse Crry protein or biologically active fragments thereof can encompass all species and strain variations. As used herein, the term “biologically active” fragment of mouse Crry protein can refer to any soluble fragment of mouse Crry lacking the transmembrane domain and the cytoplasmic domain, including fragments comprising, consisting essentially of or consisting of 1, 2, 3, 4, or 5 SCR domains, including any fragments of the full-length mouse Crry protein having some or all the complement inhibitory activity of the full-length Crry protein.

[00163] As used herein, the term “complement receptor 1,” “CR1,” or “CD35” can refer to a human gene encoding a protein of 2039 amino acids, with a predicted molecular weight of 220 kilodaltons (“kDa”), including homologs thereof. The gene can be expressed principally on erythrocytes, monocytes, neutrophils, and B cells, but may also be present on some T lymphocytes, mast cells, and glomerular podocytes. CR1 protein can be typically expressed at between 100 and 1000 copies per cell. CR1 can be the main system for processing and clearance of complement-opsonized immune complexes. CR1 can negatively regulate the complement cascade, mediate immune adherence and phagocytosis, and inhibit all complement pathways. The full-length CR1 protein may comprise a 42 amino acid signal peptide, an extracellular domain of 1930 amino acids, a 25 amino acid transmembrane domain, and a 43 amino acid C-terminal cytoplasmic domain. The extracellular domain of CR1 can include 25 potential N-glycosylation signal sequences and may comprise 30 short consensus repeat (“SCR”) domains,

also known as complement control protein (CCP) repeats, or sushi domains, each 60 to 70 amino acids long. The sequence homology between SCRs can range between 60-99 percent. The 30 SCR domains may further be grouped into four longer regions termed long homologous repeats (“LHRs”), each encoding approximately 45 kDa segments of the CR1 protein, designated LHR-A, -B, -C, and -D (*see, e.g., Krych-Goldberg et al.*, 274(44): 31160–31168, 1999). The first three LHRs can comprise seven SCR domains each, while LHR-D can comprise 9 SCR domains. The active sites on the extracellular domain of CR1 protein can include a C4b-binding site with lower affinity for C3b in SCR 1-3 comprising amino acids 42-234, a C3b-binding site with lower affinity for C4b in SCRs 8-11 comprising amino acids 490-745, a C3b-binding site with lower affinity for C4b in SCRs 15-18 comprising amino acids 940-1196, and a C1q-binding site in SCRs 22-28 comprising amino acids 1394-1842.

[00164] SEQ ID No. 8 represents an exemplary sequence for the full-length human CR1 (*see, e.g., UniProtKB/Swiss-Prot. Accession No. P17927*). Amino acids 1-41 may correspond to the signal peptide, amino acids 42-2039 may correspond to the mature protein, comprising amino acids 42-1971, that may correspond to the extracellular domain, amino acids 1972-1996, that may correspond to the transmembrane domain, and amino acids 1997-2039, that may correspond to the cytoplasmic domain. In the extracellular domain, amino acids 42-101 may correspond to SCR 1, 102-163 may correspond to SCR 2, amino acids 164-234 may correspond to SCR 3, amino acids 236-295 may correspond to SCR 4, amino acids 295-355 may correspond to SCR 5, amino acids 356-418 may correspond to SCR 6, amino acids 419-489 may correspond to SCR 7, amino acids 491-551 may correspond to SCR 8, amino acids 552-613 may correspond to SCR 9, amino acids 614-684 may correspond to SCR 10, amino acids 686-745 may correspond to SCR 11, amino acids 745-805 may correspond to SCR 12, amino acids 806-868 may correspond to SCR 13, amino acids 869-939 may correspond to SCR 14, amino acids 941-1001 may correspond to SCR 15, amino acids 1002-1063 may correspond to SCR 16, amino acids 1064-1134 may correspond to SCR 17, amino acids 1136-1195 may correspond to SCR 18, amino acids 1195-1255 may correspond to SCR 19, amino acids 1256-1318 may correspond to SCR 20, amino acids 1319-1389 may correspond to SCR 21, amino acids 1394-1454 may correspond to SCR 22, amino acids 1455-1516 may correspond to SCR 23, amino acids 1517-1587 may correspond to SCR 24, amino acids 1589-1648 may correspond to SCR 25, amino acids 1648-1708 may correspond to SCR 26, amino acids 1709-1771 may correspond to SCR 27, amino acids 1772-1842 may correspond to SCR 28, amino acids 1846-1906 may correspond to SCR 29, amino acids 1907-1967 may correspond to SCR 30. It is understood that species and strain variations exist for the disclosed peptides, polypeptides, and proteins, and that CR1 protein or biologically active fragments thereof can encompass all species and strain variations.

As used herein, the term “biologically active” fragment of CR1 protein can refer to any soluble fragment of CR1 lacking the transmembrane domain and the cytoplasmic domain, including fragments comprising, consisting essentially of or consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 SCR domains, including any fragments of the full-length CR1 protein having some or all the complement inhibitory activity of the full-length CR1 protein. Functional fragments may include SCRs 1 and 2; SCRs 1,2,3, and 4; SCRs 1, 2, 3, 4, 5, 6, 7; SCRs 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10 (“CR1 1-10”); SCRs 6, 7, 8, 9, 10, 11, and 12; SCRs 8 and 9; SCRs 8, 9, 10, and 11; SCRs 8, 9, 10,11, 12, 13, and 14; SCRs 15 and 16; SCRs 12, 13, 14, 15, 16, and 17; SCRs 15, 16, 17, 18, and 19; SCRs 1 through 17 (“CR1 1-17”); SCRs 1 through 23; SCRs 1 through 28. Example variant polypeptides comprise at least three SCRs of each of domains A and B; at least three SCRs of each of domains A, B and C; at least the first three SCRs of domains A, B, and C, or amino acid sequences at least 90% identical to any of the foregoing.

[00165] As used herein, the terms “complement factor H,” “factor H,” or “FH” can refer to complement factor H, a single polypeptide chain plasma glycoprotein, including homologs thereof. The protein may be composed of 20 conserved short consensus repeat (SCR) domains of approximately 60 amino acids, arranged in a continuous fashion like a string of beads, separated by short linker sequences of 2-6 amino acids each. Factor H may bind to C3b, accelerate the decay of the alternative pathway C3-convertase (C3bBb) as well as the alternative pathway C5 convertase (C3bBb3b), and act as a cofactor for the proteolytic inactivation of C3b. In the presence of factor H, proteolysis by factor I may result in the cleavage and inactivation of C3b. Factor H can have at least three distinct binding domains for C3b, which may be located within any one of SCRs 1-20, SCRs 1-4, SCRs 5-8, and SCRs 19-20. Each domain may bind to a distinct region within the C3b protein: the N-terminal sites may bind to native C3b; the second site, located in the middle region of factor H, may bind to the C3c fragment and the site located within SCR19 and 20 may bind to the C3d region. In addition, factor H can also contain binding sites for heparin, which may be located within SCR 7, SCRs 5-12, and SCR 20 of factor H and may overlap with those of the C3b binding sites. Structural and functional analyses have shown that the domains for the complement inhibitory activity of factor H may be located within the first four N-terminal SCR domains.

[00166] SEQ ID No. 9 represents an exemplary amino acid sequence for the full-length human factor H protein (*see, e.g.*, UniProtKB/Swiss-Prot. Accession No. P08603); SEQ ID NO: 10 represents an exemplary amino acid sequence for the full-length mouse factor H protein (*see, e.g.*, UniProtKB/Swiss-Prot. Accession No. P06909). In the human factor H sequence, amino acids 1-18 of SEQ ID NO: 9 may correspond to the signal peptide, and amino acids 19-1231 of

SEQ ID NO: 9 may correspond to the mature protein. Within that protein, amino acids 21-80 of SEQ ID NO: 9 may correspond to SCR 1, amino acids 85-141 of SEQ ID NO: 9 may correspond to SCR 2, amino acids 146-205 of SEQ ID NO: 9 may correspond to SCR 3, amino acids 210-262 of SEQ ID NO: 9 may correspond to SCR 4, and amino acids 267-320 of SEQ ID NO: 9 may correspond to SCR 5. In the mouse factor H sequence, amino acids 1-18 of SEQ ID NO: 10 may correspond to the signal peptide, and amino acids 19-1234 of SEQ ID NO: 10 may correspond to the mature protein. Within that protein, amino acids 19-82 of SEQ ID NO: 10 may correspond to SCR 1, amino acids 83-143 of SEQ ID NO: 10 may correspond to SCR 2, amino acids 144-207 of SEQ ID NO: 10 may correspond to SCR 3, amino acids 208-264 of SEQ ID NO: 10 may correspond to SCR 4, and amino acids 265-322 of SEQ ID NO: 10 may correspond to SCR 5. It is understood that species and strain variations exist for the disclosed peptides, polypeptides, and proteins, and that factor H or biologically active fragments thereof can encompass all species and strain variations. As used herein, the term “biologically active” fragment of factor H can refer to any portion of a factor H protein having some or all the complement inhibitory activity of the full-length factor H protein, and can include, but is not limited to, factor H fragments comprising SCRs 1-4, SCRs 1-5, SCRs 1-8, SCRs 1-18, SCRs 19-20, or any homolog of a naturally-occurring factor H or fragment thereof, as described in detail below. In some examples of the fusion protein constructs, the biologically active fragment of factor H may have one or more of the following properties: (1) binding to C-reactive protein (CRP), (2) binding to C3b and/or its fragments, (3) binding to heparin, (4) binding to sialic acid, (5) binding to endothelial cell surfaces, (6) binding to cellular integrin receptor, (7) binding to pathogens, (8) C3b co-factor activity, (9) C3 and C5 alternative pathway convertase decay-acceleration activity, and (10) inhibiting the alternative complement pathway.

[00167] In some examples of the fusion protein constructs, the complement modulator portion of the construct may comprise a complement inhibitor or biologically active fragment thereof. In some examples of the fusion protein constructs, the complement inhibitor may be selected from human MCP, human DAF, mouse DAF, human CD59, mouse CD59 isoform A, mouse CD59 isoform B, mouse Crry protein, human CR1, human factor H, mouse factor H, biologically active fragments thereof, and variants thereof.

[00168] In some cases, the complement inhibitor portion of the fusion protein construct may comprise the full-length human MCP (SEQ ID NO: 1). In some cases, the complement inhibitor portion of the fusion protein construct can comprise a biologically active fragment of human MCP (SEQ ID NO: 1). In some cases, the biologically active fragment of human MCP can be selected from SCRs 1-4 (amino acids 35-285 of SEQ ID NO: 1), SCRs 1-4 plus the

serine/threonine-rich domain (amino acids 35-326 of SEQ ID NO: 1), and the extracellular domain of MCP (amino acids 35-343 of SEQ ID NO: 1), and any combinations thereof.

[00169] In some cases, the complement inhibitor portion of the fusion protein construct can comprise the full-length human DAF. In some cases, the complement inhibitor portion of the fusion protein construct can comprise a biologically active fragment of human DAF (SEQ ID NO: 2). In some cases, the biologically active fragment of human DAF can be selected from SCRs 1-4 (amino acids 25-285 of SEQ ID NO: 2) and SCRs 1-4 plus the O-glycosylated serine/threonine-rich domain (amino acids 25-353 of SEQ ID NO: 2), and any combinations thereof. In some cases, the complement inhibitor portion of the construct can comprise the full-length mouse DAF (SEQ ID NO: 3). In some cases, the complement inhibitor portion of the construct can comprise a biologically active fragment of mouse DAF. In some cases, the biologically active fragment of mouse DAF can be selected from SCRs 1-4 (amino acids 35-286 of SEQ ID NO: 3) and SCRs 1-4 plus the O-glycosylated serine/threonine-rich domain (amino acids 35-362 of SEQ ID NO: 3), and any combinations thereof.

[00170] In some cases, the complement inhibitor portion of the fusion protein construct may comprise the full-length human CR1 (SEQ ID NO: 8). In some cases, the complement inhibitor portion of the fusion protein construct can comprise a biologically active fragment of human CR1 (SEQ ID NO: 8). In some cases, the biologically active fragment of human CR1 can be SCR1 (amino acids 42-101 of SEQ ID NO: 8), SCR2 (amino acid 102-163 of SEQ ID NO: 8), SCR3 (amino acids 164-234 of SEQ ID NO: 8), SCR4 (amino acids 236-295 of SEQ ID NO: 8), SCR5 (amino acids 295-355 may of SEQ ID NO: 8), SCR6 (amino acids 356-418 of SEQ ID NO: 8), SCR7 (amino acids 419-489 of SEQ ID NO: 8), SCR8 (amino acids 491-551 of SEQ ID NO: 8), SCR9 (amino acids 552-613 of SEQ ID NO: 8), SCR10 (amino acids 614-684 of SEQ ID NO: 8), SCR11 (amino acids 686-745 of SEQ ID NO: 8), SCR12 (amino acids 745-805 of SEQ ID NO: 8), SCR13 (amino acids 806-868 of SEQ ID NO: 8), SCR14 (amino acids 869-939 of SEQ ID NO: 8), SCR15 (amino acids 941-1001 of SEQ ID NO: 8), SCR16 (amino acids 1002-1063 of SEQ ID NO: 8), SCR17 (amino acids 1064-1134 of SEQ ID NO: 8), SCR18 (amino acids 1136-1195 of SEQ ID NO: 8), SCR19 (amino acids 1195-1255 of SEQ ID NO: 8), SCR20 (amino acids 1256-1318 of SEQ ID NO: 8), SCR21 (amino acids 1319-1389 of SEQ ID NO: 8), SCR22 (amino acids 1394-1454 of SEQ ID NO: 8), SCR23 (amino acids 1455-1516 of SEQ ID NO: 8), SCR24 (amino acids 1517-1587 of SEQ ID NO: 8), SCR25 (amino acids 1589-1648 of SEQ ID NO: 8), SCR26 (amino acids 1648-1708 of SEQ ID NO: 8), SCR 27 (amino acids 1709-1771 of SEQ ID NO: 8), SCR28 (amino acids 1772-1842 of SEQ ID NO: 8), SCR29 (amino acids 1846-1906 of SEQ ID NO: 8), SCR30 (amino acids 1907-1967 of SEQ ID NO: 8), or any combinations thereof.

[00171] In some cases, the complement inhibitor portion of the fusion protein construct may comprise the full-length human factor H (SEQ ID NO: 9). In some cases, the complement inhibitor portion of the fusion protein construct can comprise a biologically active fragment of human factor H (SEQ ID NO: 9). In some cases, the complement inhibitor portion of the fusion protein construct may comprise the full-length mouse factor H (SEQ ID NO: 10). In some cases, the complement inhibitor portion of the fusion protein construct can comprise a biologically active fragment of mouse factor H (SEQ ID NO: 10). The biologically active fragment of factor H can comprise SCRs 1-4, SCRs 1-5, SCRs 1-8, SCRs 1-18, SCRs 19-20 of factor H, or any homolog of a naturally-occurring factor H or fragment thereof, or any combinations thereof.

Targeting Moiety

[00172] The targeting moiety of the multivalent construct can be responsible for targeted delivery of the modulator of the complement system to the sites of action, such as the site of complement activation. The complement modulator can have a therapeutic activity such as specifically inhibiting complement activation. The multivalent construct described herein thus generally has the dual functions of binding to an epitope recognized by an antibody described herein and exerting therapeutic activity through inhibition of complement activation. The targeting moiety can be an antibody or an antigen binding fragment thereof that is human, murine, humanized, or camelized.

[00173] The epitope recognized by the antibody or antigen binding fragment thereof can be a domain of a mammalian annexin protein, a phospholipid, such as one or more of the C2 antibody-reactive phospholipids described below, or a complement protein, such as C3d, C3 fragments (*e.g.*, deposited C3 fragments – C3b, iC3b, C3d, C3dg; free or undeposited C3 fragments- C3a, C3b, C3c or C3f).

[00174] The antibody or antigen-binding fragment thereof can specifically bind to a domain of a mammalian annexin protein. The annexins are a family of calcium- (Ca^{2+}) and phospholipid-binding proteins that differ from most other Ca^{2+} binding proteins in their Ca^{2+} binding sites. The annexin family Ca^{2+} binding site has a unique architecture that enables annexin family members to reversibly dock onto the periphery of cellular and/or organellar membranes. The conserved Ca^{2+} binding site characteristic of annexin family members is located in the annexin core domain, and comprises four annexin repeats, each seventy (70) amino acids long. The annexin core domain is α -helical and forms a compact, curved disc with a convex surface comprising the Ca^{2+} and membrane-binding sites and a concave side oriented away from the membrane that is available for other types of interaction. Annexin family members also typically have an amino-

terminal domain of variable length that precedes the annexin core domain and is diverse in sequence and structure. Twelve annexin subfamilies have been characterized in vertebrates, including annexin IV and annexin 2, each having different splice variants, with different amino-terminal domains and differently positioned Ca^{2+} binding sites. The antibody or antigen-binding fragment thereof, that specifically binds to a domain within or recognizes an epitope within the annexin IV protein, can be a B4 mAb or an antigen binding fragment derived from the B4 mAb. The antibody or antigen-binding fragment thereof, that specifically binds to a domain within or recognizes an epitope within the annexin IV protein (*e.g.*, human annexin IV protein), can be a B4 mAb or an antigen binding fragment derived from the B4 mAb, described in Kulik *et al.*, J Immunol. 182(9): 5363 (2009). Exemplary CDRs of B4 mAb are provided in SEQ ID NOS: 11-16. The targeting moiety can further be an antibody or an antigen binding fragment thereof that specifically binds to or recognizes an epitope within the annexin 2 protein (*e.g.*, human annexin 2 protein).

[00175] The antibody or antigen-binding fragment thereof can also specifically bind to a phospholipid (*e.g.*, phosphatidylethanolamine (PE), cardiolipin (CL), phosphatidylcholine (PC), phosphatidylinositol, phosphatidylglycerol, phosphatidylserine, or phosphatidic acid) or malondialdehyde (MDA). The antibody or antigen-binding fragment thereof, that specifically binds to a phospholipid, can be a C2 mAb or derivative thereof. The phospholipid can be present on the surface of a cell, a basement membrane (*e.g.*, Bruch's membrane), or in a pathological structure (*e.g.*, drusen) in an individual that is in or adjacent to a tissue undergoing (or at risk of undergoing) tissue injury (such as nonischemic injury), oxidative damage, or any combinations thereof. The phospholipid can be neutral, negatively or positively charged, or oxidized. The antibody or antigen-binding fragment thereof, that specifically binds to a phospholipid, can be a C2 mAb, or an antigen binding fragment derived from the C2 mAb, described in Elvington *et al.*, J Immunol., 188(3): 1460–1468 (2012). Exemplary CDRs of C2 mAb are provided in SEQ ID NOS: 17-22. C2 mAb recognizes a subset of phospholipids that are exposed after complement activation or ischemia; this subset of phospholipids is referred to herein as “C2 antibody-reactive phospholipids.” C2 mAb has been shown to recognize a subset of phospholipids that included phosphatidylcholine, phosphatidylethanolamine and cardiolipin, but not phosphatidylglycerol or phosphatidylserine.

[00176] The targeting moiety, in some cases, can be an antibody or an antigen-binding fragment thereof, which specifically binds to deposited or opsonized C3 fragments, *e.g.*, C3b, iC3b, C3d or C3dg, but may or may not bind to free or circulating or undeposited C3 fragments, *e.g.*, C3a, C3b, C3c or C3f. In some examples, it is possible for fusion protein constructs comprising an anti-C3d or anti-C3dg antibody or an antigen-binding fragment thereof to bind with relatively

higher affinity to deposited C3 fragments compared to free C3 or C3 fragments. For example, the antibody or antigen-binding fragment thereof can bind C3 and C3b with about 5-fold, about 6-fold, about 7-fold, about 8-fold, about 9-fold, or about 10-fold lower binding affinity compared to C3d. In some embodiments, the antibody or antigen-binding fragment binds C3 and/or C3b with a K_D of 10^{-4} M or higher, 10^{-3} M, or higher, or 10^{-2} M or higher, and binds iC3b, C3dg, or both, with a binding affinity (K_D) of 10^{-8} M or less, 10^{-9} M or less, or 10^{-10} M or less.

[00177] In some examples, it is possible for fusion protein constructs comprising an anti-C3d or anti-C3dg antibody or an antigen-binding fragment thereof to bind to deposited C3 fragments as well as free C3 or C3 fragments. It is further possible that the anti-C3d or anti-C3dg antibody or an antigen-binding fragment thereof, of an exemplary fusion protein construct, can bind to complement fragment C3d and have the ability to discriminate between tissue bound C3 fragments from circulating C3 (*e.g.*, C3, C3b, or C3(H₂O)). Examples of the anti-C3d or anti-C3dg antibodies or antigen binding fragments thereof include, but are not limited to, mAbs 3d9a, 3d29 and 3d8b (*See, e.g.*, US9815890). In some instances, the anti-C3d or anti-C3dg antibodies of this disclosure can bind to C3d with greater specificity than commercially available anti-C3d antibodies, such as, for example, anti-C3d antibodies designated by the Quidel catalog numbers A207 and A250, that are commercially available from the Quidel Corporation (Quidel Corp., San Diego and Santa Clara, Calif.). In some cases, the targeting moiety can comprise an antibody specific to C3d and/or other C3 fragments (C3b, iC3b, C3c, C3dg, etc.), such as an antibody C8D3 as described in US Patent Application Publication No. 2016/0333082. The antibody C8D3 can bind to an epitope on C3d with high affinity (*see, e.g.*, Figs. 3 and 8 of US 2016/0333082), which overlaps with the CR2 binding epitope. The C8D3 heavy chain sequence can be SEQ ID NO: 154, and light chain sequence is SEQ ID NO: 155; the C8D3 CDRH1, CDRH2 and CDRH3 are SEQ ID NO: 156, 157 and 158, respectively, and CDRL1, CDRL2 and CDRL3 are SEQ ID NO: 159, 160 and 161, respectively. Also described in this publication are four hybridoma clones which produce antibodies to C3d (*i.e.*, Clones B7, C2, C6 and C8). The C6 heavy chain sequence is SEQ ID NO: 162, and light chain sequence is SEQ ID NO: 163; the C6 CDRH1, CDRH2 and CDRH3 are SEQ ID NO: 164, 165 and 166, respectively, and CDRL1, CDRL2 and CDRL3 are SEQ ID NO: 167, 168 and 169, respectively.

[00178] In some examples, the C3d antibody can be an antibody which binds C3d, but not C3c (“Neo-Anti-C3d”), as described in US Patent Application Publication No. 2015/0139899. The binding between the C3d antibody and its epitope with an affinity of about 100 pM to about 500 pM, *e.g.*, 447 pM. The C3d antibody can also be an antibody specific for the neoepitope iC3b (“Neo Anti-iC3b”), and, in some cases, bind its epitope with an affinity of about 100 pM to about 500 pM *e.g.*, 262 pM, however, said antibody does not bind C3c or C3d.

[00179] In some examples, the C3d antibody can be monoclonal antibody M130 which is specific for an antigenic determinant expressed by C3bi, C3dg, and C3d, which is almost undetectable in C3 and C3b. M130 has been shown to have higher affinity to C3d and iC3b than C3(H₂O) (J.D. Tamerius *et al.*, J. Immunol. 135(3): 2015-19 (1985)) and can bind to C3d at residues 1209-1236, and 1217-1232 (Lambris *et al.*, PNAS, 82(12): 4235-9 (1985)).

[00180] In some examples, the C3d antibody can be monoclonal antibody C3-12.2 which binds to human, rat and mouse C3dg fragments (Hidalgo *et al.*, Eur. J. Immunol. 47(3): 504-15 (2017)). It was prepared using C3 deficient mice immunized with human C3b, iC3b and C3dg protein mixture, and has K_D of about 95 nM measured by BiaCore. C3-12.2 and antibodies 3d29, 3d8b and 3d9a can recognize one or more overlapping C3 fragments or variants and the Fab appears to bind to the same or neighboring epitope as CR2.

[00181] In some examples, the C3d antibody can be monoclonal antibody 15-39-06 which was raised in wild-type rats using a synthetic peptide derived from human C3dg and conjugated to diphtheria toxin (K.J. Rassmussen *et al.*, J. Immunol. Methods, 444: 51-5 (2017)). It may have specificity to C3dg complement split product.

[00182] In some examples, the C3d antibody can be commercially available antibodies specific to C3d and/or other C3 fragments (*i.e.*, C3b, iC3b, C3c, C3dg, etc.). Examples include antibodies available from Quidel, monoclonal antibodies A250 and A209 are reported to be specific for the neoepitopes C3d and iC3b, respectively. Antibody A250 was shown to agglutinate EC3bi, EC3b and EC3d cells in an indirect hemagglutination assay, and was also shown to bind to radio-labeled purified iC3b, C3b, and C3d but not to similarly labeled C3, or C3c. Antibody A209 was shown to agglutinate EC3bi but not EC3b or EC3d cells in an indirect hemagglutination assay, and was also shown to bind to radio-labeled purified iC3b but not to similarly labeled C3, C3b, C3d, or C3c. Further examples include available from Abcam are anti-C3d antibody 7C10 with unknown epitopes and anti-C3d antibody [E28-P] (ab136916) which is reported to bind an epitope at the N-terminus of C3d. In some cases, commercial antibodies can be antibodies available from BioRad are anti-C3d antibody 053A-514.3.1.4 and iC3b antibody 013III-1.16 (f.k.a. MCA2607) are reported to be specific to neoantigens C3d and iC3b, respectively. Available from Sigma is antibody 3E7 is reported to recognize C3b and iC3b. Available from Origene, monoclonal antibody AM26358PU-N reacts with a neoantigen on iC3 (C3(H₂O)), iC3b, C3dg and/or C3g and recognizes iC3b, C3dg and C3g in plasma but does not recognize C3 or C3b. Available from U.S. Biological Life Sciences is antibody C0010-19 rat anti-C3g (recognizing iC3, iC3b, C3dg). Also available from U.S. Biological Life Sciences, C7850-13V-ML550 mouse anti-complement C3b, inactivated. This antibody is reported to recognize human inactivated complement C3b (iC3b) neoantigen in blood serum.

Available from Hycult are a number of antibodies including antibody HM2199, anti-human C3g mAb 9 (YB2/90-5-20, which reacts with a neoantigen on iC3, iC3b, C3dg and C3g, and which recognizes iC3b, C3dg and C3g in plasma but does not recognize C3 or C3b; monoclonal antibody HM2198 – anti-human C3d, mAb 3 (YB2/39-11-1-7) which is reported to react with a linear determinant in C3d found on C3, C3b, iC3b, C3dg and C3d and which recognizes C3, C3b, iC3b, C3dg and C3d, but not C3c; antibody HM2168 – anti-activated human C3, clone bH6 which is specific for a C3 neoepitope expressed on the cleavage fragments of C3b, iC3b and C3c, but not C3dg and C3f (P. Garred *et al.*, Scand J Immunol 1988, 27: 319); and antibody HM2257 – activated human C3, mAb I3/15 which recognizes activated complement protein C3 or more specifically a neoepitope on C3b, iC3b and C3dg which are not present in native C3. Available from Meridian, antibody H54189M is reported to react with the alpha chain of C3b, but not with C3a or C3d, and allows demonstration of C3 deposits in tissue, on cells, on microorganisms and in immune complexes.

[00183] Each of the 3d9a, 3d29 and 3d8b antibodies may be able to bind to kidney tissue sections exhibiting inflammation when injected into mice intravenously, and bind to C3-opsonized zymosan, which is known to express iC3b but not C3b. Thus, these antibodies may be able to distinguish between tissue bound fragment C3d and circulating native C3 and the fragment C3b. The C3 binding antibody or antigen-binding fragment thereof, can bind to C3d or C3dg from multiple species (species cross-reactive). The anti-C3d or anti-C3dg antibody or antigen-binding fragment thereof can bind to C3d or C3dg from at least one species selected from human, non-human mammals (*e.g.*, cynomolgus monkey or cynomolgus macaque, rhesus macaque, ape, baboon, chimpanzee, orangutan, or gorilla), rodents (*e.g.*, mouse, rat, hamster, Guinea pig, gerbil, or rabbit), cattle, sheep, goat, donkey, pig, dog, cat, horse, and camel. The anti-C3d or anti-C3dg antibody or antigen-binding fragment thereof can bind to cynomolgus macaque C3d or C3dg. The anti-C3d or anti-C3dg antibody or antigen-binding fragment thereof described herein binds to C3d or C3dg from at least two species selected from the above list. The anti-C3d or anti-C3dg antibody or antigen-binding fragment thereof binds to both human and cynomolgus macaque C3d or C3dg. The anti-C3d or anti-C3dg antibody or an antigen-binding fragment thereof can be an antibody selected from: 3d8b, 3d9a, 3d29, 3d11, 3d31, 3d3, 3d15, 3d10, and 3d16 (*See e.g.*, US9815890). The anti-C3d or anti-C3dg antibody or an antigen-binding fragment thereof can be an antibody selected from: 3d9a, 3d29 and 3d8b. The anti-C3d or anti-C3dg antibody or an antigen-binding fragment thereof can be 3d29.

[00184] In some examples, the anti-C3d or anti-C3dg antibody, or antigen-binding fragment thereof, of the fusion protein constructs, can compete with CR2 for binding to C3d or C3dg. Such an antibody or antigen-binding fragment thereof can reduce the ability of a CR2 protein to

bind to human complement component C3d or C3dg by greater than 50 (*e.g.*, greater than 55, 60, 65, 70, 75, 80, 85, 90, or 95 or more) %. For example, the CR2-C3d binding can be decreased to at least 60%, at least 40%, or to a % value in between. The anti-C3d or anti-C3dg antibody, or antigen-binding fragment thereof, can significantly inhibit or block CR2 binding to C3d. In some embodiments, such an antibody is 3d9a, 3d29 or 3d8b. Exemplary fusion protein constructs comprising anti-C3d or anti-C3dg targeting domains and a complement modulator, in some cases, can better compete with CR2 binding to C3d or C3dg, than an anti-C3d or anti-C3dg targeting domain alone.

Fusion Protein Construct Designs

[00185] The fusion protein constructs, comprising a targeting moiety and the complement modulator, can include an antibody or an antigen-binding fragment thereof as the targeting moiety. Examples of the targeting moiety include, but are not limited to, a monoclonal antibody or antibody fragment, a diabody, a chimerized or chimeric antibody or antibody fragment, a humanized antibody or antibody fragment, a deimmunized human antibody or antibody fragment, a fully human antibody or antibody fragment, a bispecific antibody or antibody fragment, a monovalent antibody or antibody fragment, a single chain antibody, an immunoglobulin G1 (IgG1) heavy chain, a single chain variable fragment (*i.e.*, an scFv), sc(fv)₂, a tandem scFv, a diabody, a VHH domain, a VH domain, an Fv, an Fd, an Fab heavy chain, an Fab light chain, an Fab, an Fab', and Fab' light chain, an Fab' heavy chain, and an F(ab')₂. The antibody or antigen binding fragments that form the targeting moiety, can be a human antibody, a humanized antibody, a murine antibody. The fusion protein constructs can include one or more targeting moieties, such that each targeting moiety comprising an antibody or an antigen binding fragment thereof specific for a target. In addition, it is possible that the fusion protein constructs include more than one complement modulator. When the fusion protein construct includes more than one complement modulators, it may comprise multiple molecules of the same complement modulator or it may comprise distinct types of complement modulators. Similarly, fusion protein constructs that have multiple targeting moieties, may comprise several molecules of the same type of targeting moiety, thereby being multivalent with respect to the targeting moiety, or distinct types of targeting moieties, thereby being multispecific with respect to the targeting moiety. Targets of the fusion protein constructs can be, for example, a complement protein or a fragment thereof, a domain of a mammalian annexin protein, or a phospholipid. Since the fusion protein constructs may have the ability to specifically bind to more than one target, it is contemplated that, in some examples, at least two of the above mentioned targets can be specifically bound by the fusion protein constructs described here. Accordingly, the fusion

protein construct can be a bispecific, trispecific, tetraspecific etc. Furthermore, it is possible for the fusion protein constructs to be multivalent, such as bivalent, trivalent, tetravalent etc. For instance, the targeting moiety of a fusion protein construct which is bispecific can be specific for a target such as a domain of mammalian annexin, a phospholipid, or a C3 complement protein fragment (*e.g.*, C3d), and the complement modulator of the fusion protein construct can be specific for another protein in the complement pathway. A tetravalent fusion protein construct can have a targeting moiety that is bivalent, such as a bivalent antibody or antigen binding fragment thereof that has two binding regions for a target protein, and two molecules of a complement modulator. It is further possible for the fusion protein construct to be a bispecific trivalent protein where the targeting moiety includes a bivalent antibody or antigen binding fragment thereof and a constant domain (Fc) of an antibody, and the complement modulator is fused to the bivalent antibody or to the Fc domain.

[00186] Other examples of the fusion protein construct include an Fc region which is heterodimeric, comprising various modifications that promote formation of a heterodimeric Fc region over a homodimeric Fc region. *See e.g.*, JH Ha *et al.* Immunoglobulin Fc Heterodimer Platform Technology: From Design to Applications in Therapeutic Antibodies and Proteins. Front. Immuno. 7:394 (2016). Conventional IgG antibodies are multivalent and monospecific, the assembly of which depends upon *in vivo* homodimerization of two identical heavy chains (HCs), which is mediated by homodimeric associations between CH3 domains, and subsequently disulfide linkages between each HC and each light chain (LC), in B cells. Thus, the development of bsAbs, using intact IgG formats with wild-type HCs and LCs, may involve HC–HC and HC_{VH-CH1}–LC mispairing problems. In addition, the development of trivalent fusion constructs that have a complement modulator linked to only one of two HCs, or only one of two LCs may involve mispairing problems. Accordingly, the heterodimeric Fc region of the targeting moieties disclosed herein may be advantageous in terms of avoiding HC mispairing problem. Although the wild-type Fc region is a homodimer of polypeptides, the Fc domains disclosed herein, in some examples, comprise amino acid substitutions such that they do not form homodimers. The monomeric Fc domains, Fc1 and Fc2, are in some embodiments IgG Fc. In some embodiments, the monomeric Fc domains, Fc1 and Fc2, are from other immunoglobulin subclasses including IgA, IgE, IgD, and IgM. The heterodimer Fc regions of the targeting moieties described herein comprise a variant CH3 constant domain comprising amino acid mutations that promote the formation of said heterodimer with stability comparable to a native homodimeric Fc, and a CH2 constant domain. The wild-type Fc is homodimeric in nature and this feature is driven by both hydrophobic interactions at the center of the CH3

interface and symmetric electrostatic interactions around the rim of the hydrophobic core. The Fc domains described herein can comprise amino acid substitutions such that they do not form homodimers. The Fc domains described herein can comprise amino acid substitutions that favor formation of heterodimers over homodimers. In certain examples, the heterodimeric Fc domain is created using (i) symmetric-to-asymmetric steric complementarity design (*e.g.*, KiH, HA-TF, and ZW1) (*see e.g.*, Klein *et al.* Progress in overcoming the chain association issue in bispecific heterodimeric IgG antibodies. *mAbs* 4(6): 653-66 (2012); G.L. Moore *et al.* A novel bispecific antibody format enables simultaneous bivalent and monovalent co-engagement of distinct target antigens. *mAbs* 3(6) 546-557 (2011); T.S. von Kreudenstein *et al.* Improving biophysical properties of a bispecific antibody scaffold to aid developability: Quality by molecular design. *mAbs* 5(5): 646-654 (2013); H.J. Choi *et al.* A heterodimeric Fc-based bispecific antibody simultaneously targeting VEGFR-2 and Met exhibits potent antitumor activity. *Mol Cancer Ther* 12(12):2748-59 (2013), (ii) charge-to-charge swap (*e.g.*, DD-KK), (iii) charge-to-steric complementarity swap plus additional long-range electrostatic interactions (*e.g.*, EW-RVT), and (iv) isotype strand swap [*e.g.*, strand-exchange engineered domain (SEED)]. Strand exchange mutations include, for example, IgA-derived 45 residues on IgG1 CH3-Fc1 and IgG1-derived 57 residues on IgA CH3-Fc2, or *vice versa*. Examples of symmetric-to-asymmetric sterically complementary mutations include HA-TF (S364H/F405A in Fc1-CH3 or CH3A and Y349T/T394F in Fc2-CH3 or CH3B), ZW1 (T350V/L351Y/F405A/Y407V in Fc1-CH3 or CH3A and T350V/T366L/K392L/T394W in Fc2-CH3 or CH3B). In other examples, the Fc variant can be generated using the “Knobs-into-holes (KiH)” approach where Fc1 comprises a T366W “knob” mutation, in Fc1-CH3 or CH3A, and Fc2 comprises T366S/L368A/Y407V “hole” mutations in Fc2-CH3 or CH3B domain. In additional examples, the Fc variant can be generated using the “Knobs-into-holes (KiH)” plus disulfide bond approach, KiHs-s, where Fc1 comprises a T366W/S354C “knob” mutation, in Fc1-CH3 or CH3A, and Fc2 comprises T366S/L368A/Y407V/Y349C “hole” mutations in Fc2-CH3 or CH3B domain. In such examples, the heterodimerization is favored through hydrophobic interactions at the core of the Fc1-CH3 or CH3A and Fc2-CH3 or CH3B interface. Examples of charge-charge swap mutations, where the Fc heterodimer favoring interaction is based on electrostatic complementarity include DD-KK (K409D/K392D in Fc1-CH3 or CH3A and D399K/E356K in Fc2-CH3 or CH3B, or *vice versa*). Examples of charge-to-steric complementarity swap plus additional long-range electrostatic interaction mutations include EW-RVT (K360E/K409W in Fc1-CH3 or CH3A and Q347R/D399V/F405T in Fc2-CH3 or CH3B, or *vice versa*); EW-RVTs-s (K360E/K409W/Y349C in Fc1-CH3 or CH3A and Q347R/D399V/F405T/S354C in Fc2-CH3 or CH3B, or *vice versa*), which comprises an inter-CH3 S-S bond. In yet other examples, the Fc

variant can be generated using hydrophobic or steric complementarity plus electrostatic complementarity, such as 7.8.60 (K360D/D399M/Y407A in Fc1-CH3 or CH3A and E345R/Q347R/T366V/K409V in Fc2-CH3 or CH3B, or *vice versa*). The heterodimer forming Fc variants described herein can also be generated through directed evolution combined with yeast surface display and high-throughput screening. For example, a combinatorial heterodimeric Fc library display system can be developed by mating two haploid yeast cell lines; one haploid cell line displaying an Fc chain library (CH3-Fc1 or CH3A) with mutations in one CH3 domain on the yeast cell surface, and the other cell line secreting an Fc chain library (CH3-Fc2 or CH3B) with mutations in the other CH3 domain. In the mated cells, secreted CH3-Fc2 or CH3B can be displayed on the cell surface through heterodimerization with the displayed CH3-Fc1 or CH3A. Fluorescence-based detection of this interaction enables screening of the library for heterodimeric Fc variants by flow cytometry. An antibody or an antigen binding fragment thereof, that includes a wild-type Fc domain has the ability to interact with neonatal Fc-receptor (FcRn) in a pH dependent manner; this interaction can confer extended serum half-life. The residues important for the high-affinity interaction of Fc domain and FcγR are located within the CH2 domain. Accordingly, in some instances, the Fc heterodimer of the targeting moieties comprise CH2 domains which have wild type IgG sequence.

[00187] In some examples, the “CH3 domain,” comprising the stretch of residues C-terminal to a CH2 domain in an Fc region (i.e. from an amino acid residue at about position 341 to an amino acid residue at about position 447 of an IgG), may be a native sequence CH3 domain or a variant CH3 domain (e.g. a CH3 domain with an introduced “protuberance” in one chain thereof and a corresponding introduced “cavity” in the other chain thereof). Such variant CH3 domains may, in some examples, be part of a heterodimeric Fc domain as described here. Accordingly, in some examples, the fusion protein construct comprises a protuberance-into-cavity antibody or an antigen-binding fragment thereof.

[00188] In some examples, the Fc region can comprise a human or murine IgG1 or human IgG4 sequence. In some examples, the Fc region can comprise a human IgG1 or IgG4, or murine IgG1 sequence comprising amino acid substitutions relative to the wild-type sequence. Examples of such Fc regions are provided in SEQ ID Nos. 247 and 248.

Domains and Structures of Fusion Proteins Constructs

[00189] The fusion protein construct comprises one or more polypeptides, each containing domains, and connected, for example, via one or more disulfide bonds. For instance, in some cases, the fusion protein construct can comprise a first polypeptide chain which comprises

domain A, domain B, domain C, domain D, and domain R, wherein domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, domain C comprises a heavy chain CH2 constant region amino acid sequence, domain D comprises a heavy chain CH3 constant region amino acid sequence, and domain R comprises a complement modulator polypeptide. In some embodiments, one or more of domains B, C and D are optional. The first polypeptide can further comprise a hinge region and the first polypeptide can further be connected to a second polypeptide which comprises further domains, such as domain E which comprises a light chain variable region amino acid sequence (VL), or an antigen-binding fragment thereof, and optionally domain F which comprises a light chain constant region amino acid sequence (CL1). The connection between the first and the second polypeptide can be by one or more disulfide bonds between domains B and F. In some examples, the first and the second polypeptides, as described above, are combined using various orientations to generate fusion protein constructs that are monomeric, trivalent homodimeric, trivalent homodimeric, tetravalent homodimeric, tetravalent heterodimeric, etc.

[00190] In various examples of multivalent fusion protein constructs (*e.g.*, bivalent, trivalent, tetravalent), multivalency of the fusion protein construct can improve the avidity of the fusion protein construct for a specific target. As described herein, “avidity” can refer to the overall strength of interaction between two or more molecules, *e.g.*, a fusion protein construct that comprises a bivalent targeting moiety, the avidity can be the cumulative strength of interaction provided by the affinities of two antigen binding sites. Avidity can be measured, for example, by the same methods as those used to determine affinity. In certain examples, the avidity can be the cumulative strength of interactions provided by the affinities of multiple antigen binding sites for separate antigens on a shared specific target or complex, such as separate antigens found on an individual cell. In certain examples, the avidity can be the cumulative strength of interaction provided by the affinities of multiple antigen binding sites for separate epitopes on a shared individual antigen.

Domain A (VH)

[00191] Domain A of the fusion protein constructs described here can comprise a VH amino acid sequence, such as antibody heavy chain variable domain sequences. In a typical antibody arrangement in both nature and in the fusion protein constructs described herein, a specific VH amino acid sequence can associate with a specific VL amino acid sequence to form an antigen-binding site. In various examples, VH amino acid sequences are mammalian sequences, including human sequences, and synthesized sequences, or combinations of non-human

mammalian, mammalian, and synthesized sequences. In various examples, VH amino acid sequences can be mutated sequences of naturally occurring sequences that retain sufficient CDR sequence to retain the desired antigen-binding affinity. In some examples, the VH sequences can be from an IgA1, IgA2, IgD, IgE, IgG1, IgG2, IgG3, IgG4, or IgM isotype. In some examples, the VH sequences can be from an IgG1 isotype.

Domain E (VL)

[00192] Domain E of the fusion protein constructs described herein, can comprise a VL amino acid sequence, such as antibody light chain variable domain sequences. In a typical arrangement in both natural antibodies and the fusion protein constructs described herein, a specific VL amino acid sequence can associates with a specific VH amino acid sequence to form an antigen-binding site. In various examples, the VL amino acid sequences can be mammalian sequences, including human sequences, synthesized sequences, or combinations of human, non-human mammalian, mammalian, and synthesized sequences. In various examples, VL amino acid sequences can be mutated sequences of naturally occurring sequences that retain at least 70%, 75%, 80%, 85%, 90%, 95% or more amino acid identity. In certain examples, the VL amino acid sequences can be lambda (λ) light chain variable domain sequences. In certain examples, the VL amino acid sequences can be kappa (κ) light chain variable domain sequences. In some examples, the VL sequences can be from an IgA1, IgA2, IgD, IgE, IgG1, IgG2, IgG3, IgG4, or IgM isotype. In some examples, the VL sequences can be from an IgG1 isotype

Domain B (CH1)

[00193] The CH1 amino acid sequences of the fusion protein constructs described herein can be sequences of the second domain of an antibody heavy chain, with reference from the N-terminus to C-terminus. In certain examples, the CH1 sequences can be endogenous sequences or mutated sequences thereof that retain at least 70%, 75%, 80%, 85%, 90%, 95% or more amino acid identity. In some examples, the CH1 sequences can be mammalian sequences, including, but not limited to mouse, rat, hamster, rabbit, camel, donkey, goat, and human sequences. In some examples, the CH1 sequences can be human sequences. In some examples, the CH1 sequences can be from an IgA1, IgA2, IgD, IgE, IgG1, IgG2, IgG3, IgG4, or IgM isotype. In some examples, the CH1 sequences can be from an IgG1 isotype. In some examples, the CH1 sequences can be from an IgG4 isotype.

Domain F (CL1)

[00194] The CL amino acid sequences of the fusion protein constructs described herein can be antibody light chain constant domain sequences. In certain examples, the CL sequences can be endogenous sequences or mutated sequences thereof that retain at least 70%, 75%, 80%, 85%, 90%, 95% or more amino acid identity. In some examples, the CL sequences can be mammalian

sequences, including, but not limited to mouse, rat, hamster, rabbit, camel, donkey, goat, and human sequences. In some examples, CL sequences can be human sequences. In certain examples, the CL amino acid sequences can be lambda (λ) light chain constant domain sequences. In some examples, the CL amino acid sequences can be human lambda light chain constant domain sequences. In certain embodiments, the CL amino acid sequences are kappa (κ) light chain constant domain sequences. In a preferred embodiment, the CL amino acid sequences are human kappa (κ) light chain constant domain sequences.

Domain C (CH2)

[00195] In the fusion protein constructs described herein, domain C can have a CH2 amino acid sequence. CH2 sequences can be endogenous sequences or mutated sequences thereof that retain at least 70%, 75%, 80%, 85%, 90%, 95% or more amino acid identity. In some examples, the CH2 sequences can be mammalian sequences, including, but not limited to human sequences. In some examples, the CH2 amino acid sequence can have an N-terminal hinge region that connects domain C to domain B, *e.g.*, connecting the C-terminus of domain B (CL1 sequence), to the N-terminus of domain C (CH2 sequence). In some examples, the CH2 sequences can be from an IgA1, IgA2, IgD, IgE, IgG1, IgG2, IgG3, IgG4, or IgM isotype. In some examples, the CH2 sequences can be from an IgG1 isotype. In some examples, the CH2 sequences can be from an IgG4 isotype.

Domain D (CH3)

[00196] In the fusion protein constructs described herein, domain D can comprise a constant region domain amino acid sequence, such as a CH3 amino acid sequence. CH3 sequences can be endogenous sequences or mutated sequences thereof that retain at least 70%, 75%, 80%, 85%, 90%, 95% or more amino acid identity. In some examples, the CH3 sequences can be mammalian sequences, including, but not limited to human sequences. In some examples, domain D can comprise a constant region sequence that is a CH3 sequence comprising knob-hole orthogonal mutations; isoallotype mutations; and either a S354C or a Y349C mutation that forms an engineered disulfide bridge with a CH3 domain containing an orthogonal mutation, or any combinations thereof. In some examples, the knob-hole orthogonal mutations combined with isoallotype mutations can comprise the following mutational changes: D356E, L358M, T366S, L368A, and Y407V. In some examples, the CH3 sequences can be from an IgA1, IgA2, IgD, IgE, IgG1, IgG2, IgG3, IgG4, or IgM isotype. In some examples, the CH3 sequences can be from an IgG1 isotype. In some examples, the CH3 sequences can be from an IgG4 isotype. In any of these examples, the CH1, CH2 and CH3 sequences can be from the same isotype, *e.g.* IgG1 or IgG3.

Complementarity Determining Regions within Domain A and Domain F

[00197] The VH (domain A) and VL (domain F) amino acid sequences of the various fusion protein constructs described herein can comprise highly variable sequences termed “complementarity determining regions” (CDRs), typically three CDRs (CDR1, CDR2, and CDR3). In a variety of examples, the CDRs can be mammalian sequences, including, but not limited to, mouse, rat, hamster, rabbit, camel, donkey, goat, and human sequences. In some examples, the CDRs can be human sequences. In some examples, the CDRs can be naturally occurring sequences. In some examples, the CDRs can be naturally occurring sequences that have been mutated to alter the binding affinity of the antigen-binding site for a particular antigen or epitope. In certain examples, the naturally occurring CDRs may have been mutated in an *in vivo* host through affinity maturation and somatic hypermutation. In certain examples, the CDRs may have been mutated *in vitro* through methods including, but not limited to, PCR-mutagenesis and chemical mutagenesis. In various examples, the CDRs can comprise synthesized sequences including, but not limited to, CDRs obtained from random sequence CDR libraries and rationally designed CDR libraries.

Framework Regions and CDR Grafting

[00198] The VH and VL amino acid sequences can further comprise “framework region” (FR) sequences. FRs generally can be conserved sequence regions that can act as a scaffold for interspersed CDRs, typically in a FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4 arrangement (from N-terminus to C-terminus). In a variety of examples, the FRs can be mammalian sequences, including, but not limited to mouse, rat, hamster, rabbit, camel, donkey, goat, and human sequences. In some examples, the FRs can be human sequences. In various examples, the FRs can be naturally occurring sequences. In various examples, the FRs can be synthesized sequences including, but not limited, rationally designed sequences.

[00199] In a variety of examples, the FRs and the CDRs can both be from the same naturally occurring variable domain sequence. In a variety of embodiments, the FRs and the CDRs can be from different variable domain sequences, wherein the CDRs can be grafted onto the FR scaffold with the CDRs providing specificity for a particular antigen. In certain examples, the grafted CDRs can all be derived from the same naturally occurring variable domain sequence. In certain examples, the grafted CDRs can be derived from different variable domain sequences. In certain examples, the grafted CDRs can be synthesized sequences including, but not limited to, CDRs obtained from random sequence CDR libraries and rationally designed CDR libraries. In certain examples, the grafted CDRs and the FRs can be from the same species. In certain example, the grafted CDRs and the FRs can be from different species. In certain examples, the various domains of the fusion protein constructs can be “humanized”, wherein the grafted CDRs

are non-human mammalian sequences including, but not limited to, mouse, rat, hamster, rabbit, camel, donkey, and goat sequences, and the FRs are human sequences. In various examples, portions or specific sequences of FRs from one species can be used to replace portions or specific sequences of another species' FRs.

Homodimeric or Heterodimeric pairing of two domain Ds (CH3 domains)

[00200] In the fusion protein constructs described herein, two domain Ds can be associated to form a dimeric construct. In various examples, the amino acid sequences of all domain Ds are identical. In certain examples, domain D comprises an endogenous CH3 sequence. In some examples, where the fusion protein constructs are heterodimers or heterodimeric, two domain Ds with different amino acid sequences can associate, and separately comprise respectively orthogonal modifications in an endogenous CH3 sequence, wherein one domain D interacts with another domain D having a different sequence, and wherein neither of the two domains significantly interacts with another domain D (CH3 domain) lacking the orthogonal modification.

[00201] “Orthogonal modifications” or synonymously “orthogonal mutations” as described herein can be one or more engineered mutations in an amino acid sequence of an antibody domain that can increase the affinity of binding of a first domain having orthogonal modification for a second domain having a complementary orthogonal modification. In certain examples, the orthogonal modifications can decrease the affinity of a domain having the orthogonal modifications for a domain lacking the complementary orthogonal modifications. In certain examples, orthogonal modifications can be mutations in an endogenous antibody domain sequence. In a variety of examples, orthogonal modifications can be modifications of the N-terminus or C-terminus of an endogenous antibody domain sequence including, but not limited to, amino acid additions or deletions. In some examples, orthogonal modifications can include, but are not limited to, engineered disulfide bridges, knob-in-hole mutations, and charge-pair mutations. In some cases, orthogonal modifications can include a combination of orthogonal modifications selected from, but not limited to, engineered disulfide bridges, knob-in-hole mutations, and charge-pair mutations. In some examples, the orthogonal modifications can be combined with amino acid substitutions that reduce immunogenicity, such as isoallotype mutations.

[00202] In certain examples, where the fusion protein constructs are heterodimers, the orthogonal modifications can comprise mutations that generate engineered disulfide bridges between a first and a second domain. As described herein, “engineered disulfide bridges” can

comprise mutations that provide non-endogenous cysteine amino acids in two or more domains such that a non-native disulfide bond forms when the two or more domains associate. In certain examples, engineered disulfide bridges can improve orthogonal association between specific domains. In some examples, the mutations that can generate engineered disulfide bridges can comprise a K392C mutation in one of a first or second CH3 domains, and a D399C in the other CH3 domain. In one example, the mutations that can generate engineered disulfide bridges can comprise a S354C mutation in one of a first or second CH3 domains, and a Y349C in the other CH3 domain. In another example, the mutations that can generate engineered disulfide bridges can comprise a 447C mutation in both the first and second CH3 domains that are provided by extension of the C-terminus of a CH3 domain incorporating a KSC tripeptide sequence.

[00203] In some examples, orthogonal modifications can comprise knob-hole (synonymously, knob-in-hole) mutations. As described herein, knob-hole mutations can comprise mutations that change the steric features of a first domain's surface such that the first domain will preferentially associate with a second domain having complementary steric mutations relative to association with domains without the complementary steric mutations. In various examples, knob-hole mutations can be combined with engineered disulfide bridges. In various embodiments, knob-hole mutations, isoallotype mutations, and engineered disulfide mutations can be combined to generate heterodimer fusion protein constructs. In certain examples, the knob-in-hole mutations can comprise a T366Y mutation in one CH3 domain, and a Y407T mutation in another CH3 domain. In certain examples, the knob-in-hole mutations can comprise a F405A in one CH3 domain, and a T394W in another CH3 domain. In certain embodiments, the knob-in-hole mutations can comprise a T366Y mutation and a F405A in one CH3 domain, and a T394W and a Y407T in another CH3 domain. In certain examples, the knob-in-hole mutations can comprise a T366W mutation in one CH3 domain, and a Y407A in another CH3 domain. In certain embodiments, the combined knob-in-hole mutations and engineered disulfide mutations can comprise S354C and T366W mutations in one CH3 domain, and a Y349C, T366S, L368A, and a Y407V mutation in another CH3 domain. In some examples, the combined knob-in-hole mutations, isoallotype mutations, and engineered disulfide mutations can comprise a S354C and T366W mutations in one CH3 domain, and a Y349C, D356E, L358M, T366S, L368A, and a Y407V mutation in another CH3 domain. In a variety of embodiments, orthogonal modifications can be charge-pair mutations. As used herein, charge-pair mutations can be mutations that affect the charge of an amino acid in a domain's surface such that the domain will preferentially associate with a second domain having complementary charge-pair mutations relative to association with domains without the complementary charge-pair mutations. In certain embodiments, charge-pair mutations can improve orthogonal association between

specific domains. In certain embodiments, charge-pair mutations can improve stability between specific domains. In some examples, the charge-pair mutations are a T366K mutation in one CH3 domain, and a L351D mutation in another CH3 domain.

Monomeric Fusion Protein Constructs

[00204] An exemplary monomeric fusion protein construct is illustrated in **FIGS. 2-3**, comprising a first and a second polypeptide, wherein the first polypeptide comprises the following domains: domain A, domain B, and domain R; and the second polypeptide comprises the following domains: domain E and domain F. In the illustrated fusion protein construct of **FIG. 2**, domain A comprises a heavy chain variable region amino acid sequence (VH), or an antigen-binding fragment thereof, domain B comprises a heavy chain CH1 constant region amino acid sequence, and domain R comprises a complement modulator polypeptide, domain E comprises a light chain variable region amino acid sequence (VL), or an antigen binding fragment thereof, and domain F comprises a light chain constant region amino acid sequence (CL1). Further, domains B and F, of the first and second polypeptides, respectively, can be linked *via* one or more disulfide bonds. The domains of the first polypeptide are arranged, from N-terminus to C-terminus, in an A-B-R orientation or an R-A-B orientation, and the domains of the second polypeptide are arranged, from N-terminus to C-terminus, in an E-F orientation. In the example shown in **FIG. 2**, the monomeric fusion protein construct comprises a linkage between domains A and R, for example, a chemical linkage or through a peptide linker. In an additional example is provided a monomeric fusion protein construct, as in **FIG. 3**, comprising linkage between domain R and domain B.

[00205] A further exemplary monomeric fusion protein construct is illustrated in **FIGS. 1 and 4**, comprising a first and a second polypeptide, wherein the first polypeptide comprises the following domains: domain A, and domain B; and the second polypeptide comprises the following domains: domain E, domain F, and domain R. The domains B and F, of the first and second polypeptides, respectively, can be linked *via* one or more disulfide bonds. The domains of the first polypeptide are arranged, from N-terminus to C-terminus, in an A-B orientation, and the domains of the second polypeptide are arranged, from N-terminus to C-terminus, in an E-F orientation. In the example shown in **FIG. 4**, the monomeric fusion protein construct comprises a linkage between domains F and R, for example, a chemical linkage or through a peptide linker. In an additional example is provided a monomeric fusion protein construct, as in **FIG. 1** comprising a linkage between domains E and R.

[00206] In additional examples, are provided fusion protein constructs comprising more than complement modulator polypeptide, *i.e.*, more than one domain R. In such cases, the fusion

protein construct comprises a first polypeptide with domains A, B, and a first complement modulator polypeptide (domain R1); a second polypeptide with domains E, F, and a second complement modulator polypeptide (domain R2); wherein the fusion protein construct comprises a linkage between domain R1 and domain A, or between domain R1 and domain B; and between domain R2 and domain F, or between domain R2 and domain E.

[00207] In a further example, the fusion protein construct comprises a first polypeptide comprising domain A, domain B, a first complement modulator polypeptide (domain R1), and a second complement modulator polypeptide (domain R2); a second polypeptide comprising domain E, domain F, a third complement modulator polypeptide (domain R3), and a fourth complement modulator polypeptide (domain R4). The fusion protein construct can comprise linkages between domain R1 and domain B and between domain R2 and domain A, or between domain R2 and domain B and between domain R1 and domain A; and between domain R3 and domain E and between domain R4 and domain F; or between domain R4 and domain E and between domain R3 and domain E.

Homodimer Fusion Protein Constructs comprising complement modulators attached to a heavy chain polypeptide

[00208] Exemplary tetravalent homodimer fusion protein constructs are illustrated in **Figs. 5-6**, comprising two polypeptides, each comprising a first polypeptide comprising domain A, domain B, a hinge region, domain C, domain D, and domain R; a second polypeptide comprising domain E, and domain F, wherein the first polypeptide is arranged, from N-terminus to C-terminus, in an A-B-hinge domain-C-D-R orientation comprising a linkage between domain D and domain R; or in an R-A-B-hinge region-C-D orientation comprising a linkage between domain R and domain A. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds. The second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation. The two first polypeptides can be linked together via one or more disulfide bonds at the hinge region. Further exemplary tetravalent homodimer fusion protein constructs comprise two polypeptides, each comprising a first polypeptide comprising domain A, domain B, a hinge region, domain C, and domain R; a second polypeptide comprising domain E, and domain F, wherein the first polypeptide is arranged, from N-terminus to C-terminus, in an A-B-hinge domain-C-R orientation comprising a linkage between domain D and domain R; or in an R-A-B-hinge region-C orientation comprising a linkage between domain R and domain A. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds. The second polypeptide can

be arranged, from N-terminus to C-terminus, in an E-F orientation. The two first polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[00209] Further exemplary tetravalent homodimer fusion protein construct comprise two polypeptides, each polypeptide chain comprising a first polypeptide comprising domain A, domain B, a hinge region, and domain R; a second polypeptide comprising domain E, and domain F, wherein the first polypeptide is arranged, from N-terminus to C-terminus, in an A-B-hinge domain-R orientation comprising a linkage between the hinge region and domain R; or in an R-A-B-hinge region orientation comprising a linkage between domain R and domain A. The second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F orientation. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds. The two first polypeptides can be linked together via one or more disulfide bonds at the hinge region.

Heterodimer Fusion Protein Constructs comprising complement modulators attached to a heavy chain polypeptide

[00210] Exemplary trivalent heterodimer fusion protein constructs are illustrated in **Figs. 7-8**, comprising a first polypeptide, a second polypeptide, a third polypeptide, and a fourth polypeptide, the first polypeptide comprising: domain A, domain B, hinge region, domain C, domain D, and domain R, arranged, from N-terminus to C-terminus in a R-A-B-hinge region-C-D orientation comprising a linkage between domain A and domain R (as in **FIG. 8**), or in an A-B-hinge region-C-D-R orientation comprising a linkage between domain D and domain R (as in **FIG. 7**); the second polypeptide comprising domain E, and domain F, arranged from N-terminus to C-terminus in an E-F orientation; the third polypeptide comprising domain A, domain B, hinge region, domain C, and domain D, arranged from N-terminus to C-terminus in an A-B-hinge region-C-D orientation; and the fourth polypeptide comprising domain E and domain F, arranged from N-terminus to C-terminus in an E-F orientation. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds and domains B and F of the third and fourth polypeptide can be linked via one or more disulfide bonds. The first and the third polypeptide can be linked together via one or more disulfide bonds, at the hinge region.

[00211] Further exemplary trivalent heterodimer fusion protein constructs comprise a first polypeptide, a second polypeptide, a third polypeptide, and a fourth polypeptide, the first polypeptide comprising: domain A, domain B, hinge region, domain C, and domain R, arranged, from N-terminus to C-terminus in a R-A-B-hinge region-C orientation comprising a linkage between domain A and domain R, or in an A-B-hinge region-C- orientation comprising a linkage between domain C and domain R; the second polypeptide comprising domain E, and

domain F, arranged from N-terminus to C-terminus in an E-F orientation; the third polypeptide comprising domain A, domain B, hinge region, and domain C, arranged from N-terminus to C-terminus in an A-B-hinge region-C orientation; and the fourth polypeptide comprising domain E and domain F, arranged from N-terminus to C-terminus in an E-F orientation. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds and domains B and F of the third and fourth polypeptide can be linked via one or more disulfide bonds. The first and the third polypeptide can be linked together via one or more disulfide bonds, at the hinge region.

[00212] Further exemplary trivalent heterodimer fusion protein construct comprise a first polypeptide, a second polypeptide, a third polypeptide, and a fourth polypeptide, the first polypeptide comprising: domain A, domain B, hinge region, and domain R, arranged, from N-terminus to C-terminus in a R-A-B-hinge region orientation comprising a linkage between domain A and domain R, or in an A-B-hinge region-R orientation comprising a linkage between the hinge region and domain R; the second polypeptide comprising domain E, and domain F, arranged from N-terminus to C-terminus in an E-F orientation; the third polypeptide comprising domain A, domain B, and hinge region, arranged from N-terminus to C-terminus in an A-B-hinge region orientation; and the fourth polypeptide comprising domain E and domain F, arranged from N-terminus to C-terminus in an E-F orientation. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds and domains B and F of the third and fourth polypeptide can be linked via one or more disulfide bonds. The third polypeptide can be linked together via one or more disulfide bonds, at the hinge region.

Fusion protein constructs comprising complement modulators attached to a light chain polypeptide

[00213] Further exemplary tetravalent homodimeric fusion protein construct, illustrated in **FIG. 9**, comprises two polypeptides, each comprising a first polypeptide and a second polypeptide, the first polypeptide comprises domain A, domain B, a hinge region, domain C and domain D; a second polypeptide comprising domain E, domain F, and domain R, wherein the first polypeptide is arranged, from N-terminus to C-terminus, in an A-B-hinge domain-C-D orientation; the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F-R orientation comprising a linkage between domain F and domain R (as shown in **FIG. 9**), or in an R-E-F orientation comprising a linkage between domain E and domain R (as shown in **FIG. 10**). Domains B and F of the first polypeptide and the second polypeptide can be linked via one

or more disulfide bonds. The two first polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[00214] Further exemplary tetravalent homodimeric fusion protein constructs comprise two polypeptides, each comprising a first polypeptide and a second polypeptide, the first polypeptide comprises domain A, domain B, a hinge region, and domain C; a second polypeptide comprising domain E, domain F, and domain R, wherein the first polypeptide is arranged, from N-terminus to C-terminus, in an A-B-hinge domain-C orientation; the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F-R orientation comprising a linkage between domain F and domain R, or in an R-E-F orientation comprising a linkage between domain E and domain R. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds. The two first polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[00215] Further exemplary tetravalent homodimeric fusion protein constructs comprise two polypeptides, each comprising a first polypeptide and a second polypeptide, the first polypeptide comprises domain A, domain B, and a hinge region; a second polypeptide comprising domain E, domain F, and domain R, wherein the first polypeptide is arranged, from N-terminus to C-terminus, in an A-B-hinge region orientation; the second polypeptide can be arranged, from N-terminus to C-terminus, in an E-F-R orientation comprising a linkage between domain F and domain R, or in an R-E-F orientation comprising a linkage between domain E and domain R. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds. The two first polypeptides can be linked together via one or more disulfide bonds at the hinge region.

[00216] Provided are exemplary heterodimeric constructs comprising a first polypeptide, a second polypeptide, a third polypeptide, and a fourth polypeptide, the first polypeptide comprising: domain A, domain B, hinge region, domain C, domain D; the second polypeptide comprises domain E, domain F, and domain R; the third polypeptide comprises domain A, domain B, hinge region, domain C, and domain D; the fourth polypeptide comprises domain E and domain F; wherein the first polypeptide and the third polypeptides are arranged, from N-terminus to C-terminus, in an A-B-hinge region-C-D orientation; the second polypeptide is arranged, from N-terminus to C-terminus in an E-F-R orientation comprising a linkage between domain F and domain R (as shown in **FIG. 12**), or in an R-E-F orientation comprising a linkage between domain E and domain R (as shown in **FIG. 11**); and the fourth polypeptide is arranged, from the N-terminus to C-terminus, in an E-F orientation. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds and domains B and F of the third and fourth polypeptide can be linked via one or more disulfide

bonds. The first and the third polypeptide can be linked together via one or more disulfide bonds, at the hinge region.

[00217] Provided are exemplary heterodimeric constructs comprising a first polypeptide, a second polypeptide, a third polypeptide, and a fourth polypeptide, the first polypeptide comprising: domain A, domain B, hinge region, and domain C; the second polypeptide comprises domain E, domain F, and domain R; the third polypeptide comprises domain A, domain B, hinge region, and domain C; the fourth polypeptide comprises domain E and domain F; wherein the first polypeptide and the third polypeptide are arranged, from N-terminus to C-terminus, in an A-B-hinge region-C orientation; the second polypeptide is arranged, from N-terminus to C-terminus in an E-F-R orientation comprising a linkage between domain F and domain R, or in an R-E-F orientation comprising a linkage between domain E and domain R; and the fourth polypeptide is arranged, from the N-terminus to C-terminus, in an E-F orientation. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds and domains B and F of the third and fourth polypeptide can be linked via one or more disulfide bonds. The first and the third polypeptide can be linked together via one or more disulfide bonds, at the hinge region.

[00218] Provided are exemplary heterodimeric constructs comprising a first polypeptide, a second polypeptide, a third polypeptide, and a fourth polypeptide, the first polypeptide comprising: domain A, domain B, and hinge region; the second polypeptide comprises domain E, domain F, and domain R; the third polypeptide comprises domain A, domain B, and hinge region; the fourth polypeptide comprises domain E and domain F; wherein the first polypeptide and the third polypeptide are arranged, from N-terminus to C-terminus, in an A-B-hinge region orientation; the second polypeptide is arranged, from N-terminus to C-terminus in an E-F-R orientation comprising a linkage between domain F and domain R, or in an R-E-F orientation comprising a linkage between domain E and domain R; and the fourth polypeptide is arranged, from the N-terminus to C-terminus, in an E-F orientation. Domains B and F of the first polypeptide and the second polypeptide can be linked via one or more disulfide bonds and domains B and F of the third and fourth polypeptide can be linked via one or more disulfide bonds. The first and the third polypeptide can be linked together via one or more disulfide bonds, at the hinge region.

Fusion protein constructs comprising complement modulators attached to the constant region of an antibody

[00219] Provided herein is an exemplary fusion protein, illustrated in **FIG. 13**, comprising a first polypeptide, a second polypeptide, and a third polypeptide; the first polypeptide comprising: domain R, a hinge region, domain C, and a domain D; the second polypeptide comprising: domain A, domain B, a hinge region, domain C, and domain D; the third polypeptide comprising: domain E and domain F, wherein, the first polypeptide can be arranged, from N-terminus to C-terminus in an R-hinge region-C-D orientation comprising a linkage between domain R and the hinge region; the second polypeptide is arranged, from N-terminus to C-terminus in an A-B-hinge region-C-D orientation; the third polypeptide can be arranged, from N-terminus to C-terminus in an E-F orientation. Domains B and F of the second polypeptide and the third polypeptide, respectively, can be linked via one or more disulfide bonds. The first and the second polypeptide can be linked together via one or more disulfide bonds, at the hinge region. In some examples, the fusion protein comprising a linkage between the complement modulator and the constant region, wherein the complement modulator can be CR1 (1-10), CR1 (1-17), factor H, MCP, or DAF connected to the constant region of an immunoglobulin molecule, comprising, for example, two CH3 domains, two CH2 domains, and the hinge region.

Exemplary Constructs

[00220] Certain examples of the fusion protein constructs can include, but are not limited to constructs illustrated in **FIG. 30**, comprising complement modulators CR1 (1-10), CR1 (1-17), and fusions with C2 antibodies or antigen binding fragments thereof, such as C2scFv-CR1 1-10, C2scFv-CR1 1-17, C2scFv-Crry, C2 IgG1 heavy chain – CR1 1-10, C2 IgG1 heavy chain – CR1 1-17, C2 IgG1 heavy chain (hole) – CR1 1-10 [pairs with an Fc domain containing a knob], C2 IgG1 heavy chain (hole) – CR1 1-17 [pairs with an Fc domain containing a knob], C2 IgG1 heavy chain (knob) [pairs with an Fc domain containing a hole]), C2 IgG1 Fab heavy chain – Crry, C2 IgG1 Fab heavy chain – CR1 1-10, C2 IgG1 Fab heavy chain – CR1 1-17, CR1 1-10-IgG1 Fc (hole) [pairs with an Fc domain containing a knob], CR1 1-17-IgG1 Fc (hole) [pairs with an Fc domain containing a knob], CR1 1-10 – C2 IgG1 heavy chain (hole) [pairs with a construct comprising an Fc domain with a knob], CR1 1-17 – C2 IgG1 heavy chain (hole) [pairs with a construct comprising an Fc domain with a knob], CR1 1-10 – C2 IgG1 Fab heavy chain, CR1 1-17 – C2 IgG1 Fab heavy chain, CR1 1-10 - C2 kappa light chain, CR1 1-17 - C2 kappa light chain; constructs illustrated in **FIG. 31**, comprising complement modulator factor H and fusions with anti-C3d antibody (3d29) or antigen binding fragments thereof, such as, 3d29 kappa light chain, 3d29 Fab heavy chain murine IgG1, 3d29 Fab heavy chain murine IgG1 – Crry, 3d29 Fab heavy chain murine IgG1 – CR1 1-10, 3d29 Fab heavy chain murine IgG1 – CR1 1-17, 3d29 Fab heavy chain murine IgG1 – fH 1-5, 3d29 heavy chain murine IgG1 (knob), 3d29

heavy chain murine IgG1 (hole) – fH 1-5, 3d29 heavy chain murine IgG1 – fH 1-5; constructs illustrated in **FIG. 32**, comprising fusions with anti-C3d antibody (3d8b) or antigen binding fragments thereof, 3d8b Fab heavy chain murine IgG1 – Crry, 3d8b Fab heavy chain murine IgG1 – CR1 1-10, 3d8b Fab heavy chain murine IgG1 – fH 1-5, 3d8b heavy chain murine IgG1, 3d8b kappa light chain – CR1 1-10, 3d8b kappa light chain – CR1 1-17, 3d8b heavy chain murine IgG1 (knob) paired with 3d8b heavy chain murine IgG1 (hole), 3d8b heavy chain murine IgG1 – CR1 1-10, 3d8b heavy chain murine IgG1 – CR1 1-17, 3d8b heavy chain murine IgG1 (hole) – fH 1-5 paired with 3d8b heavy chain murine IgG1 (knob), 3d8b heavy chain murine IgG1 – fH 1-5, CR1 1-10 - 3d8b heavy chain murine IgG1, CR1 1-10 - 3d8b kappa light chain, CR1 1-17 - 3d8b kappa light chain, 3d29 heavy chain murine IgG1 – CR1 1-10, 3d29 heavy chain murine IgG1 – CR1 1-10 +His tag, 3d29 heavy chain murine IgG1 (knob) – CR1 1-10 +His tag, 3d29 heavy chain murine IgG1 (hole), 3d29 heavy chain murine IgG1 – CR1 1-17, 3d29 heavy chain murine IgG1 – CR1 1-17 +His tag, 3d29 heavy chain murine IgG1 (knob) – CR1 1-17 +His tag, 3d29 heavy chain murine IgG1 (hole), fH 1-5 - 3d8b heavy chain murine IgG1, 3d8b kappa light chain – fH 1-5, and fH 1-5 - 3d8b kappa light chain; CR1 1-10- murine IgG1 Fc (knob); 3d8b heavy chain murine IgG1 (hole); 3d8b kappa light chain (murine); fH 1-5 - murine IgG1 Fc (knob); 3d8b Fab heavy chain murine IgG1 – CR1 1-17; 3d8b heavy chain murine IgG1 (hole) – CR1 1-17; 3d8b heavy chain murine IgG1 (knob); 3d8b heavy chain murine IgG1 – CR1 1-17; 3d8b heavy chain murine IgG1; 3d8b kappa light chain – CR1 1-17; CR1 1-17 - 3d8b heavy chain murine IgG1; CR1 1-17 - 3d8b kappa light chain. Amino acid sequences for exemplary constructs are provided in SEQ ID Nos. 103-149, and Figures 30-35 provide exemplary illustrations of the same.

[00221] Table 1 provides a list of exemplary constructs comprising anti-C3d antibodies or antigen binding fragments thereof; and fusion protein constructs comprising anti-C3d antibodies or antigen binding fragments thereof and complement modulators or biologically active fragments thereof. Sequences are provided for heavy chain and light chain of the antibodies, including sequences of complement modulator polypeptides or biologically active fragments thereof that are conjugated to the anti-C3d antibodies (*e.g.*, one or more complement modulators conjugated to heavy chains of an exemplary anti-C3d antibody, C-terminally or N-terminally; one or more complement modulators conjugated to light chains of an exemplary anti-C3d antibody, C-terminally or N-terminally; one or more complement modulators conjugated to the hinge region of an anti-C3d antibody). The fusion protein constructs comprising the anti-C3d antibodies, in some instances, comprise an anti-C3d antibody comprising two heavy chains and two light chains; in some instances comprise an anti-C3d Fab fragment, in some instances comprise an anti-C3d scFv. In some instances, the constructs comprise two molecules of the

first polypeptide (two heavy chains identified in the table as HC1 or HC1+complement modulator and HC2 or HC2+complement modulator) and two molecules of the second polypeptide (two light chains identified in the table as LC1 or LC1+complement modulator and LC2 or LC2+complement modulator).

[00222] Table 1: Exemplary protein constructs

Exemplary Fusion Construct No.	First polypeptide (heavy chain sequence 1 (HC1))/(HC1+ complement modulator)	Second polypeptide (light chain sequence (LC1))/(LC1 + complement modulator)	First polypeptide (heavy chain sequence (HC2))/(HC2+ complement modulator)	Second polypeptide (light chain sequence (LC2))/(LC2+ complement modulator)
Exemplary Fusion Construct 35	SEQ ID No. 60	SEQ ID No. 59		
Exemplary Fusion Construct 36	SEQ ID No. 61	SEQ ID No. 59		
Exemplary Fusion Construct 37	SEQ ID No. 58 conjugated to SEQ ID No. 72	SEQ ID No. 59		
Exemplary Fusion Construct 38	SEQ ID No. 65	SEQ ID No. 59	SEQ ID No. 64	SEQ ID No. 59
Exemplary Fusion Construct 39	SEQ ID No. 65	SEQ ID No. 59	SEQ ID No. 65	SEQ ID No. 59
Exemplary Fusion Construct 40	SEQ ID No. 243 conjugated to SEQ ID No. 72	SEQ ID No. 59	SEQ ID No. 64	SEQ ID No. 59
Exemplary Fusion Construct 41	SEQ ID No. 64 conjugated to SEQ ID No. 72	SEQ ID No. 59	SEQ ID No. 64 conjugated to SEQ ID No. 72	SEQ ID No. 59
Exemplary Fusion Construct 42	SEQ ID No. 67	SEQ ID No. 68		
Exemplary Fusion Construct 43	SEQ ID No. 70	SEQ ID No. 68		
Exemplary Fusion Construct 44	SEQ ID No. 71	SEQ ID No. 68		
Exemplary Fusion Construct 45	SEQ ID No. 75	SEQ ID No. 68	SEQ ID No. 74	SEQ ID No. 68
Exemplary Fusion Construct 46	SEQ ID No. 76	SEQ ID No. 68	SEQ ID No. 76	SEQ ID No. 68
Exemplary Fusion Construct 47	SEQ ID No. 82	SEQ ID No. 68	SEQ ID No. 74	SEQ ID No. 68
Exemplary Fusion Construct 48	SEQ ID No. 71	SEQ ID No. 68	SEQ ID No. 71	SEQ ID No. 68
Exemplary Fusion Construct 50	SEQ ID No. 78	SEQ ID No. 68	SEQ ID No. 78	SEQ ID No. 68
Exemplary Fusion Construct 51	SEQ ID No. 73	SEQ ID No. 79	SEQ ID No. 73	SEQ ID No. 79

Exemplary Fusion Construct 52	SEQ ID No. 73	SEQ ID No. 77	SEQ ID No. 73	SEQ ID No. 77
Exemplary Fusion Construct 59	SEQ ID No. 85	SEQ ID No. 68	SEQ ID No. 85	SEQ ID No. 68
Exemplary Fusion Construct 60	SEQ ID No. 73	SEQ ID No. 84	SEQ ID No. 73	SEQ ID No. 84
Exemplary Fusion Construct 61	SEQ ID No. 73	SEQ ID No. 86	SEQ ID No. 73	SEQ ID No. 86
Exemplary Fusion Construct 62	SEQ ID No. 132	SEQ ID No. 68		
Exemplary Fusion Construct 63	SEQ ID No. 133	SEQ ID No. 68		
Exemplary Fusion Construct 64	SEQ ID No. 134	SEQ ID No. 68	SEQ ID No. 134	SEQ ID No. 68
Exemplary Fusion Construct 65	SEQ ID No. 73	SEQ ID No. 135	SEQ ID No. 73	SEQ ID No. 135
Exemplary Fusion Construct 68	SEQ ID No. 80	SEQ ID No. 68	SEQ ID No. 81	SEQ ID No. 68
Exemplary Fusion Construct 69	SEQ ID No. 87	SEQ ID No. 68	SEQ ID No. 88	SEQ ID No. 68
Exemplary Fusion Construct 94	SEQ ID No. 282 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 95	SEQ ID No. 282	SEQ ID No. 279 conjugated to SEQ ID No. 41 via SEQ ID No. 138 (linker)	SEQ ID No. 282	SEQ ID No. 279 conjugated to SEQ ID No. 41 via SEQ ID No. 138 (linker)
Exemplary Fusion Construct 96	SEQ ID No. 282 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 97	SEQ ID No. 282 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 99	SEQ ID No. 284 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 284 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 279

Exemplary Fusion Construct 100	SEQ ID No. 284 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 284 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 104	SEQ ID No. 284 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 284	SEQ ID No. 279
Exemplary Fusion Construct 106	SEQ ID No. 284 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 279 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 284 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)
Exemplary Fusion Construct 107	SEQ ID No. 284 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 284 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)
Exemplary Fusion Construct 116	SEQ ID No. 69	SEQ ID No. 68	SEQ ID No. 69	SEQ ID No. 68
Exemplary Fusion Construct 118	SEQ ID No. 73 conjugated to SEQ ID No. 291, via SEQ ID No. 138 (linker)	SEQ ID No. 68	SEQ ID No. 73 conjugated to SEQ ID No. 291, via SEQ ID No. 138 (linker)	SEQ ID No. 68
Exemplary Fusion Construct 129	SEQ ID No. 286 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 286 conjugated to SEQ ID No. 42, via SEQ ID No. 138 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 133	SEQ ID No. 286 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 286 conjugated to SEQ ID No. 41, via SEQ ID No. 138 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 135	SEQ ID No. 286 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 286 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279

Exemplary Fusion Construct 138	SEQ ID No. 282 conjugated to SEQ ID No. 41, via SEQ ID No. 164 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 41, via SEQ ID No. 164 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 139	SEQ ID No. 282 conjugated to SEQ ID No. 41, via SEQ ID No. 241 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 41, via SEQ ID No. 241 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 140	SEQ ID No. 282 conjugated to SEQ ID No. 42, via SEQ ID No. 164 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 42, via SEQ ID No. 164 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 141	SEQ ID No. 282 conjugated to SEQ ID No. 42, via SEQ ID No. 241 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 42, via SEQ ID No. 241 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 142	SEQ ID No. 282 conjugated to SEQ ID No. 72, via SEQ ID No. 164 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 72, via SEQ ID No. 164 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 143	SEQ ID No. 282 conjugated to SEQ ID No. 72, via SEQ ID No. 241 (linker)	SEQ ID No. 279	SEQ ID No. 282 conjugated to SEQ ID No. 72, via SEQ ID No. 241 (linker)	SEQ ID No. 279
Exemplary Fusion Construct 146	SEQ ID No. 285 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279	SEQ ID No. 285 conjugated to SEQ ID No. 72, via SEQ ID No. 138 (linker)	SEQ ID No. 279

Variable Domain and CDR Sequences within fusion protein constructs

[00223] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID Nos: 11, 12

and 13, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 11, 12 or 13; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 14, 15 and 16 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs 14, 15 or 16. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00224] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 11, 12 and 13, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 14, 15 and 16. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 11, 12 and 13, with a single conservative amino acid substitution within heavy chain CDR2, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 14, 15 and 16. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 11, 12 and 13, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 14, 15 and 16.

[00225] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID Nos: 17, 18 and 19, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 17, 18 or 19; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 20, 21 and 22 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID Nos: 20, 21 or 22. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00226] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 17, 18 and 19, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 20, 21 and 22. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 17, 18 and 19, with a single conservative amino acid substitution within heavy chain CDR2, and a second

polypeptide comprising the three light chain CDRs of SEQ ID NOs: 20, 21 and 22. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 17, 18 and 19, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 20, 21 and 22.

[00227] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 23, 24 and 25, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 23, 24 and 25; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID Nos. 26, 27 and 28 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID Nos: 26, 27 and 28. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00228] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 23, 24 and 25, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 26, 27 and 28. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 23, 24 and 25, with a single conservative amino acid substitution within heavy chain CDR2, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 26, 27 and 28. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 23, 24 and 25, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 26, 27 and 28.

[00229] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 29, 30 and 31, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 29, 30 and 31; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 32, 33 and 34 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 32, 33 and 34. In some embodiments, there is a single conservative

amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00230] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 30 and 31, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 30 and 31, with a single conservative amino acid substitution within heavy chain CDR2, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 30 and 31, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34.

[00231] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 29, 259 and 31, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 29, 259 and 31; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 32, 33 and 34 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 32, 33 and 34. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00232] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 259 and 31, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 259 and 31, with a single conservative amino acid substitution within heavy chain CDR2, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 259 and 31, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34.

[00233] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 29, 260 and 31, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 29, 260 and 31; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 32, 33 and 34 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 32, 33 and 34. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00234] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 260 and 31, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 260 and 31, with a single conservative amino acid substitution within heavy chain CDR2, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 29, 260 and 31, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 32, 33 and 34.

[00235] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 35, 36 and 37, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 35, 36 and 37; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 38, 39 and 40 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 38, 39 and 40. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00236] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 35, 36 and 37, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light

chain CDRs of SEQ ID NOs: 38, 39 and 40. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 35, 36 and 37, with a single conservative amino acid substitution within heavy chain CDR2, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 38, 39 and 40. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 35, 36 and 37, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 38, 39 and 40.

[00237] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 147, 148 and 149, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 150, 151 and 152; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 147, 148 and 149 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 150, 151 and 152. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00238] In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 147, 148 and 149, with a single conservative amino acid substitution within heavy chain CDR1, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 150, 151 and 152. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 147, 148 and 149, with a single conservative amino acid substitution within heavy chain CDR2, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 150, 151 and 152. In some embodiments, the fusion protein construct has a first polypeptide comprising the three heavy chain CDRs of SEQ ID NOs: 147, 148 and 149, with a single conservative amino acid substitution within heavy chain CDR3, and a second polypeptide comprising the three light chain CDRs of SEQ ID NOs: 150, 151 and 152.

[00239] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID Nos: 188, 199 and 190, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 188, 189 and 190; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID Nos. 191, 192 and 193 or (ii) three light chain CDRs having amino acid

sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID Nos. 191, 192 and 193. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions (substitution of the original residue with histidine) within the CDRs.

[00240] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 196, 197 and 198, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 196, 197 and 198; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID Nos: 199, 200 and 201 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 199, 200 and 201. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00241] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 204 or 343, 205 and 206, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 204 or 343, 205 and 206; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 207, 208 and 209, or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 207, 208 and 209. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00242] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 212, 213 and 214, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 212, 213 and 214; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 215, 216 and 217, or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID Nos. 215, 216 and 217. In some embodiments, there is a single conservative

amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00243] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NO: 220, 221 and 222, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 220, 221 and 222; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 223, 224 and 225 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 223, 224 and 225. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00244] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) three heavy chain CDRs having the amino acid sequences of SEQ ID NOs: 228, 229, and 230, or (ii) three heavy chain CDRs having amino acid sequences that differ by a one, two, or three conservative amino acid substitution within one or more of SEQ ID NOs: 228, 229, and 230; and the second polypeptide may comprise (i) three light chain CDRs having the amino acid sequences of SEQ ID NOs: 231, 232, and 233 or (ii) three light chain CDRs having amino acid sequences that differ by a one, two or three conservative amino acid substitution within one or more of SEQ ID NOs: 231, 232, and 233. In some embodiments, there is a single conservative amino acid substitution within one or more of the CDRs. In other embodiments, there are one, two, three or four additional histidine substitutions within the CDRs.

[00245] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a heavy chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 194, 202, 210, 218, 226, 234, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, and 274; and (ii) a light chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 195, 203, 211, 219, 227, 235, 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, and 278, or (i) a heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos: 194, 202, 210, 218, 226, 234, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, and 274; and (ii) a light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within at least one of SEQ ID Nos: 195, 203, 211, 219, 227, 235, 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, and 278.

[00246] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, and 274; and (ii) a humanized light chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, and 278, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos: 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 261, 262, 263, 264, 265, 270, 271, 272, 273, and 274; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within at least one of SEQ ID Nos: 256, 257, 258, 266, 267, 268, 269, 275, 276, 277, and 278.

[00247] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 246, 247, 248, 249, 250, 251, 252, 253, 254, and 255; and (ii) a light chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 256, 257, and 258, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos: 246, 247, 248, 249, 250, 251, 252, 253, 254, and 255; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within at least one of SEQ ID Nos: 256, 257, and 258.

[00248] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of SEQ ID No: 254; and (ii) a light chain variable region comprising the amino acid sequence of SEQ ID No: 258, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within SEQ ID No: 254; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within SEQ ID No: 258.

[00249] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of SEQ ID No: 251; and (ii) a light chain variable region comprising the amino acid sequence of SEQ ID No: 258, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within SEQ ID No: 251; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within SEQ ID No: 258.

[00250] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 261, 262, 263, 264, and 265; and (ii) a light chain variable region comprising the amino acid sequence of at least one of SEQ ID Nos: 266, 267, 268, and 269, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos: 261, 262, 263, 264, and 265; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within at least one of SEQ ID Nos: 266, 267, 268, and 269.

[00251] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of SEQ ID No: 264; and (ii) a light chain variable region comprising the amino acid sequence of SEQ ID No: 269, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within SEQ ID No: 264; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within SEQ ID No: 269.

[00252] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of SEQ ID No: 264; and (ii) a light chain variable region comprising the amino acid sequence of SEQ ID No: 268, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within SEQ ID No: 264; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within SEQ ID No: 268.

[00253] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain variable region comprising the amino acid sequence of SEQ ID No: 263; and (ii) a light chain variable region comprising the amino acid sequence of SEQ ID No: 269, or (i) a humanized heavy chain variable region comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within SEQ ID No: 263; and (ii) a humanized light chain variable region comprising an amino acid sequence that differs by one or more conservative amino acid substitution within SEQ ID No: 269.

[00254] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a humanized heavy chain sequence comprising the amino acid sequence of at least one of SEQ ID Nos: 280, 281, 282, 237, 283, 284, 285, and 286; and (ii) a light chain sequence comprising the amino acid sequence of SEQ ID No: 279, or (i) a humanized heavy chain sequence comprising an amino acid sequence that differs by a one or more conservative amino

acid substitution within at least one of SEQ ID Nos: 280, 281, 282, 237, 283, 284, 285, and 286; and (ii) a humanized light chain sequence comprising an amino acid sequence that differs by one or more conservative amino acid substitution within SEQ ID No. 279.

[00255] A fusion protein construct described herein comprises, in some embodiments, a humanized heavy chain sequence comprising the amino acid sequence of at least one of SEQ ID Nos: 280, 281, 282, 283, 284, 285, and 286 or a humanized heavy chain sequence comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos: 280, 281, 282, 237, 283, 284, 285, and 286. A fusion protein construct described herein comprises, in some embodiments, a humanized light chain sequence comprising the amino acid sequence of SEQ ID No. 279, or a humanized light chain sequence comprising an amino acid sequence that differs by one or more conservative amino acid substitution within SEQ ID No. 279.

[00256] In any of the fusion protein constructs described herein, the first polypeptide may comprise (i) a murine heavy chain sequence comprising the amino acid sequence of at least one of SEQ ID Nos. 73, 288, 244, 290, and 342; and (ii) a murine light chain sequence comprising the amino acid sequence of at least one of SEQ ID Nos. 68, 287, 59, and 289 or (i) a murine heavy chain sequence comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos. 73, 288, 244, 290, and 342; and (ii) a murine light chain sequence comprising an amino acid sequence that differs by one or more conservative amino acid substitution within at least one of SEQ ID Nos. 68, 287, 59, and 289.

[00257] A fusion protein construct described herein comprises, in some embodiments, a murine heavy chain sequence comprising the amino acid sequence of at least one of SEQ ID Nos. 73, 288, 244, 290, and 342 or a murine heavy chain sequence comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos. 73, 288, 244, 290, and 342. A fusion protein construct described herein comprises, in some embodiments, a murine light chain sequence comprising the amino acid sequence of at least one of SEQ ID Nos. 68, 287, 59, and 289 or a murine light chain sequence comprising an amino acid sequence that differs by a one or more conservative amino acid substitution within at least one of SEQ ID Nos. 68, 287, 59, and 289.

[00258] A conservative amino acid substitution is a substitution that changes a given amino acid to a different amino acid with similar biochemical properties (*e.g.*, charge, hydrophobicity, size). For example, any one of the amino acids within the following categories are considered conservative amino acid substitutions: Polar (hydrophilic) neutral amino acids: serine (Ser), threonine (Thr), cysteine (Cys), histidine (His), asparagine (Asn), glutamine (Gln), and tyrosine

(Tyr); Polar negatively charged amino acids: aspartic acid (Asp), glutamic acid (Glu); Polar positively charged amino acids: histidine (His), lysine (Lys), arginine (Arg); Hydrophobic amino acids: glycine (Gly), alanine (Ala), valine (Val), leucine (Leu), isoleucine (Ile), proline (Pro), phenylalanine (Phe), methionine (Met), and tryptophan (Trp); Hydrophobic amino acids with aliphatic side chains: alanine (Ala), valine (Val), leucine (Leu), isoleucine (Ile); Hydrophobic amino acids with aromatic side chains: phenylalanine (Phe), tryptophan (Trp); Amino acids that are small in size: alanine (Ala), cysteine (Cys), glycine (Gly), proline (Pro), serine (Ser) and threonine (Thr).

Conjugation of Targeting Moiety and Complement Modulator

[00259] The linkage between the targeting moiety and the complement modulator can comprise a conjugation via: (1) a direct fusion of the two protein sequences; or (2) a fusion with an intervening linker/linker sequence/spacer/tethering sequence. The terms “linker,” “linker sequence,” “spacer,” or “tethering sequence,” as used herein can mean a molecule or group of molecules (such as a monomer or polymer) that connects two molecules and often serves to place the two molecules in a preferred configuration. A number of strategies may be used to covalently link molecules together. These include but are not limited to polypeptide linkages between N- and C-termini of proteins or protein domains, linkage via disulfide bonds, and linkage via chemical cross-linking reagents. In one aspect, the linker is a peptide bond, generated by recombinant techniques or peptide synthesis.

[00260] In some examples, the complement modulator and the targeting moiety may be conjugated via a linker peptide, *e.g.*, a linker peptide that may directly link a targeting moiety and a complement modulator. The linker peptide may contain amino acid residues that provide flexibility. Thus, the linker peptide may include the following amino acid residues: glycine, serine, alanine, or threonine. The linker peptide should have a length that is adequate to link two molecules in such a way that they assume the correct conformation relative to one another so that they retain the desired activity. Suitable lengths for this purpose may include at least one to about 100 amino acid residues or more. The linker can be from about 1 to 30 amino acids in length. The linker can be from about 1 to 20 amino acids in length. Linker peptides can be included as spacers between two protein moieties. Linker peptides can promote proper protein folding, stability, expression, and bioactivity of the component protein moieties. Long flexible linker peptides can be composed of glycine, serine, or threonine, with multiple glycine residues providing a highly flexible conformation. Serine or threonine residues provide polar surface area to limit hydrophobic interaction within the peptide or with the component fusion protein moieties. The amino acid residues selected for inclusion in the linker peptide can exhibit

properties that do not interfere significantly with the activity of the polypeptide. Thus, the linker peptide may not exhibit a charge that would be inconsistent with the activity of the polypeptide, or interfere with internal folding, or form bonds or other interactions with amino acid residues in the targeting moiety or the complement modulator that would seriously impede the binding of the moieties to their targets. Non-limiting examples of sequences which may serve as the linker can include short peptides of about 2 to about 15 amino acids in length. Among the peptide sequences that can be used as linkers in this disclosure are (Gly-Ser)_n, where n=0,1, 2, 3, 4, 5, 6, 7, or 8 (SEQ ID NO: 292); (GlyGlyGlySer)_n, where n=1, 2, 3, or 4 (SEQ ID NO: 293); (GlySerSerGly)_n, where n=1, 2, 3, or 4 (SEQ ID NO: 294). In some fusion protein constructs, the linker sequence is (GlyGlyGlyGlySerGlyGlyGlyGlySer) (SEQ ID NO: 138). In some cases, glycine-alanine polymers, alanine-serine polymers, and other flexible linkers such as a tether blocker for the shaker potassium channel, comprising, a panel of quaternary ammoniums (QA) linked to maleimides with varying length poly-glycine tethers, *see, e.g.*, T.J. Morin and W.R. Kobertz Tethering Chemistry and K⁺ Channels J. Biol. Chem. 283(37): 25105-25109 (2008), and a large variety of other flexible linkers can be used. Glycine-serine polymers can be used since both amino acids are relatively unstructured, and therefore may be able to serve as a neutral tether between components. Secondly, serine is hydrophilic and therefore able to solubilize what could be a globular glycine chain. In some cases, the linker can comprise a sequence as set forth in any one of SEQ ID NOs: 171-193, where, in some examples, n can be at least 4; in some examples, n can be between 1 and 8, between 1 and 5. For instance, in SEQ ID NO: 161, n can be at least 4; in SEQ ID NO: 164, n = 1-8; in SEQ ID NO: 165, n = 1-5; in SEQ ID NO: 166, n = 1-5. In SEQ ID NO: 168, X can be A (alanine), K (lysine), or E (glutamic acid), and n = 5-17. In some cases, n in SEQ ID Nos.: 161, 164, 165, 166, 168, 170, 171, 174, and 179 can range from 1 to 17, 1 to 8, 1 to 5, at least 4, or 5 to 17.

[00261] Suitable linkers may also be identified by screening databases of known three-dimensional structures for naturally occurring motifs that can bridge the gap between two polypeptide chains, such as linkers derived from naturally occurring multidomain proteins. In some examples, the linker is not immunogenic when administered in a human patient. Thus, linkers may be chosen such that they have low immunogenicity or are thought to have low immunogenicity. For example, a linker may be chosen that exists naturally in a human. In some examples, the linker can have a sequence of the hinge region of an antibody, that is the sequence that links the antibody Fab and Fc regions; alternatively, the linker can have a sequence that comprises part of the hinge region, or a sequence that is substantially similar to the hinge region of an antibody. Another way of obtaining a suitable linker is by optimizing a simple linker, *e.g.*, (Gly₄Ser)_n (SEQ ID NO: 295), through random mutagenesis. Alternatively, once a suitable

polypeptide linker is defined, additional linker polypeptides can be created to select amino acids that more optimally interact with the domains being linked. Other types of linkers that may be used in the present invention include artificial polypeptide linkers and inteins. In some cases, the complement modulator and the targeting moiety may be conjugated using an enzymatic site-specific conjugation method which involves the use of a mammalian or bacterial transglutaminase enzyme. Microbial transglutaminases (mTGs) are versatile tools in modern research and biotechnology. The availability of large quantities of relatively pure enzymes, ease of use, and lack of regulation by calcium and guanosine-5'-triphosphate (GTP) has propelled mTG to be the main cross-linking enzyme used in both the food industry and biotechnology. Currently, mTGs are used in many applications to attach proteins and peptides to small molecules, polymers, surfaces, DNA, as well as to other proteins. See, *e.g.*, Pavel Strop, Veracity of microbial transglutaminase, *Bioconjugate Chem.* 25(5): 855-862.

[00262] In some examples are provided fusion protein construct comprising targeting moieties comprising an acceptor glutamine in a constant region, which can then be conjugated to a complement protein via a lysine-based linker (*e.g.*, any primary amine chain which is a substrate for TGase, *e.g.*, comprising an alkylamine, oxoamine) wherein the conjugation occurs exclusively on one or more acceptor glutamine residues present in the targeting moiety outside of the antigen combining site (*e.g.*, outside a variable region, in a constant region). Conjugation thus does not occur on a glutamine, *e.g.*, an at least partly surface exposed glutamine, within the variable region. The conjugate may be formed by reacting the targeting moiety and a lysine-based linker in the presence of a TGase. The lysine-based linker may comprise, for example, in addition to a primary amine, *e.g.*, alkylamine, oxoamine, a peptide, polypeptide, any organic molecule, a drug or diagnostic moiety, or may comprise a reactive moiety that can subsequently be reacted with the complement modulator.

[00263] In another aspect, disulfide bonds can be designed to link the two molecules. In some cases, linkers are chemical cross-linking agents. For example, a variety of bifunctional protein coupling agents may be used, including but not limited to N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl) cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, 1971, *Science* 238:1098. Chemical linkers may enable chelation of an isotope. For example, Carbon-14-labeled 1-

isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody (see, *e.g.*, WO 94/11026). The linker may be cleavable, facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, dimethyl linker or disulfide-containing linker (Chari et al., 1992, Cancer Research 52: 127-131) may be used. Alternatively, a variety of nonproteinaceous polymers, including but not limited to polyethylene glycol (PEG), polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, may find use as linkers, that is may find use to link the targeting moieties of the present disclosure to a fusion or conjugate partner, such as a complement modulator to generate a fusion protein construct of this disclosure.

[00264] Where the targeting and active moieties are directly joined, a hybrid vector can be made where the DNA encoding the targeting moiety and the complement modulator are themselves directly ligated to each other. Where a linker is used, a hybrid vector can be made where the DNA encoding the targeting moiety is ligated to the DNA encoding one end of the linker moiety; and the DNA encoding the complement modulator is ligated to the other end of the linker moiety. Such ligation may be performed either in series, or as a three-way ligation.

Production, Purification and Characterization Methods

[00265] The fusion protein constructs described herein can be produced using a variety of techniques. For example, a nucleic acid encoding a fusion protein construct described herein can be inserted into an expression vector that contains transcriptional and translational regulatory sequences, which include, *e.g.*, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, transcription terminator signals, polyadenylation signals, and enhancer or activator sequences. The regulatory sequences include a promoter and transcriptional start and stop sequences. In addition, the expression vector can include more than one replication system such that it can be maintained in two different organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification.

[00266] Several possible vector systems are available for the expression of fusion proteins from nucleic acids in mammalian cells. One class of vectors relies upon the integration of the desired gene sequences into the host cell genome. Cells which have stably integrated DNA can be selected by simultaneously introducing drug resistance genes such as *E. coli* gpt (*See* Mulligan and Berg Proc. Natl. Acad. Sci. USA 78:2072 (1981)) or Tn5 neo (*See* Southern and Berg Mol. Appl. Genet. 1:327 (1982)). The selectable marker gene can be either linked to the DNA gene sequences to be expressed or introduced into the same cell by co-transfection (Wigler *et al.* Cell

16:77 (1979)). A second class of vectors utilizes DNA elements which confer autonomously replicating capabilities to an extrachromosomal plasmid. These vectors can be derived from animal viruses, such as bovine papillomavirus (Sarver *et al.* Proc. Natl. Acad. Sci. USA, 79:7147 (1982)), polyoma virus (Deans *et al.* Proc. Natl. Acad. Sci. USA 81:1292(1984)), or SV40 virus (Lusky and Botchan Nature 293:79 (1981)).

[00267] The expression vectors can be introduced into cells in a manner suitable for subsequent expression of the nucleic acid. The method of introduction is largely dictated by the targeted cell type, discussed below. Exemplary methods include calcium phosphate precipitation, liposome fusion, lipofectin, electroporation, viral infection, dextran-mediated transfection, polybrene-mediated transfection, protoplast fusion, and direct microinjection.

[00268] Appropriate host cells for the expression of the fusion proteins include yeast, bacteria, insect, plant, and, as described above, mammalian cells. Of interest are bacteria such as *E. coli*, fungi such as *Saccharomyces cerevisiae* and *Pichia pastoris*, insect cells such as SF9, mammalian cell lines (*e.g.*, human cell lines), as well as primary cell lines (*e.g.*, primary mammalian cells). In some embodiments, the fusion proteins can be expressed in Chinese hamster ovary (CHO) cells or in a suitable myeloma cell line such as (NS0). Suitable cell lines also include, for example, HEK cells (Human embryonic kidney 293 cells), BHK-21 (baby hamster kidney) cells; 293 (human embryonic kidney) cells; HMEpC (Human Mammary Epithelial cells; 3T3 (mouse embryonic fibroblast) cells.

[00269] As will be recognized by the skilled artisan, some complement modulators that may be used in the disclosure occur in nature as secreted proteins in conjunction with a signal or leader peptide, as a pro-peptide, or both, and undergo further intra- or extra-cellular processing. In such cases, the hybrid vectors of this disclosure may include one or more DNA sequences encoding such signal or leader peptides, one or more DNA sequences encoding such pro-peptide sequence, or both, depending upon whether such secretion, processing, or a combination of secretion and processing is desired. Alternatively, the hybrid vectors of the present disclosure may include DNA sequences encoding a different signal or leader peptide, pro-peptide, or both, sequence chosen to optimize the expression and localization of the fusion protein. In most cases, the signal peptide may be omitted, as the targeting moiety will supply sufficient information for targeting of the complement modulator to the desired tissue and cells within a subject's body.

[00270] In exemplary production methods, a fusion protein construct described herein can be expressed in, and purified from, transgenic animals (*e.g.*, transgenic mammals). For example, a fusion protein described herein can be produced in transgenic non-human mammals (*e.g.*, rodents, sheep or goats) and isolated from milk as described in, *e.g.*, Houdebine Curr. Opin. Biotechnol. 13(6):625-629 (2002); van Kuik-Romeijn *et al.* Transgenic Res. 9(2):155-159 (2000); and Pollock *et al.* J Immunol. Methods 231(1-2):147-157 (1999).

[00271] The fusion protein constructs described herein can be produced from cells by culturing a host cell transformed with the expression vector containing nucleic acid encoding the antibodies or antigen binding fragments thereof, under conditions, and for an amount of time, sufficient to allow expression of the proteins. For example, polypeptides expressed in *E. coli* can be refolded from inclusion bodies (*see e.g.*, Hou *et al.* Cytokine 10:319-30 (1998)). Bacterial expression systems and methods for their use are well known in the art (*see* Current Protocols in Molecular Biology, Wiley & Sons, and Molecular Cloning—A Laboratory Manual—3rd Ed., Cold Spring Harbor Laboratory Press, New York (2001)). The choice of codons, suitable expression vectors and suitable host cells will vary depending on a number of factors and may be easily optimized as needed. A fusion protein construct described herein can be expressed in mammalian cells or in other expression systems including but not limited to yeast, baculovirus, and in vitro expression systems (*see e.g.*, Kaszubska *et al.* Protein Expression and Purification 18:213-220 (2000)).

[00272] Following expression, the fusion protein constructs can be isolated. The term “purified” or “isolated” as applied to any of the proteins described herein (*e.g.*, a fusion protein constructs described herein) may refer to a polypeptide that has been separated or purified from components (*e.g.*, proteins or other naturally-occurring biological or organic molecules) which naturally accompany it, *e.g.*, other proteins, lipids, and nucleic acid in a prokaryote expressing the proteins. Typically, a polypeptide is purified when it constitutes at least 60 (*e.g.*, at least 65, 70, 75, 80, 85, 90, 92, 95, 97, or 99) %, by weight, of the total protein in a sample. A fusion protein construct described herein can be isolated or purified in a variety of ways depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography. For example, a fusion protein can be purified using a standard anti-fusion protein antibody affinity column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. *See e.g.*, Scopes (1994) “Protein Purification, 3rd edition,” Springer-Verlag, New York City, N.Y. The degree of purification necessary will vary depending on the desired use. In some instances, no purification of the expressed polypeptide thereof will be necessary.

[00273] Methods for determining the yield or purity of a purified polypeptide can include, *e.g.*, Bradford assay, UV spectroscopy, Biuret protein assay, Lowry protein assay, amido black protein assay, high pressure liquid chromatography (HPLC), mass spectrometry (MS), and gel electrophoretic methods (*e.g.*, using a protein stain such as Coomassie Blue or colloidal silver stain).

[00274] In other exemplary production methods, a fusion protein construct described herein can be synthesized *de novo* in whole or in part, using chemical methods. For example, the component amino acid sequences can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high-performance liquid chromatography followed by chemical linkage to form a desired polypeptide. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing.

[00275] Once expressed, purified, or after being purified following expression, a fusion protein construct described herein can be assayed for any one of a number of desired properties using *in vitro* or *in vivo* assays such as any of those described herein. For example, a fusion protein described herein can be assayed for its ability to inhibit C5 convertase as described in, *e.g.*, Heinen *et al.* Factor H-related protein 1 (CFHR-1) inhibits complement C5 convertase activity and terminal complex formation. Blood 114(12):2439-47 (2009). Endotoxins can be removed from the fusion protein construct preparations using a variety of commercially available reagents including, without limitation, the ProteoSpin™ Endotoxin Removal Kits (Norgen Biotek Corporation), Detoxi-Gel Endotoxin Removal Gel (Thermo Scientific; Pierce Protein Research Products), MiraCLEAN® Endotoxin Removal Kit (Mirus), or Acrodisc™-Mustang® E membrane (Pall Corporation).

[00276] Methods for detecting and/or measuring the amount of endotoxin present in a sample (both before and after purification) can be based on commercial kits that are available. For example, the concentration of endotoxin in a protein sample can be determined using the QCL-1000 Chromogenic kit (BioWhittaker), the *limulus amoebocyte* lysate (LAL)-based kits such as the Pyrotell®, Pyrotell®-T, Pyrochrome®, Chromo-LAL, and CSE kits available from the Associates of Cape Cod Incorporated.

[00277] Following expression and purification, the fusion protein constructs described herein can be modified. The modifications can be covalent or non-covalent modifications. Such modifications can be introduced into the fusion proteins by, *e.g.*, reacting targeted amino acid residues of the polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or terminal residues. Suitable sites for modification can be chosen using any of a variety of criteria including, *e.g.*, structural analysis or amino acid sequence analysis of the fusion proteins described herein.

[00278] In some exemplary production methods, a fusion protein construct as described herein can be conjugated to a heterologous moiety. The heterologous moiety can be, *e.g.*, a heterologous polypeptide, a therapeutic agent (*e.g.*, a toxin or a drug), or a detectable label such as, but not limited to, a radioactive label, an enzymatic label, a fluorescent label, or a luminescent label. Suitable heterologous polypeptides can include, *e.g.*, an antigenic tag (*e.g.*,

FLAG, polyhistidine, hemagglutinin (HA), glutathione-S-transferase (GST), or maltose-binding protein (MBP)) for use in purifying the antibodies. Heterologous polypeptides can also include polypeptides that are useful as diagnostic or detectable markers, for example, luciferase, green fluorescent protein (GFP), or chloramphenicol acetyl transferase (CAT). Where the heterologous moiety is a polypeptide, the moiety can be incorporated into a fusion protein described herein, resulting in a fusion protein.

Pharmaceutical Formulations

[00279] Also provided in this disclosure are pharmaceutical formulations comprising a fusion protein construct as described here. Pharmaceutical formulations of the fusion protein constructs of this disclosure are typically prepared for parenteral administration, *i.e.*, bolus, intravenous, intratumor, subcutaneous injection with a pharmaceutically acceptable parenteral vehicle and in a unit dosage injectable form. A fusion protein construct can be optionally mixed with pharmaceutically acceptable diluents, carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences (1980) 16th edition, Osol, A. Ed.), in the form of a lyophilized formulation or an aqueous solution. Acceptable diluents, carriers, excipients, and stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG), or any combinations thereof.

[00280] The fusion protein constructs may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

[00281] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi permeable matrices of solid hydrophobic polymers containing a fusion protein construct, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinyl alcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

[00282] The formulations to be used for *in vivo* administration are sterile, which can be accomplished by filtration through sterile filtration membranes. The formulations include those suitable for the foregoing administration routes. The formulations may conveniently be presented in unit dosage form and may be prepared by any of the methods usually practiced in preparation of pharmaceutical formulations as unit dosage. Techniques and formulations generally are found in Remington's Pharmaceutical Sciences (Mack Publishing Co., Easton, Pa.). Such methods include the step of bringing into association the active ingredient with the carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the fusion protein constructs with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaking the product.

[00283] Aqueous suspensions of this disclosure contain the fusion protein constructs in admixtures with excipients suitable for the manufacture of aqueous suspensions. Such excipients include a suspending agent, such as sodium carboxymethylcellulose, croscarmellose, povidone, methylcellulose, hydroxypropyl methylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia, and dispersing or wetting agents such as a naturally occurring phosphatide (*e.g.*, lecithin), a condensation product of an alkylene oxide with a fatty acid (*e.g.*, polyoxyethylene stearate), a condensation product of ethylene oxide with a long chain aliphatic alcohol (*e.g.*, heptadecaethyleneoxycetanol), a condensation product of ethylene oxide with a partial ester derived from a fatty acid and a hexitol anhydride (*e.g.*, polyoxyethylene sorbitan monooleate). The aqueous suspension may also contain one or more preservatives such as ethyl or n-propyl p-hydroxy-benzoate, one or more coloring agents, one or more flavoring agents and one or more sweetening agents, such as sucrose or saccharin.

[00284] The pharmaceutical formulations containing the fusion protein constructs may be in the form of a sterile injectable preparation, such as a sterile injectable aqueous or oleaginous suspension. This suspension may be formulated according to methods using those suitable

dispersing or wetting agents and suspending agents which have been mentioned above. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally acceptable diluent or solvent, such as a solution in 1,3-butane-diol or prepared as a lyophilized powder. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile fixed oils may conventionally be employed as a solvent or suspending medium. For this purpose, any bland fixed oil may be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid may likewise be used in the preparation of injectables.

[00285] The amount of active ingredient that may be combined with the carrier material to produce a single dosage form will vary depending upon the host treated and the particular mode of administration. For example, an aqueous solution intended for intravenous infusion may contain from about 3 to 500 µg of the active ingredient per milliliter of solution in order that infusion of a suitable volume at a rate of about 30 mL/hour can occur.

[00286] Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents.

[00287] Although oral administration of protein therapeutics is disfavored due to hydrolysis or denaturation in the gut, formulations of fusion protein constructs suitable for oral administration may be prepared as discrete units such as capsules, cachets or tablets each containing a predetermined amount of the fusion protein construct.

[00288] The formulations may be packaged in unit-dose or multi-dose containers, for example sealed ampoules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example water, for injection immediately prior to use. In some cases, the formulations may be packaged in an infusion device, such as an infusion pump, *e.g.*, for controlled delivery. Extemporaneous injection solutions and suspensions are prepared from sterile powders, granules and tablets of the kind previously described.

Preferred unit dosage formulations are those containing a daily dose or unit daily sub-dose, as herein above recited, or an appropriate fraction thereof, of the active ingredient.

[00289] The disclosure further provides veterinary compositions comprising at least one active ingredient as above defined together with a veterinary carrier therefore. Veterinary carriers are materials useful for the purpose of administering the composition and may be solid, liquid or gaseous materials which are otherwise inert or acceptable in the veterinary art and are compatible with the active ingredient. These veterinary compositions may be administered parenterally, orally or by any other desired route.

Methods of Treating Complement Associated Diseases, Disorders, or Conditions

[00290] The fusion protein constructs described herein can be used to treat a variety of complement-associated disorders such as, but not limited to: ischemia-reperfusion injury, rheumatoid arthritis (RA); lupus nephritis; ischemia-reperfusion injury; atypical hemolytic uremic syndrome (aHUS); typical or infectious hemolytic uremic syndrome (tHUS); dense deposit disease (DDD); paroxysmal nocturnal hemoglobinuria (PNH); multiple sclerosis (MS); macular degeneration (*e.g.*, age-related macular degeneration (AMD), geographic atrophy (also known as atrophic age-related macular degeneration or advanced dry AMD); hemolysis, elevated liver enzymes, and low platelets (HELLP) syndrome; sepsis; dermatomyositis; diabetic retinopathy; thrombotic thrombocytopenic purpura (TTP); spontaneous fetal loss; Pauci-immune vasculitis; epidermolysis bullosa; recurrent fetal loss; multiple sclerosis (MS); and traumatic brain injury.

[00291] Complement-mediated vascular disorder can also be treated using the fusion protein construct of this disclosure, such as, but not limited to, a cardiovascular disorder, myocarditis, a cerebrovascular disorder, a peripheral (*e.g.*, musculoskeletal) vascular disorder, a renovascular disorder, a mesenteric/enteric vascular disorder, revascularization to transplants and/or replants, vasculitis, Henoch-Schönlein purpura nephritis, systemic lupus erythematosus-associated vasculitis, vasculitis associated with rheumatoid arthritis, immune complex vasculitis, Takayasu's disease, capillary leak syndrome, dilated cardiomyopathy, diabetic angiopathy, thoracic-abdominal aortic aneurysm, Kawasaki's disease (arteritis), venous gas embolus (VGE), and restenosis following stent placement, rotational atherectomy, and percutaneous transluminal coronary angioplasty (PTCA).

[00292] The complement-associated disorder can also be myasthenia gravis, cold-agglutinin disease (CAD), paroxysmal cold hemoglobinuria (PCH), idiopathic inflammatory myopathies including dermatomyositis and polymyositis, scleroderma, warm autoimmune hemolytic anemia, Graves' disease, Hashimoto's thyroiditis, type I diabetes, psoriasis, pemphigus, autoimmune hemolytic anemia (AIHA), idiopathic thrombocytopenic purpura (ITP), Goodpasture's syndrome, antiphospholipid syndrome (APS), Degos disease, and catastrophic APS (CAPS).

[00293] Ischemia-reperfusion (IR) injury can refer to damage to a tissue caused when the blood supply returns to the tissue after a period of ischemia (restriction in blood supply). The absence of oxygen and nutrients from the blood creates a condition in which the restoration of circulation results in inflammation and oxidative damage, rather than restoration of normal function.

Ischemia-reperfusion injury can be associated with traumatic injury, including hemorrhagic shock, as well as many other medical conditions such as stroke or large vessel occlusion (e.g. middle cerebral artery), and is a major medical problem. More particularly, ischemia-reperfusion injury is important in heart attacks, stroke, kidney failure following vascular surgery, post-transplantation injury and chronic rejection, as well as in various types of traumatic injury, where hemorrhage will lead to organ hypoperfusion, and then subsequent reperfusion injury during fluid resuscitation. Ischemia-reperfusion injury, or an injury due to reperfusion and ischemic events, is also observed in a variety of autoimmune and inflammatory diseases. Independently of other factors, ischemia-reperfusion injury may lead to increased mortality. Ischemia-reperfusion injury, as well as hypovolemic shock and subsequent tissue damage, has been shown to be caused by complement and Fc receptor activation and the recruitment and activation of neutrophils and other inflammatory cells. *See e.g.*, S. Rehrig *et al.*, 2001, J. Immunol. 167:5921-5927. It had also been shown that single monoclonal antibodies that react broadly with phospholipids and other extracellular or intracellular antigens such as DNA can cause ischemia-reperfusion injury in mice that lack other antibodies (i.e., B cell- deficient mice).

[00294] Renal disease, such as albuminuria, or more broadly, proteinuria, can refer to abnormalities in kidney function that leads to increased levels of protein excretion in the urine. Increased protein levels in the urine is a marker of kidney failure, or kidney damage caused by immune disorders, glomerulonephritis, multiple myeloma, cardiovascular diseases, or kidney trauma. The ratio of albumin and creatinine present in the urine are used to detect potential kidney failure; persistent elevated urine protein levels is indicative of kidney failure.

[00295] In some cases, an albumin to creatine ratio is determined. In some embodiments, an albumin to creatine ratio is determined for a subject having a disease (e.g., renal disease). In some embodiments, an albumin to creatine ratio is determined in a biological sample. In some embodiments, the biological sample is urine. In some embodiments, an albumin to creatine ratio determined for a subject having a disease is compared to an albumin to creatine ratio from another subject or the same subject (e.g., another subject with the same disease, or the same subject at different time points, or another subject not having the disease). In some embodiments, the albumin to creatine ratio is determined at some point after the subject is administered with any of the fusion protein construct of this disclosure. In some embodiments, the another subject is administered with a comparable fusion protein construct. In some embodiments, the comparable fusion protein construct does not comprise the antibody or the antigen binding fragment thereof but is otherwise identical to a fusion protein construct of this disclosure. In some embodiments, the albumin to creatinine ratio is determined from a biological sample (e.g., urine sample) from a subject (e.g., a subject having a disease). In some embodiments, the albumin to

creatinine ratio from a subject having a disease is at least about 1%, 2%, 3%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% lower than the albumin to creatinine ratio from a comparable biological sample from the same subject collected at a different time point or from another subject (e.g., another subject administered with a comparable fusion protein construct).

[00296] In certain instances, an anti-C3d/C3dg antibody or antigen-binding fragment thereof or a fusion protein construct comprising such antibody or an antigen-binding fragment thereof as the targeting moiety described herein, alone or in combination with a second anti-inflammatory agent, can be used to treat an inflammatory disorder such as, but not limited to, RA (above), inflammatory bowel disease, sepsis (above), septic shock, acute lung injury, disseminated intravascular coagulation (DIC), or Crohn's disease. In some embodiments, the second anti-inflammatory agent can be one selected from NSAIDs, corticosteroids, methotrexate, hydroxychloroquine, anti-TNF agents such as etanercept and infliximab, a B cell depleting agent such as rituximab, an interleukin-1 antagonist, and a T cell costimulatory blocking agent such as abatacept.

[00297] In some embodiments, the complement-associated disorder is a complement-associated neurological disorder such as, but not limited to, amyotrophic lateral sclerosis (ALS), brain injury, Alzheimer's disease, and chronic inflammatory demyelinating neuropathy.

[00298] Complement-associated disorders also include complement-associated pulmonary disorders such as, but not limited to, asthma, bronchitis, a chronic obstructive pulmonary disease (COPD), an interstitial lung disease, α -1 anti-trypsin deficiency, emphysema, bronchiectasis, bronchiolitis obliterans, alveolitis, sarcoidosis, pulmonary fibrosis, and collagen vascular disorders.

[00299] The fusion protein constructs of this disclosure can be used to treat one or more indications selected from: Paroxysmal nocturnal hemoglobinuria (PNH), Atypical hemolytic uremic syndrome (aHUS), myasthenia gravis, Antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis (AAV), C3 glomerulonephritis (C3G), cold agglutinin disease (CAD), warm antibody hemolytic anemia, antibody mediated transplant rejection, Neuromyelitis Optica (NMOSD), dense deposit disease, IgA Nephropathy (IgAN), Membranous Nephropathy (MN), thrombotic microangiopathy, hereditary angioedema (HAE), systemic lupus, lupus nephritis, discoid lupus, psoriatic arthritis, psoriasis, atopic dermatitis, alopecia areata, hidradenitis suppurativa, vitiligo, rheumatoid arthritis, periodontal disease, bone disorders (osteoarthritis, fracture, osteomyelitis), Dry macular degeneration, Wet macular degeneration, glaucoma, uveitis, geographic atrophy, heart and lung surgery, cardiac regeneration, lung cancer, neurodegeneration, ALS, MS, traumatic brain injury, spinal cord injury, schizophrenia, major

depressive disorder, bipolar disorder, scleroderma, scleroderma renal crisis, cutaneous vasculitis, blistering skin diseases (endemic pemphigus, bullous pemphigoid, Pemphigus erythematosus, pemphigus vulgaris), and drusen-related disease.

[00300] While preferred embodiments of this disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from this disclosure. It should be understood that various alternatives to the embodiments of this disclosure described herein may be employed in practicing the disclosure. It is intended that the claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

Certain Definitions

[00301] Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. The meaning and scope of the terms should be clear, however, in the event of any latent ambiguity, definitions provided herein take precedent over any dictionary or extrinsic definition. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. In this application, the use of “or” means “and/or” unless stated otherwise. Furthermore, the use of the term “including”, as well as other forms, such as “includes” and “included”, is not limiting.

[00302] The term “complement modulator,” as used herein, means any molecule that can stimulate or inhibit activity of a complement pathway.

[00303] The term “antibody”, as used herein, means any antigen-binding molecule comprising at least one complementarity determining region (CDR). The term “antibody” includes immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, as well as multimers thereof (*e.g.*, IgM). Each heavy chain comprises a heavy chain variable region (abbreviated herein as HCVR or VH) and a heavy chain constant region. The heavy chain constant region comprises three domains, CH1, CH2 and CH3. Each light chain comprises a light chain variable region (abbreviated herein as LCVR or VL) and a light chain constant region. The light chain constant region comprises one domain (CL1). The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in

the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In different embodiments of the disclosure, the FRs of the targeting moiety (or antigen-binding portion thereof) may be identical to the human germline sequences or may be naturally or artificially modified. An amino acid consensus sequence may be defined based on a side-by-side analysis of two or more CDRs.

[00304] The terms “antigen-binding portion” of an antibody, “antigen-binding fragment” of an antibody, and the like, as used herein, include any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex. Antigen-binding fragments of an antibody may be derived, *e.g.*, from intact antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and optionally constant domains. Such DNA is known and/or is readily available from, *e.g.*, commercial sources, DNA libraries (including, *e.g.*, phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, etc.

[00305] Non-limiting examples of antigen-binding fragments include: (i) Fab fragments; (ii) F(ab')₂ fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single-chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units consisting of the amino acid residues that mimic the hypervariable region of an antibody (*e.g.*, an isolated complementarity determining region (CDR) such as a CDR3 peptide), or a constrained FR3-CDR3-FR4 peptide.

[00306] The term “variable region” or “variable domain” of an antibody, or fragment thereof, as used herein refers to the portions of the light and heavy chains of antibody molecules that include amino acid sequences of complementarity determining regions (CDRs; *i.e.*, CDR1, CDR2, and CDR3), and framework regions (FRs). VH refers to the variable domain of the heavy chain. VL refers to the variable domain of the light chain. According to the methods used in this disclosure, the amino acid positions assigned to CDRs and FRs may be defined according to Kabat *et al.* (Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md., 1987 and 1991)). Amino acid numbering of antibodies or antigen binding fragments is also according to that of Kabat.

[00307] The term “complementarity determining regions” or “CDRs” as used herein refers to the complementarity determining region within antibody variable sequences. There are three CDRs in each of the variable regions of the heavy chain and the light chain, which are designated CDR1, CDR2 and CDR3, for each of the variable regions. The term “CDR set” as

used herein refers to a group of three CDRs that occur in a single variable region capable of binding the antigen. The exact boundaries of these CDRs have been defined differently according to different systems. The system described by Kabat (Kabat *et al.*, Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md. (1987) and (1991)) not only provides an unambiguous residue numbering system applicable to any variable region of an antibody, but also provides precise residue boundaries defining the three CDRs. These CDRs may be referred to as Kabat CDRs. Chothia and coworkers (Chothia *et al.*, J. Mol. Biol. 196:901-917 (1987) and Chothia *et al.*, Nature 342:877-883 (1989)) found that certain sub-portions within Kabat CDRs adopt nearly identical peptide backbone conformations, despite having great diversity at the level of amino acid sequence. These sub-portions were designated as L1, L2 and L3 or H1, H2 and H3 where the “L” and the “H” designates the light chain and the heavy chains regions, respectively. These regions may be referred to as Chothia CDRs, which have boundaries that overlap with Kabat CDRs. Other boundaries defining CDRs overlapping with the Kabat CDRs have been described by Padlan (FASEB J. 9:133-139 (1995)) and MacCallum (J Mol Biol 262(5):732-45 (1996)). Still other CDR boundary definitions may not strictly follow one of the above systems, but will nonetheless overlap with the Kabat CDRs, although they may be shortened or lengthened in light of prediction or experimental findings that particular residues or groups of residues or even entire CDRs do not significantly impact antigen binding. The methods used herein may utilize CDRs defined according to any of these systems, although preferred embodiments use Kabat or Chothia defined CDRs.

[00308] ImMunoGeneTics (IMGT) also provides a numbering system for the immunoglobulin variable regions, including the CDRs. *See, e.g.*, M. P. Lefranc *et al.*, Dev. Comp. Immunol. 27: 55-77(2003). The IMGT numbering system is based on an alignment of more than 5,000 sequences, structural data, and characterization of hypervariable loops and allows for easy comparison of the variable and CDR regions for all species. According to the IMGT numbering schema, VH-CDR1 can be at positions 26 to 35, VH-CDR2 can be at positions 51 to 57, VH-CDR3 can be at positions 93 to 102, VL-CDR1 can be at positions 27 to 32, VL-CDR2 can be at positions 50 to 52, and VL-CDR3 can be at positions 89 to 97. In some examples, the antibodies or antigen binding fragment thereof described in this disclosure can include a combination of heavy chain and light chain complementarity determining regions (CDRs) selected from the CDR sequences shown in the Sequence table, where the CDRs shown in the Sequence Table are defined according to the IMGT nomenclature. In some cases, the CDR sequences of the antibodies or antigen binding fragments thereof were analyzed from the cDNA amplified sequences using IMGT software (on the world wide web at http://imgt.org/IMGT_vquest/vquest).

[00309] The term “framework regions” (hereinafter FR) as used herein refers to those variable domain residues other than the CDR residues. Each variable domain typically has four FRs identified as FR1, FR2, FR3 and FR4. Common structural features among the variable regions of antibodies, or functional fragments thereof, are well known in the art. The DNA sequence encoding a particular antibody can generally be found following well known methods such as those described in Kabat, *et al.* 1987 Sequence of Proteins of Immunological Interest, U.S. Department of Health and Human Services, Bethesda MD, which is incorporated herein as a reference. In addition, a general method for cloning functional variable regions from antibodies can be found in Chaudhary, V.K., *et al.*, 1990 Proc. Natl. Acad. Sci. USA 87:1066, which is incorporated herein as a reference.

[00310] The term “Fc region” herein is used to as used herein is meant the polypeptide comprising the constant region of an antibody excluding the first constant region immunoglobulin domain and, in some cases, part of the hinge region. Thus Fc region refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM, Fc may include the J chain. For IgG, Fc can comprise immunoglobulin domains CH2 and CH3 and the hinge between CH1 and CH2 (Cgamma 2). Fc may refer to this region in isolation, or this region in the context of an Fc fusion protein. The term Fc region includes, for example, native sequence Fc regions, recombinant Fc regions, and variant Fc regions. Although the boundaries of the Fc region of an antibody heavy chain might vary, the human IgG heavy chain Fc region is often defined to stretch from an amino acid residue at position Cys226, or from Pro230, to the carboxyl-terminus thereof, wherein the numbering is according to the EU index as in Kabat. The C-terminal lysine (residue 447 according to the EU numbering system) of the Fc region may be removed, for example, during production or purification of the antibody, or by recombinantly engineering the nucleic acid encoding a heavy chain of the antibody. Accordingly, the fusion protein constructs described herein may comprise targeting moieties comprising Fc regions where K447 residues are removed, or where no K447 residues are removed, or fusion protein constructs where some of the Fc regions have K447 residues removed while some do not have K447 residues removed.

[00311] As used herein, “Fc polypeptide” can refer to a polypeptide that comprises all or part of an Fc region. Fc polypeptides can include antibodies, Fc fusions, isolated Fcs, and Fc fragments. Immunoglobulins may be Fc polypeptides. The term “Fc fusion” as used herein is meant a protein wherein one or more polypeptides is operably linked to Fc. Fc fusion is herein meant to be synonymous with the terms “immunoadhesin,” “Ig fusion,” “Ig chimera,” and “receptor globulin” (or “receptor-globulin”) as used, for example, in Chamow et al., 1996,

Trends Biotechnol 14:52-60; Ashkenazi et al., 1997, Curr. Opin. Immunol 9:195-200. An Fc fusion can combine the Fc region of an immunoglobulin with a fusion partner, which can be a complement modulator protein, polypeptide or small molecule. In some examples, the role of the non-Fc part of an Fc fusion, *i.e.*, the fusion partner, such as a complement modulator protein, is to mediate target binding, and thus it is functionally analogous to the variable regions of an antibody. Protein fusion partners may include, but are not limited to, the target-binding region of a receptor, an adhesion molecule, a ligand, an enzyme, a cytokine, a chemokine, a complement modulator protein or polypeptide, or some other protein or protein domain. Small molecule fusion partners may include any therapeutic agent that directs the Fc fusion to a therapeutic target. Such targets may be any molecule, *e.g.*, an extracellular receptor that is implicated in disease.

[00312] The terms “Fc gamma receptor” or “Fcgamma R” as used herein can mean any member of the family of proteins that bind the IgG antibody Fc region and are substantially encoded by the Fcgamma R genes. In humans this family includes but is not limited to Fcgamma RI (CD64), including isoforms Fcgamma RIa, Fcgamma RIb, and Fcgamma RIc; Fcgamma RII (CD32), including isoforms Fcgamma RIIa (including allotypes H131 and R131), Fcgamma RIIb (including Fcgamma RIIb-1 and Fcgamma RIIb-2), and Fcgamma RIIC; and Fcgamma RIII (CD16), including isoforms Fcgamma RIIIa (including allotypes V158 and F158) and Fcgamma RIIIb (including allotypes Fcgamma RIIIb-NA1 and Fcgamma RIIIb-NA2) (Jefferis et al., 2002, Immunol Lett 82:57-65, incorporated entirely by reference), as well as any undiscovered human Fcgamma Rs or Fcgamma R isoforms or allotypes. An Fcgamma R may be from any organism, including but not limited to humans, mice, rats, rabbits, and monkeys. Mouse Fcgamma Rs include but are not limited to Fcgamma RI (CD64), Fcgamma RII (CD32), Fcgamma RIII (CD16), and Fcgamma RIII-2 (CD16-2), as well as any undiscovered mouse Fcgamma Rs or Fcgamma R isoforms or allotypes.

[00313] An “Fc ligand” or “Fc receptor” as used herein can mean a molecule, *e.g.*, a polypeptide, from any organism that binds to the Fc region of an antibody to form an Fc-ligand complex. Fc ligands include but are not limited to Fcgamma Rs, Fcgamma Rs, Fcgamma Rs, FcRn, C1q, C3, mannan-binding lectin, mannose receptor, staphylococcal protein A, streptococcal protein G, and viral Fcgamma R. Fc ligands also include Fc receptor homologs (FcRH), which are a family of Fc receptors that are homologous to the Fcgamma Rs (Davis et al., 2002, Immunological Reviews 190:123-136). Fc ligands may include undiscovered molecules that bind Fc.

[00314] The term “humanized antibody” as used herein can refer to an antibody or a variant, derivative, analog or fragment thereof, which can immunospecifically bind to an antigen of

interest (*e.g.*, a domain of a mammalian annexin protein, a phospholipid, a complement protein or a fragment thereof, such as C3d), and which comprises a framework (FR) region having substantially the amino acid sequence of a human antibody and a complementary determining region (CDR) having substantially the amino acid sequence of a non-human antibody.

Humanized forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins that contain minimal sequences derived from non-human immunoglobulin. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin sequence. The humanized antibody can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin consensus sequence. Any suitable methods of antibody humanization can be used. See, *e.g.*, Riechmann *et al.*, 1988, *Nature* 332:323-7; U.S. Patent Nos: 5,530,101; 5,585,089; 5,693,761; 5,693,762; and 6,180,370 to Queen *et al.*; EP239400; PCT publication WO 91/09967; U.S. Patent No. 5,225,539; EP592106; EP519596; Padlan, 1991, *Mol. Immunol.*, 28:489-498; Studnicka *et al.*, 1994, *Prot. Eng.* 7:805-814; Roguska *et al.*, 1994, *Proc. Natl. Acad. Sci.* 91:969-973; and U.S. Patent No. 5,565,332, all of which are hereby incorporated by reference in their entireties.

[00315] The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible mutations, *e.g.*, naturally occurring mutations that may be present in minor amounts. Thus, the modifier “monoclonal” indicates the character of the antibody as not being a mixture of discrete antibodies. In certain embodiments, such a monoclonal antibody typically includes an antibody comprising a polypeptide sequence that binds a target, wherein the target-binding polypeptide sequence was obtained by a process that includes the selection of a single target binding polypeptide sequence from a plurality of polypeptide sequences. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, or recombinant DNA clones. In contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal-antibody preparation is directed against a single epitope on an antigen.

[00316] The term “chimeric antibody” as used herein refers to antibodies (immunoglobulins) that have a portion of the heavy and/or light chain identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging

to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; and Morrison *et al.*, Proc. Natl. Acad. Sci. USA 81 :6851-6855 (1984)).

[00317] The term “epitope” as used herein refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be defined as structural or functional. Functional epitopes are generally a subset of the structural epitopes and have those residues that directly contribute to the affinity of the interaction. Epitopes may also be conformational, that is, composed of non-linear amino acids. In certain embodiments, epitopes may include determinants that are chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl groups, or sulfonyl groups, and, in certain embodiments, may have specific three-dimensional structural characteristics, and/or specific charge characteristics.

[00318] As used herein, the term “annexin,” refers to a large family calcium-dependent membrane binding-proteins that are widely distributed among eukaryotes but are typically absent in prokaryotes and yeasts. The term “annexin,” includes more than about 100 annexins that have so far been identified in many species. *See, e.g.*, Gerke V, Moss SE. Annexins: from structure to function. *Physiol Rev.* 2002; 82:331–371. Included within the meaning of the term “annexin,” are annexin proteins identified in humans, annexins 1-11 and annexin-13. All annexins share a conserved C-terminal core domain made up of at least four similar repeats, each about 70 amino acids long. These subunits usually contain characteristic type 2 calcium binding sites. The number and location of these sites generally vary between different annexin families, with variation and replacement with other motifs. Calcium-independent annexin membrane interactions involve a switch from a helix-loop-helix motif to the transmembrane helix, which drives a reversible membrane insertion. In contrast to the core domain, individual vertebrate annexins have a unique N-terminal domain of variable length, amino acid sequences, and determinants of hydrophobicity.

[00319] The term “annexin IV,” refers to proteins of the annexin A4 subfamily, which are the smallest annexin family members containing a short N-terminal region, which have been shown to be involved in repair of plasma membrane stress induced lesions. *See, e.g.*, Boye *et al.*, *Nature Communications* 8, Article No: 1623 (2017). As used herein, the term “biologically-active fragment” of annexin IV, annexin 4, can refer to a fragment of annexin IV which can be recognized by pathogenic natural antibodies that recognize annexin IV, or antibodies or antigen binding fragments thereof that are derived from such natural antibodies (*e.g.*, the C2 antibody,

the B4 antibody) which leads to development of intestinal ischemia-reperfusion injury, as has been shown by Kulik *et al.* J. Immunol. 2009; 182:5363-5373. Natural antibodies exist in an immune competent individual and can be found in the serum or plasma of an individual not known to have been stimulated by a specific antigen to which the antibody binds. Previous studies by the present inventors and colleagues have shown that certain types of natural antibodies recognize epitopes on ischemic tissue and catalyze the initiation and subsequent development of ischemia-reperfusion injury. *See, e.g.*, Fleming *et al.*, 2002, J. Immunol. 169:2126-2133; Rehrig *et al.*, 2001, J. Immunol. 167:5921-5927). The ability of a biologically-active fragment of annexin IV to interact with or bind such pathological natural antibodies can be assayed by a variety of methods, including gel mobility shift assays, Western blot, immunoprecipitation, surface plasmon resonance, and the like.

[00320] The terms “annexin A2,” “annexin II,” or “annexin 2” refer to proteins of the annexin A2 subfamily, which have been shown to associate with diverse sites of actin attachment at cell membranes and serve as receptors for plasminogen and tissue plasminogen activator, positively modulating the fibrinolytic cascade, among other activities. Annexin A2 has also been identified as a component of drusen in monkeys affected with both early- and late-onset macular degeneration. *See* S. Umeda *et al.*, FASEB J. (2005) 19(12): 1683-1685. As used herein, the term “biologically-active fragment” of annexin A2, annexin II, or annexin 2, refers to a fragment of annexin A2 capable of interacting with or binding to renal tubules in the kidney and interacting with or binding to factor H or a biologically active fragment thereof. The ability of a biologically-active fragment of annexin A2 to interact with or bind renal tubules or factor H can be assayed by a variety of methods, including gel mobility shift assays, Western blot, immunoprecipitation, surface plasmon resonance, and the like.

[00321] As used herein, percent (%) amino acid sequence identity is defined as the percentage of amino acids in a candidate sequence that are identical to the amino acids in a reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared can be determined by known methods.

[00322] Specificity of a fusion protein construct can refer to selective recognition of the construct for a particular epitope of an antigen. Natural antibodies, for example, are monospecific. “Bispecific,” according to the disclosure are fusion protein constructs, or

targeting moieties within said constructs, which have two different antigen-binding specificities. Where a fusion protein construct has more than one specificity, the recognized epitopes may be associated with a single antigen or with more than one antigen. The term “valent” as used within the present disclosure can denote the presence of a specified number of binding sites in a fusion protein construct, or a targeting moiety within said construct. A natural antibody for example has two binding sites and is bivalent. As such, the terms “trivalent” denotes the presence of three binding sites in a fusion protein construct, or a targeting moiety within said construct, such as an antibody or an antigen binding fragment thereof. The term “trivalent, bispecific” antibody as used herein denotes an antibody that has three antigen-binding sites of which two bind to the same antigen (or the same epitope of the antigen) and the third binds to a different antigen or a different epitope of the same antigen. The term “tetraivalent,” as used herein refers to the fusion protein construct that has four binding sites that are capable of binding to the same target, such as an antigen. In some cases, CrossMab technology as described in WO 2010/145792 A1 can be used to ensure correct light chain pairing for antibodies that are bispecific.

EXAMPLES

[00323] The examples below further illustrate the described embodiments without limiting the scope of this disclosure.

Example 1: Generation of Exemplary -Complement Modulator Fusion Protein Constructs according to this disclosure

[00324] An exemplary phospholipid binding immunoglobulin sequence (*e.g.*, C2 antibody) was obtained from hybridomas. Variable regions were fused onto a murine IgG1 framework using recombinant DNA technology, to generate a C2-IgG1 (SEQ ID NO: 51) and various antigen binding fragments, such as C2-scFv, C2-Fab. **Table 2** provides a list of exemplary C2 antibodies or antigen binding fragments thereof. Such exemplary C2 antibodies or antigen binding constructs were used to generate fusion protein constructs, *e.g.*, by linking a complement modulator protein (or a fragment thereof) to the C2 antibody or antigen binding fragment thereof. **Table 3** provides a list of exemplary complement modulators that were used in generating the C2-complement modulator fusion protein constructs. **Table 4** provides exemplary linkers that were used to link the exemplary C2 antibodies or antigen binding fragments thereof to the exemplary complement modulators. Orientation of the fusion protein in relation to the N-terminus or C-terminus of the C2 antibodies or antigen binding fragment thereof was explored. After codon optimization and synthesis, each DNA construct was

transiently transfected in serum free media using standard methods. After harvest of culture supernatant, protein constructs were purified in a suitable manner relative to their protein structure. Some examples of the C2 constructs generated are described herein, comprising a phospholipid binding sequence or fragment thereof (exemplary sequences shown in **Table 2**), fused to a complement modulator (exemplary sequences shown in **Table 3**), optionally connected by a linker (exemplary sequences shown in **Table 4**). Specific examples of constructs include for instance: C2 scFv-CR1 (1-10) is a monomeric fusion protein construct comprising a CR1 (1-10) complement modulator protein connected to the light chain variable region of C2 scFv; C2 scFv-Crry is a monomeric fusion protein construct comprising a Crry complement modulator protein connected to the light chain variable region of C2 scFv; C2 Fab-Crry is a monomeric fusion protein construct comprising a Crry complement modulator protein connected to the CH1 domain of a C2-Fab; C2 Fab-CR1 (1-10) is a monomeric fusion protein comprising a CR1 (1-10) complement protein connected to the CH1 domain of a C2-Fab; C2 Fab-CR1 (1-17) is a monomeric fusion protein comprising a CR1 (1-17) complement protein connected to the CH1 domain of a C2-Fab; CR1 (1-10)-C2 Fab is a monomeric fusion protein comprising a CR1 (1-10) complement protein connected to the VH domain of a C2-Fab; CR1 (1-17)-C2 Fab is a monomeric fusion protein comprising a CR1 (1-17) complement protein connected to the VH domain of a C2-Fab; C2-IgG1-CR1 (1-10), HC C-term x 2 is a tetravalent homodimeric fusion protein comprising two CR1 (1-10) complement modulator proteins, each connected to a heavy chain of C2-IgG1; C2-IgG1-CR1 (1-10), HC C-term x 1 is a trivalent heterodimeric fusion protein comprising one CR1 (1-10) complement modulator protein connected to a heavy chain of C2-IgG1; C2-CR1 bispecific is a fusion protein comprising a CR1 complement modulator protein connected to the hinge region of a C2 IgG1 fragment; C2-IgG1-CR1 (1-10), HC N-term x 1 is a trivalent heterodimeric fusion protein comprising a CR1 (1-10) complement protein connected to a VH domain of a C2 IgG1; C2-IgG1-CR1 (1-10), LC N-term x 1 is a trivalent heterodimeric fusion protein comprising a CR1 (1-10) connected to a VL domain of a C2 IgG1; C2-IgG1-CR1 (1-10), HC N-term x 2 is a tetravalent homodimeric fusion protein construct comprising two CR1 (1-10) complement proteins, each connected to a VH domain of a C2 IgG1; C2-IgG1-CR1 (1-10), LC N-term x 2 is a tetravalent homodimeric fusion protein comprising two CR1 (1-10) complement modular proteins, each connected to a VL domain of a C2 IgG1. **FIG. 14** illustrates the structures of some of the exemplary C2 fusion protein construct as described in this example. It is contemplated that additional constructs can be prepared using complement modulators as described herein (*e.g.*, MCP, DAF, factor H, CD59)

[00325] Table 2: C2-Antibodies or Antigen Binding Fragments Thereof

Description	SEQ ID NO:
C2 IgG1 heavy chain	51
C2 IgG1 heavy chain with knob	54
C2 IgG1 heavy chain with hole	238
C2 kappa light chain	45
C2 scFv	239
C2 Fab heavy chain	240
Humanized C2 variable heavy chain	261

[00326] Table 3: Complement Modulator

Description	SEQ ID NO:
CR1 (1-10)	41
CR1 (1-17)	42
Crry	7

[00327] Table 4: Exemplary Linkers

Description	SEQ ID NO:
GGGSGGGSGGGGS	241
GGGSGGGGS	242

Example 2: Generation of Exemplary C3d-Complement Modulator Fusion Protein Constructs according to this disclosure

[00328] Exemplary anti-C3d sequences were obtained from hybridomas. Variable regions of heavy and light chain were ligated onto murine IgG1, kappa constant domain frameworks, respectively, using recombinant DNA technology. Exemplary clones such as C3d8b, C3d29 full length antibodies or antigen binding fragments thereof were generated. **Table 5** provides a list of exemplary anti-C3d antibodies or antigen binding fragments thereof. Such exemplary anti-C3d antibodies or antigen binding constructs were used to generate fusion protein constructs, *e.g.*, by linking a complement modulator protein (or a fragment thereof) to the anti-C3d antibody or antigen binding fragment thereof. **Table 6** provides a list of exemplary complement modulators that were used in generating the anti-C3d-complement modulator fusion protein constructs. **Table 7** provides exemplary linkers that were used to link the exemplary anti-C3d antibodies or antigen binding fragments thereof to the exemplary complement modulators. Orientation of the fusion protein in relation to the N-terminus or C-terminus of the C3d antibodies or antigen binding fragments thereof was explored. After codon optimization and synthesis, each DNA construct was transiently transfected in serum free media using standard methods. After harvest of culture supernatant, protein constructs were purified in a suitable manner relative to their protein structure. Some examples of the anti-C3d constructs generated are described herein, comprising a C3d binding sequence or fragment thereof (exemplary sequences shown in **Table 5**), fused to a complement modulator (exemplary sequences shown in

Table 6), optionally connected by a linker (exemplary sequences shown in **Table 7**). Specific examples of the anti-C3d constructs generated are described herein, for instance: 3d29-Fab-Crry is a monomeric fusion protein construct comprising an anti-C3d Fab, the CH1 domain of which is connected to the complement modulator protein Crry. 3d29 Fab-CR1 1-10 is a monomeric fusion protein construct comprising an anti-C3d Fab, the CH1 domain of which is connected to the complement modulator protein fragment CR1 (1-10). 3d29-IgG1-CR1 (1-10), HC C-term x 1 is a trivalent heterodimeric fusion protein construct comprising a CR1 (1-10) connected to a CH3 domain of an anti-C3d IgG1. 3d29-IgG1-CR1 (1-10), HC C-term x 1, KIH is a trivalent heterodimeric fusion protein construct comprising a CR1 (1-10) connected to a CH3 domain of an anti-C3d IgG1, wherein the Fc region of the anti-C3d IgG1 comprises a knob into hole structure. 3d29-IgG1-CR1 (1-10), HC C-term x 2 is a tetravalent homodimeric fusion protein comprising two CR1 (1-10) complement modulator proteins, each connected to a heavy chain of an anti-C3d IgG1. 3d8b-Fab-Crry is a monomeric fusion protein construct comprising an anti-C3d Fab, the CH1 domain of which is connected to the complement modulator protein Crry. 3d8b-Fab-CR1 (1-10) is a monomeric fusion protein construct comprising an anti-C3d Fab, the CH1 domain of which is connected to the complement modulator protein fragment CR1 (1-10). 3d8b Fab-fH 1-5 is a monomeric fusion protein construct comprising an anti-C3d Fab, the CH1 domain of which is connected to the complement modulator protein fragment factor H (1-5). 3d8b-IgG1-CR1 (1-10), HC C-term x 1, KIH is a trivalent heterodimeric fusion protein construct comprising a CR1 (1-10) connected to a CH3 domain of an anti-C3d IgG1, wherein the Fc region of the anti-C3d IgG1 comprises a knob into hole structure. 3d8b-IgG1-CR1 (1-10), HC C-term x 2 is a tetravalent homodimeric fusion protein comprising two CR1 (1-10) complement modulator proteins, each connected to a heavy chain of an anti-C3d IgG1. 3d8b-IgG1-CR1 (1-10), HC N-term x 2 is a tetravalent homodimeric fusion protein comprising two CR1 (1-10) complement modulator proteins, each connected to the VH domain of a heavy chain of an anti-C3d IgG1. 3d8b-IgG1-CR1 (1-10), LC N-term x 2 is a tetravalent homodimeric fusion protein comprising two CR1 (1-10) complement modulator proteins, each connected to the VL domain of a heavy chain of an anti-C3d IgG1. 3d8b-IgG1-CR1 (1-10), bispecific is a fusion protein comprising a CR1 complement modulator protein connected to the hinge region of an anti-C3d IgG1 fragment, wherein the Fc region of the anti-C3d IgG1 comprises a knob into hole structure. 3d8b-IgG1-fH (1-5), HC C-term x 1, KIH is a trivalent heterodimeric fusion protein construct comprising a factor H (1-5) connected to a CH3 domain of an anti-C3d IgG1, wherein the Fc region of the anti-C3d IgG1 comprises a knob into hole structure. 3d8b-IgG1-fH (1-5), HC C-term x 2 is a tetravalent homodimeric fusion protein comprising two factor H (1-5) complement modulator proteins, each connected to a heavy chain of an anti-C3d IgG1. 3d8b-IgG1-fH (1-5),

LC C-term x 2 is a tetravalent homodimeric fusion protein comprising two factor H (1-5) complement modulator proteins, each connected to a light chain of an anti-C3d IgG1. 3d8b-IgG1-fH (1-5), HC N-term x 2 is a tetravalent homodimeric fusion protein comprising two factor H (1-5) complement modulator proteins, each connected to a VH domain of a heavy chain of an anti-C3d IgG1. 3d8b-IgG1-fH (1-5), LC N-term x 2 is a tetravalent homodimeric fusion protein comprising two factor H (1-5) complement modulator proteins, each connected to a VL domain of a light chain of an anti-C3d IgG1. 3d8b-IgG1-fH (1-5), bispecific is a fusion protein comprising a factor H (1-5) complement modulator protein connected to the hinge region of an anti-C3d IgG1 fragment, wherein the Fc region of the anti-C3d IgG1 comprises a knob into hole structure. **FIGs. 15-18** illustrate the structures of some of the exemplary anti-C3d fusion protein construct as described in this example. Examples of the format of fusion protein construct displayed in **FIGs. 15-18** are tested in several assays, including hemolytic assays, LPS activation assay, assays measuring deposition of complement activation products (such as C3, C4), C1 inhibitor tests using quantitative chromogenic assays, immunochemical assays (such as ELISA, Western Blotting) for individual complement components and each fusion protein construct displays comparable activity to the complement modulator protein alone.

[00329] Table 5: Anti-C3d Antibodies or Antigen Binding Fragments Thereof

Description	SEQ ID NO:
3d29-IgG1 Fab heavy chain	58
3d29 kappa light chain	59
3d29 heavy chain murine IgG1	62
3d29 heavy chain (hole) IgG1	64
3d29 heavy chain (knob) IgG1	254
3d29- Fab	244
3d29 IgG1 heavy chain	62
3d8b-Fab heavy chain murine IgG1	69
3d8b kappa light chain	68
3d8b heavy chain murine IgG1	73
3d8b heavy chain murine IgG1 (knob)	74
3d8b heavy chain murine IgG1 (hole)	81
3d8b heavy chain murine IgG1 Fc (hole)	88
3d8b heavy chain murine IgG1 Fc (knob)	245

[00330] Table 6: Complement Modulator

Description	SEQ ID NO:
CR1 (1-10)	41
Factor H (1-5)	72
Crry	7

[00331] Table 7: Exemplary Linkers

Description	SEQ ID NO:
GGGSGGGSGGGGS	241

GGGGS GGGGS	242

Example 3: Generation of Exemplary B4-Complement Modulator Fusion Protein

Constructs according to this disclosure

[00332] Exemplary annexin domain binding sequences (for example, a B4 antibody or fragment thereof) are obtained from hybridomas. Variable regions of heavy and light chain were ligated onto murine IgG1, kappa constant domain frameworks, respectively, using recombinant DNA technology, to generate exemplary B4 full length antibodies and antigen binding fragments thereof. **Table 8** provides a list of exemplary B4 antibodies or antigen binding fragments thereof. Such exemplary B4 antibodies or antigen binding constructs are used to generate fusion protein constructs, *e.g.*, by linking a complement modulator protein (or a fragment thereof) to the B4 antibody or antigen binding fragment thereof. **Table 9** provides a list of exemplary complement modulators that are used in generating the B4-complement modulator fusion protein constructs. **Table 10** provides exemplary linkers that are used to link the exemplary B4 antibodies or antigen binding fragments thereof to the exemplary complement modulators. Orientation of the fusion protein in relation to the N-terminus or C-terminus of the B4 antibodies or antigen binding fragments thereof is explored.

[00333] Some examples of B4 antibody or fragment constructs generated are described herein, comprising an annexin domain binding sequence or fragment thereof (exemplary sequences shown in **Table 8**), fused to a complement modulator (exemplary sequences shown in **Table 9**), optionally connected by a linker (exemplary sequences shown in **Table 10**).

[00334] Table 8: B4-Antibodies or Antigen Binding Fragments Thereof

Description
B4-IgG1
B4-Fab
B4-scFv

[00335] Table 9: Complement Modulators

Description	SEQ ID NO:
CR1 (1-10)	41
CR1 (1-17)	42
Factor H (1-5)	72
Crry	7
MCP (1-4)	187
Map44	186
CD59	185
DAF (1-4)	184

[00336] Table 10: Exemplary Linkers

Description	SEQ ID NO:
GGGSGGGSGGGGS	241
GGGSGGGGS	242

Example 4: Design of an Exemplary Bifunctional Protein Construct according to this disclosure, containing a Knob-Hole heterodimeric Fc region

[00337] An exemplary fusion protein construct was designed, comprising an exemplary anti-C3d antibody (3d8b) connected to a CR1 (1-10) complement modulator polypeptide, illustrated in **FIG. 13**. Numbering of amino acid positions mentioned in the below exemplary design is according to the EU index as in Kabat. The anti-C3d antibody comprises a light chain (domains VL and CK) comprising the sequence in SEQ ID NO: 69, a first heavy chain (domains VH-hinge-CH1-CH2-CH3; as in the sequence in SEQ ID NO: 89) comprising amino acid substitutions Thr366Ser, Met368Ala, and Tyr407Val, forming an Fc region comprising a hole, which pairs with a second heavy chain (domains hinge-CH2-CH3) Fc region comprising amino acid substitution Thr366Trp, forming an Fc region with a knob, the second heavy chain is connected to the CR1 (1-10) complement modulator polypeptide at the hinge region, via the linker (G₄SG₄S) (SEQ ID NO: 242), as in the sequence of SEQ ID NO: 90.

Example 5: Design of an Exemplary Bifunctional mAb Fusion Protein Construct according to this disclosure, containing a Knob-Hole heterodimeric Fc region

[00338] An exemplary mAb-fusion protein construct was designed, comprising an exemplary anti-C3d antibody (3d8b) connected to a complement modulator polypeptide, such as CR1 (1-10) CR1 (1-17), factor H (1-5), MCP (1-4), DAF, or CD59. In the example illustrated in **FIG. 19**, a full-length exemplary anti-C3d antibody C3d8b is connected to a first exemplary complement modulator polypeptide (such as a factor H (1-5) fragment), via one of its CH3 domain and a second exemplary complement modulator polypeptide (such as CR (1-10) fragment) via the other CH3 domain. Numbering of amino acid positions mentioned in the below exemplary design is according to the EU index as in Kabat. The exemplary anti-C3d antibody comprises light chains (domains VL and CK) comprising the sequence in SEQ ID NO: 69, a first heavy chain (domains VH-CH1-hinge-CH2-CH3) comprising amino acid substitutions Thr366Ser, Met368Ala, and Tyr407Val, forming an Fc region comprising a hole, which pairs with a second heavy chain (domains VH-hinge-CH1-CH2-CH3) Fc region comprising amino acid substitution Thr366Trp, forming an Fc region with a knob, the first heavy chain is connected to factor H at the CH3 region, via the linker (G₄SG₄S) (SEQ ID NO: 242), as in the sequence of SEQ ID NO: 139, the second heavy chain is connected to the CR1 (1-10)

complement modulator polypeptide at the CH3 region, via the linker (G4SG4S) (SEQ ID NO: 242), as in the sequence of SEQ ID NO: 140.

Example 6: Design of an Exemplary Fusion Protein Constructs according to this disclosure containing anti-C3d antibody or an antigen binding fragment thereof

[00339] An exemplary mAb-fusion protein construct was designed, comprising an exemplary anti-C3d antibody (3d8b) connected to an exemplary complement modulator polypeptide (such as decay-accelerating factor, DAF (1-4)). Numbering of amino acid positions mentioned in the below exemplary design is according to the EU index as in Kabat. The anti-C3d antibody comprises light chains (domains VL and CK) comprising the sequence in SEQ ID NO: 69, and heavy chains (domains VH-CH1-hinge-CH2-CH3). The heavy chains are connected to the DAF (1-4) at the CH3 regions, via the linker (G4SG4S) (SEQ ID NO: 242), as in the sequence of SEQ ID NO: 141.

[00340] Another exemplary mAb-fusion protein construct was designed, comprising an anti-C3d antibody (3d8b) connected to an exemplary complement modulator (such as CD59 polypeptide). Numbering of amino acid positions mentioned in the below exemplary design is according to the EU index as in Kabat. The anti-C3d antibody comprises light chains (domains VL and CK) comprising the sequence in SEQ ID NO: 69, and heavy chains (domains VH-CH1-hinge-CH2-CH3). The heavy chains are connected to the CD59 at the CH3 regions, via the linker (G4SG4S) (SEQ ID NO: 242), as in the sequence of SEQ ID NO: 142.

[00341] A further exemplary mAb-fusion protein construct was designed, comprising an exemplary anti-C3d antibody (3d8b) connected to an exemplary complement modulator (such as MAp44 polypeptide). Numbering of amino acid positions mentioned in the below exemplary design is according to the EU index as in Kabat. The anti-C3d antibody comprises light chains (domains VL and CK) comprising the sequence in SEQ ID NO: 69, and heavy chains (domains VH-CH1-hinge-CH2-CH3). The heavy chains are connected to the MAp44 at the CH3 regions, via the linker (G4SG4S) (SEQ ID NO: 242), as in the sequence of SEQ ID NO: 143.

[00342] An exemplary mAb-fusion protein construct was designed, comprising an exemplary anti-C3d antibody (3d8b) connected to an exemplary (such as MCP 1-4 polypeptide). The anti-C3d antibody comprises light chains (domains VL and CK) comprising the sequence in SEQ ID NO: 69, and heavy chains (domains VH-CH1-hinge-CH2-CH3). The heavy chains are connected to the MCP 1-4 at the CH3 regions, via the linker (G4SG4S) (SEQ ID NO: 242), as in the sequence of SEQ ID NO: 144.

[00343] Further examples of any of the fusion protein constructs illustrated in **FIGs. 1-19** can comprise (a) the complement modulator sequences set out below, (b) the CDRs or the VH and

VL sequences set out below, and (c) constant regions comprising at least one of CH1, hinge, CH2 or CH3 domains of human or murine immunoglobulin constant regions, or comprising one or more mutations in at least one of CH1, hinge, CH2 or CH3 domains of human or murine immunoglobulin constant regions.

[00344] Table 11:

Complement modulator sequence	CDRs Or VH, VL
SEQ ID NO: 184	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO:108	SEQ ID NOS: 11, 12, and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO:72	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO: 41	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO:42	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO: 91	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO: 92	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO: 185	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO: 186	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO: 187	SEQ ID NOS: 11, 12 and 13; and SEQ ID NOS: 14, 15 and 16
SEQ ID NO:184	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO:108	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO:72	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO:41	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO:42	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO: 91	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO: 92	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22

SEQ ID NO: 185	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO: 186	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO: 187	SEQ ID NOS: 17, 18 and 19; and SEQ ID NOS: 20, 21 and 22
SEQ ID NO: 184	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258.
SEQ ID NO: 108	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258.
SEQ ID NO: 72	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258.
SEQ ID NO: 41	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258.
SEQ ID NO: 42	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258.
SEQ ID NO: 91	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258
SEQ ID NO: 92	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258
SEQ ID NO: 185	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258
SEQ ID NO: 186	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258
SEQ ID NO: 187	SEQ ID NO: 246, 247, 248, 249, 250, 251, 252, 253, 254, or 255; and SEQ ID NO: 256, 257, or 258
SEQ ID NO: 184	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 108	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 72	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 41	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 42	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 91	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267,

	268, 269.
SEQ ID NO: 92	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 185	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 186	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 187	SEQ ID NO: 262, 263, 264, or 265; and SEQ ID NO: 266, 267, 268, 269.
SEQ ID NO: 184	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 108	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 72	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 41	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 42	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 91	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 92	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 185	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 186	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.
SEQ ID NO: 187	SEQ ID NO: 270, 271, 272, 273, or 274; and SEQ ID NO: 275, 276, 277, or 278.

Example 7: Assessment of binding of anti-C3d antibody, 3d8b, and its fusion proteins

[00345] Binding of the anti-C3d antibody, 3d8b, and its complement regulator fusions, was measured by Enzyme-Linked ImmunoSorbent Assay (ELISA) binding assays. The binding affinity of constructs was measured by surface plasmon resonance using Biacore.

Antibody preparations

[00346] Murine IgG1 Fc, human IgG4 Fc, antibody fragments containing a His₆ epitope tag (SEQ ID NO: 296) or CR1 fusion partner containing constructs were prepared in 1X PBS containing 0.1% Bovine Serum Albumin (BSA).

[00347] Secondary antibodies were used to detect 1) murine IgG1, 2) human IgG4, 3) antibody fragments (His₆ epitope tag) (SEQ ID NO: 296), or 4) antibody fusion proteins containing a CR1 fusion partner. Secondary antibodies specific for murine IgG1 Fc (anti-mouse IgG light-chain kappa) (Novus) were diluted 1:20,000 in 1X PBS containing 0.1% BSA. Secondary antibodies specific for human IgG4 (anti-human pFc') (Abcam) were diluted 1: 30,000 in 1X PBS containing 0.1% BSA. Secondary antibodies specific for the His₆ epitope tag (Abcam) (SEQ ID NO: 296) were diluted 1:5000 in 1X PBS containing 0.1% BSA. Secondary antibodies specific for CR1 (anti-CR1-biotin, Thermo Fisher) were diluted 1:2500 1X PBS containing 0.1% BSA. For detection of biotinylated antibodies, streptavidin-horseradish peroxidase (Strep-HRP, Thermo Fisher) was diluted 1:5000 in 1X PBS containing 0.1% BSA.

[00348] For detection of murine IgG1, human IgG4, or antibody fragments (His₆ epitope tag (SEQ ID NO: 296)) or antibody fusion proteins containing a CR1 fusion partner, the ELISA assays were performed in 1X PBS unless otherwise noted. 2.5 µg/mL of human (Comptech Technologies), mouse (Genscript), or cyno- (Atum) C3d was coated onto the surface of microtiter plates in sodium bicarbonate buffer at pH 8 (Alfa Aesar) at 4°C, overnight. C3d-coated microtiter plates (Thermo Fisher) were washed three times with 1X Phosphate Buffered Saline with 0.05% Tween-20 (Sigma) (PBS-T, KPL). Coated microtiter plates were blocked overnight by addition of 1X PBS containing 2% BSA. After blocking, coated plates were washed three times with PBS-T. 100 µL of diluted antibody constructs was added and incubated between 1- 2 hours. Coated plates were washed three times with PBS-T. 100 µL of the appropriate secondary antibodies were added to the coated plates. If necessary, 100 µL of diluted strep-HRP was added. Plates were washed three times with PBS-T. 100 µL of 3,3',5,5'-tetramethyl-benzidine (TMB, Surmodics) was added and incubated in the dark at room temperature for 10-15 minutes. Reactions were terminated by addition of an equal volume of stop solution (Surmodics). The absorbance of each well was measured at 450 nm.

[00349] Binding experiments were performed on Biacore™ 3000 at 25 °C. The Assay Buffer used was 10 mM HEPES buffer (pH 7.4), 150 mM NaCl, 3mM EDTA, 0.05% P20 (polyoxyethylenesorbitan); Regeneration Buffer was 10 mM Glycine buffer (pH 1.75); and Conjugation Buffer used was 10 mM sodium acetate buffer (pH 5). The flow rate used for capturing the ligand was 10 µL/min. The flow rate for kinetics analysis is 30µL/min.

[00350] Flow cells 2, 3 and 4 of the CM5 chip were coated with human C3d at response units (RU) levels as indicated using EDC/NHS (N-ethyl-N'- (3-dimethyl aminopropyl carbodiimide/N-hydroxy succinimide) amine coupling method as per GE manufacturers instruction. The unoccupied sites were blocked with 1M ethanol amine. Binding of exemplary humanized antibodies to the antigen was monitored in real time. From the observed k_{on} and k_{off} , K_D was determined. For the interactions with fast off rate, steady state kinetics was used to determine K_D .

[00351] Tables 12, 13, and 14 show the ELISA EC_{50} values for various exemplary anti-C3d antibodies and fusion protein constructs comprising the same. Table 15 shows the K_D of exemplary antibody fusion constructs measured by BIAcore measuring binding of antibody constructs to immobilized human C3d.

[00352] Table 12: Human C3d EC_{50} data of various fusion protein constructs: summary of average Data

Description/Mutation	EC_{50} (nM)
Exemplary construct 32	0.28
Exemplary construct 33	1.11
Exemplary construct 34	0.32
Exemplary fusion construct 35	3.52
Exemplary fusion construct 36	2.59
Exemplary fusion construct 38	0.68
Exemplary fusion construct 39	1.82
Exemplary fusion construct 42	0.96
Exemplary fusion construct 43	1.31
Exemplary fusion construct 44	1.41
Exemplary fusion construct 45	0.70
Exemplary fusion construct 46	0.99
Exemplary fusion construct 47	1.04
Exemplary fusion construct 48	0.99
Exemplary construct 49	2.28
Exemplary fusion construct 50	0.90
Exemplary fusion construct 51	1.31
Exemplary fusion construct 52	1.03
Exemplary construct 53	0.80
Exemplary construct 54	1.42
Exemplary construct 55	0.24
Exemplary construct 56	0.55
Exemplary construct 58	0.83
Exemplary fusion construct 59	0.79
Exemplary fusion construct 60	0.47
Exemplary fusion construct 61	0.94
Exemplary fusion construct 62	1.40
Exemplary fusion construct 63	1.50
Exemplary fusion construct 64	1.15

Exemplary fusion construct 65	1.34
Exemplary fusion construct 68	1.00
Exemplary fusion construct 69	1.05
Exemplary fusion construct 116	0.55
Exemplary fusion construct 118	0.84

*Unless otherwise noted, tested proteins were expressed in CHO cells

[00353] Table 13: Human C3d EC₅₀ data: Effect of humanization on target affinity

Description/Mutation	EC₅₀, nM
Exemplary construct 73	0.021
Exemplary construct 74	0.017
Exemplary construct 75	0.029
Exemplary construct 76	0.018
Exemplary construct 77	0.011
Exemplary construct 78	0.018
Exemplary construct 79	0.020
Exemplary construct 86	0.03

[00354] Table 14: Human C3d EC₅₀ data of humanized fusion constructs

Description/ Mutation	EC₅₀, nM
Exemplary construct 86	0.03
Exemplary construct 87	0.02
Exemplary construct 93	0.02
Exemplary fusion construct 94	0.14
Exemplary fusion construct 95	0.04
Exemplary fusion construct 96	0.09
Exemplary fusion construct 99	1.54
Exemplary fusion construct 101	1.55
Exemplary fusion construct 106	1.62
Exemplary fusion construct 107	4.20
Exemplary fusion construct 129	0.13
Exemplary fusion construct 133	0.07
Exemplary fusion construct 135	0.06
Exemplary fusion construct 138	0.09
Exemplary fusion construct 139	0.06
Exemplary fusion construct 140	0.08
Exemplary fusion construct 141	0.11
Exemplary fusion construct 142	0.04
Exemplary fusion construct 143	0.05
Exemplary fusion construct 97	0.074
Exemplary fusion construct 146	0.061

[00355] Table 15: Surface Plasmon Resonance Data from Biacore™ 3000 Instrument using CM5 Sensor Chip with C3d antigen immobilized

Analyte	K _D (M)	Conc. of Analyte (nM)
Exemplary construct 32	3.10E-09	0-50
Exemplary construct 33	2.43E-10	0-50
Exemplary construct 34	8.88E-10	0-50
Exemplary fusion construct 35	2.66E-07	0-1500
Exemplary fusion construct 36	3.59E-07	0-1500
Exemplary fusion construct 43	5.24E-09	0-50
Exemplary fusion construct 46	2.72E-08	0-100
Exemplary construct 49	3.34E-07	0-1500
Exemplary fusion construct 52	1.55E-08	0-100
Exemplary construct 53	5.99E-09	0-100
Exemplary construct 54	5.01E-08	0-100
Exemplary construct 56	9.10E-10	0-100
Exemplary construct 58	7.02E-09	0-100
Exemplary fusion construct 62	3.41E-08	0-100
Exemplary fusion construct 64	1.84E-08	0-100
Exemplary construct 72	No Binding	125-2000
Exemplary construct 73	9.18E-10	0-100
Exemplary construct 74	1.34E-09	0-100
Exemplary construct 75	1.63E-09	0-100
Exemplary construct 86	1.47E-08	0-100
Exemplary construct 87	7.57E-09	0-100
Exemplary construct 93	1.02E-08	1.56-200
Exemplary fusion construct 97	1.19E-08	1.56-200
Exemplary fusion construct 116	1.06E-08	1.56-200
Exemplary fusion construct 118	9.36E-09	1.56-200
Exemplary fusion construct 129	3.72E-08	1.56-200
Exemplary fusion construct 133	3.80E-08	1.56-200
Exemplary fusion construct 135	3.89E-08	1.56-200

Example 8: Complement inhibition of anti-C3d antibody, 3d8b, and fusion proteins

[00356] The Wieslab® Alternative and Classical pathway ELISA's (ALPCO) were performed according to manufacturer's instructions. Briefly, complement preserved human serum (CompTech) was diluted 1:18 or 1:101 in the appropriate dilution buffer provided for the Alternative or Classical kit, respectively. Test analogs were diluted into PBS (Gibco) and a dose response was generated by diluting test analogs 2-4-fold in PBS. Diluted test analogs were then added at 25x to the diluted human serum. 96 well flat bottom Wieslab plates were incubated for 1 hour at 37° C (Thermo) and washed 3x with wash buffer provided by the kit. Antibody conjugate was then added, and the plate was incubated for 30 minutes followed by a second wash. Finally, substrate was added, the plate was incubated for another 30 minutes, and absorbance was read at 405nm. IC50 curves were generated using PRISM software.

[00357] **Table 16** shows the complement activity of different CR11-10 complement regulator fusion proteins. **Table 17** shows the complement activity of CR11-17 fusion proteins for the alternative and classical pathways. **Table 18** shows the complement activity of fH1-5 fusion proteins in the alternative and classical pathways.

[00358] Table 16: Functional analysis of exemplary constructs with CR1₁₋₁₀ complement modulator

Construct ID	Alternative Pathway		Classical Pathway	
	IC ₅₀ (nM)	SD	IC ₅₀ (nM)	SD
Exemplary fusion construct 106	4	1	90	44
Exemplary fusion construct 95	11	4	105	30
Exemplary fusion construct 96	11	6	107	40
Exemplary fusion construct 52	12	2	63	29
Exemplary fusion construct 46	12	4	79	6
Exemplary fusion construct 36	13	0	156	65
Exemplary fusion construct 133	13	n/a	n/a	n/a
Exemplary fusion construct 139	14	2	n/a	n/a
Exemplary fusion construct 138	15	3	n/a	n/a
Exemplary fusion construct 39	17	5	95	47
Exemplary fusion construct 99	23	12	140	47
Exemplary fusion construct 43	29	10	62	14
Exemplary fusion construct 51	30	12	147	45
Exemplary fusion construct 50	35	12	169	31
Exemplary fusion construct 38	43	19	190	124
Exemplary fusion construct 45	51	9	119	13
Exemplary construct 19	71	31	76	24
Exemplary construct 70	80	26	70	41
Exemplary fusion construct 68	89	3	606	118
Exemplary construct 58	>300	n/a	>300	n/a

[00359] Table 17: Functional analysis of exemplary constructs with CR1₁₋₁₇ complement modulator

	Alternative Pathway		Classical Pathway	
	IC ₅₀ (nM)	SD	IC ₅₀ (nM)	SD
Exemplary fusion construct 107	4	2	51	14
Exemplary fusion construct 94	6	3	34	3
Exemplary fusion construct 141	6	0	n/a	n/a
Exemplary fusion construct 64	6	2	55	16
Exemplary fusion construct 140	6	3	n/a	n/a
Exemplary construct 72	6	3	35	12
Exemplary fusion construct 129	7	n/a	n/a	n/a
Exemplary fusion construct 100	7	5	65	13
Exemplary fusion construct 63	9	2	84	17
Exemplary fusion construct 65	10	4	84	3
Exemplary fusion construct 62	19	2	112	10

Exemplary construct 58	>300	n/a	>300	n/a

[00360] Table 18: Functional analysis of exemplary constructs with factor H complement modulator

Construct ID	Alternative Pathway		Classical Pathway	
	IC ₅₀ (nM)	SD	IC ₅₀ (nM)	SD
Exemplary fusion construct 143	50	29	n/a	n/a
Exemplary fusion construct 142	54	16	n/a	n/a
Exemplary fusion construct 135	56	n/a	n/a	n/a
Exemplary fusion construct 97	58	13	n/a	n/a
Exemplary fusion construct 48	73	22	166	14
Exemplary fusion construct 61	125	17	n/a	n/a
Exemplary fusion construct 60	144	24	n/a	n/a
Exemplary fusion construct 44	206	91	3041	944
Exemplary fusion construct 59	488	315	n/a	n/a
Exemplary fusion construct 69	492	96	n/a	n/a
Exemplary fusion construct 47	615	85	n/a	n/a
Exemplary construct 71	1772	430	n/a	n/a
Exemplary construct 58 (used as control)	>300	n/a	>300	n/a
Exemplary fusion construct 97	73.4	18.9	n/a	n/a
Exemplary fusion construct 146	88.1	7.0	n/a	n/a

Example 9: Analyzing the inhibition of the alternative complement pathway using rabbit erythrocytes using antibody fusions containing complements regulators

Erythrocyte Preparation

[00361] 45 ml of Dulbecco's Phosphate Buffered Saline (without Ca²⁺ or Mg²⁺) (dPBS, Life Technologies) was added to 0.5 ml of rabbit whole blood (BioIVT) in a 50 ml conical tube. The cellular suspension was centrifuged at 4°C for 10 minutes at 2000 RPM. The supernatant and buffy coat were removed by decanting. The cell pellet was resuspended with 0.5 ml of dPBS.

[00362] To quantify the number of erythrocytes in the cell suspension, 50 μ L of suspended cells were added to 700 μ L of distilled water. The cell suspension was vortexed until the cells lysed. The optical density of the lysate was measured at 541 nm. The OD₅₄₁ of the lysed cell sample was used to adjust the concentration of the 0.5ml of resuspended cells to 2.9×10^9 cells/ml by dividing the OD₅₄₁ by 0.2 and multiplying by 2.9×10^9 .

Reagent Preparation

[00363] All reagents were maintained at 4°C. All tubes, plates, and solutions were maintained on ice. A fresh solution of Mg-EGTA was prepared by mixing 0.25 mL of 1M MgCl₂ (Boston BioProducts) and 0.5 mL of 0.5M EGTA (Boston BioProducts) at pH 7.4. A diluted Mg-EGTA solution was prepared by mixing 0.45 mL Mg-EGTA with 0.55 mL dPBS. 10 μ L of diluted Mg-

EGTA was added to each sample well of the assay plate. Human serum (BioIVT) was thawed in a 37°C water bath. The references and controls required for this assay are a positive control, serum background, and CAP block control. The solution were prepared in the appropriate concentration and diluted in a separate plate. 100µL of each control in duplicate was transferred to the corresponding wells on the TEST plate.

[00364] Test constructs were diluted in normal human serum to a concentration of 10 µM. Serial dilutions were prepared at 1:2 with normal human serum. 100 µL of diluted inhibitors were added to the respective wells in the assay plate (R&D Systems). 5 µL of dPBS was added to serum background wells. 5 µL diluted erythrocytes are added to all remaining wells in the assay plate. Wells were gently mixed by gentle pipetting. The assay plate was sealed and incubated for 30 minutes at 37°C.

Preparation of Stop Solution

[00365] A 25 mM EDTA solution in water (EDTA-H₂O) was prepared by adding 20 µL of 0.5 M EDTA (Corning) into 380 µL of water (1:20). A 25 mM EDTA solution in dPBS (EDTA-PBS) was prepared by adding 400 µL of 0.5 M EDTA into 7.6 mL of dPBS (1:20).

[00366] In order to terminate the complement activity, 100 µL of EDTA-H₂O was added to the water controls, whereas 100 µL of EDTA-PBS was added to the remaining wells. The plate was spun at 1800 rpm for 10 minutes at 4°. 100 µL of the well volume was transferred to a new microplate and was measured at 415nm (SpectraFluorPlus, Tecan). Data was exported and analyzed by calculating the Percent Lysis with the following equation:

$$\text{Percent lysis} = \frac{A_{415(\text{test construct})} - A_{415(\text{serum background})}}{A_{415(\text{water})}} \times 100$$

[00367] The data was plotted as percent lysis versus log(inhibitor concentration)

The data was normalized to positive and negative controls and IC₅₀ calculated with the following parameters and equation: variable slope and 4 parameter fit.

$$Y = \text{Bottom} + \frac{\text{Top} - \text{Bottom}}{(1 + 10^{((\log(\text{IC}_{50}) - X) * \text{HillSlope}))}}$$

[00368] IC₅₀ values for soluble CR₁₁₋₁₀, CR₁₁₋₁₇, and fH₁₋₅ complement regulators and their fusion proteins are shown in **Tables 19, 20, and 21**.

[00369] **Table 19: IC₅₀ data: Targeted vs. non-targeted CR₁₁₋₁₀ constructs from complement alternative pathway, averaged data**

Compound ID	Targeted/Non-targeted	IC ₅₀ , µM	SD
Exemplary construct 19	Non-targeted	1.16	0.16
Exemplary construct 70	Non-targeted	1.01	0.36
Exemplary fusion construct 38	Targeted	0.58	0.10

Exemplary fusion construct 39	Targeted	0.18	0.02
Exemplary fusion construct 43	Targeted	0.37	0.01
Exemplary fusion construct 45	Targeted	0.28	0.02
Exemplary fusion construct 46	Targeted	0.12	0.02
Exemplary fusion construct 50	Targeted	0.26	0.01
Exemplary fusion construct 51	Targeted	0.42	0.04
Exemplary fusion construct 52	Targeted	0.16	0.01
Exemplary construct 58	Targeted	>10	NA
Exemplary fusion construct 68	Targeted	0.67	0.08
Exemplary construct 93	Targeted	>10	NA
Exemplary fusion construct 95	Targeted	0.26	0.04
Exemplary fusion construct 96	Targeted	0.20	0.05
Exemplary fusion construct 99	Targeted	0.34	0.04
Exemplary fusion construct 106	Targeted	0.17	0.11
Exemplary fusion construct 138	Targeted	0.57	NA
Exemplary fusion construct 139	Targeted	0.64	NA

[00370] Table 20: IC₅₀ data: Targeted vs. non-targeted CR1₁₋₁₇ constructs from complement alternative pathway, averaged data

Compound ID	Targeted/Non-targeted	IC ₅₀ , μ M	SD
Exemplary construct 20	Non-targeted	0.09	0.02
Exemplary construct 72	Non-targeted	0.09	0.01
Exemplary construct 58	Targeted	>10	NA
Exemplary fusion construct 62	Targeted	0.13	0.02
Exemplary fusion construct 63	Targeted	0.13	0.02
Exemplary fusion construct 64	Targeted	0.31	0.10
Exemplary fusion construct 65	Targeted	0.26	0.23
Exemplary construct 93	Targeted	>10	NA
Exemplary fusion construct 94	Targeted	0.29	0.12
Exemplary fusion construct 107	Targeted	0.21	0.07
Exemplary fusion construct 140	Targeted	0.91	NA
Exemplary fusion construct 141	Targeted	1.3	NA

[00371] Table 21: IC₅₀s: Targeted vs. non-targeted fH₁₋₅ constructs from complement alternative pathway, averaged data

Compound ID	Targeted/Non-targeted	IC ₅₀ , μ M	SD
Exemplary construct 71	Non-targeted	4.54	0.53
Exemplary construct 58	Targeted	>10	NA
Exemplary fusion construct 44	Targeted	0.90	0.15
Exemplary fusion construct 47	Targeted	2.26	0.63
Exemplary fusion construct 48	Targeted	0.26	0.06
Exemplary fusion construct 59	Targeted	>10	NA
Exemplary fusion construct 60	Targeted	0.93	0.26
Exemplary fusion construct 61	Targeted	6.08	3.63
Exemplary fusion construct 69	Targeted	8.32	2.23
Exemplary construct 93	Targeted	>10	NA
Exemplary fusion construct 97	Targeted	0.30	0.01

Exemplary fusion construct 142	Targeted	0.97	NA
Exemplary fusion construct 143	Targeted	0.99	NA
Exemplary fusion construct 97	Targeted	0.64	0.04
Exemplary fusion construct 146	Targeted	0.46	0.02

Example 10: Analyzing inhibition of the classical complement pathway using sheep erythrocytes

Sensitization of sheep red blood cells (SRBC) with hemolysin

[00372] 2 mL of SRBCs (BioIVT) were added to 3 mL of GVB⁺⁺ buffer (Boston BioProducts) and mixed gently. The SRBC suspension was centrifuged at 4°C for 5 minutes at 2000 RPM. The supernatant was decanted, and the pellet resuspended in GVB⁺⁺ buffer. The SRBC suspension was centrifuged for 5 minutes at 4°C at 2000 RPM. The supernatant was decanted again. 9 mL of GVB⁺⁺ buffer was added to the pellet to prepare a 10% cell suspension. Hemolysin (Rockland) was prepared by resuspending dry powder with 2 mL milliQ water and stored at -20°C, at an estimated concentration of about 80 mg/mL (lyophilized powder reconstituted in 2 mL per manufacturer's instructions). An equal volume of hemolysin (equal to the volume of 10% SRBC suspension) was prepared by diluting the stock hemolysin 1:100 in GVB⁺⁺ buffer. Diluted hemolysin was added dropwise to the 10% SRBC suspension and mixed gently by swirling. The solution was incubated at 30°C for 30 minutes in a water bath and swirled every 15 minutes. Sensitized SRBCs were stored overnight at 4°C.

Determination of CH₅₀

[00373] The CH₅₀ test was used to determine the optimal concentration of serum to use in the inhibitor assay. A 1:2 dilution series of human serum was prepared in GVB⁺⁺ buffer. Serum was initially diluted 1:4 in GVB⁺⁺ buffer (100 µL serum in 300 µL GVB⁺⁺). 200 µL of diluted serum was added to the dilution series tubes. After generating the serum dilutions, 200 µL of sensitized sheep SRBC (sSRBC) was added to each diluted serum tube. 200 µL of water was added to serve as a 100% lysis control. The negative control was prepared by addition of sRBCs to GVB⁺⁺ without serum. The samples were incubated in a 37°C water bath. Samples were centrifuged for 5 minutes at 2000 RPM to pellet sSRBCs. 100 µL of the supernatant was transferred to a 96-well microtiter plates and 100 µL of water was added to each well. The absorbance was measured at 541 nm. 50% lysis (CH₅₀) was calculated by plotting % lysis versus serum dilution.

Assessment of inhibitors of the classical complement pathway

[00374] Test constructs were diluted in 2X human serum. All test constructs were diluted to 10 µM. A 12-point 1:2 dilution series of the test constructs by diluting with 2X human serum. 100

μL of sample was transferred to a fresh tube. 100 μL of GVB⁺⁺ buffer was added to each tube. 100 μL of sSRBC was added to each tube. The appropriate 100% lysis and GVB⁺⁺ buffer controls were prepared. Samples were incubated at 37°C for 30 minutes in a water bath. Samples were centrifuged for 10 minutes at 2000 RPM. 100 μL of supernatant was transferred to a 96-well microtiter plate. 100 μL of diH₂O was added to each well and the absorbance measured at 541 nm.

[00375] The averages for each sample was obtained and the background absorbance was subtracted from the GVB⁺⁺ buffer control well. Percent lysis was calculated for each dilution with the following equation:

$$\% \text{ lysis} = 100 \times \frac{OD_{541}(\text{test construct}) - OD_{541}(\text{GVB control})}{OD_{541}(100\% \text{ lysis}) - OD_{541}(\text{GVB control})}$$

[00376] Table 22 shows the IC₅₀ of the classical complement pathway test constructs.

[00377] Table 22: Inhibition of the complement classical pathway

Compound ID	IC ₅₀ , μM
Exemplary construct 19	3.43E-02
Exemplary fusion construct 38	3.13E-02
Exemplary fusion construct 39	3.03E-03
Exemplary fusion construct 43	2.69E-02
Exemplary fusion construct 45	3.98E-02
Exemplary fusion construct 46	5.02E-04
Exemplary fusion construct 50	4.80E-02
Exemplary fusion construct 52	2.07E-03
Exemplary fusion construct 68	2.90E-01
Exemplary construct 70	5.23E-03
Exemplary construct 20	1.02E-02
Exemplary fusion construct 62	3.60E-02
Exemplary fusion construct 64	2.16E-02
Exemplary fusion construct 65	5.51E-02
Exemplary construct 72	1.32E-02
Exemplary fusion construct 44	>1
Exemplary fusion construct 47	>1
Exemplary fusion construct 48	4.32E-01
Exemplary fusion construct 59	>1
Exemplary construct 71	>1
Exemplary construct 58	>1
Exemplary construct 92	1.09E-01
BB5.1, Hycult (anti-mouse C5 antibody)	1.06E-01

Example 11: Evaluation of anti-phospholipid antibody, C2, binding to cardiolipin

[00378] 96-well plates (Thermofisher) were coated with 50 μL of Cardiolipin (Sigma) in coating buffer (100% ethanol) (Sigma). Plates were incubated overnight while loosely covered (USA Scientific) to enable evaporation of ethanol. Coated plates were blocked with 300 μL of Echelon custom blocking buffer (Echelon) and incubated for at least 2 hours at room temperature. Wells

were aspirated and 100 μ L of diluted sample in Echelon custom buffer was added to each well. Wells were incubated for at least 90 minutes at room temperature. Plates were washed three times with PBS and dried on paper towels. 100 μ L of PBS-diluted secondary antibodies were added to the appropriate wells. For detections of C2-IgM, goat anti-mouse IgM (Southern Biotech) was diluted at 1:5,000. For detection of C2 IgG1 (murine), rabbit anti-mouse light chain kappa (Abcam) was diluted at 1:10,000. For detection of C2-IgG1 (human), mouse anti-human pFc' (Abcam) was diluted at 1:20,000. For detection of C2 fragments with a His₆ epitope tag (SEQ ID NO: 296), goat anti-6XHis (Abcam) was diluted at 1:5,000. After addition and incubation of secondary antibodies, plates were washed three times with PBS. Plates were developed by addition of 100 μ L of BioFx Supersensitive TMB (Surmodics). Plates were incubated in the dark for 15 minutes. The reactions were terminated by addition of 100 μ L of stop solution (Surmodics) and the absorbance was measured at 450 nm.

[00379] Table 23 shows EC₅₀ values obtained for the C2 constructs assayed in the cardiolipin ELISA binding assay. **Table 24** shows EC₅₀ values obtained for the humanized variants (human IgG4) in the cardiolipin ELISA binding assay.

[00380] Table 23: Cardiolipin EC₅₀ for C2 constructs

Construct Description	EC ₅₀ , nM
C2 IgM	0.154
C2 scFv-Crry	5.4
C2 scFv-Crry	3.9
C2-hIgG4	2.9
C2-muIgG1	5.7
CR1 ₁₋₁₀	30.8
CR1 ₁₋₁₇	14
C2 scFv-CR1 ₁₋₁₀	2.8
C2-muIgG1	6.4
C2 Fab-CR1 ₁₋₁₀ , C-term	2.65
C2 Fab-CR1 ₁₋₁₀ , N-term	2.9
C2 muIgG1, CR1 ₁₋₁₀ , C-term HC x 1	0.37
C2 muIgG1, CR1 ₁₋₁₀ , N-term HC x 1	0.95
C2 muIgG1, CR1 ₁₋₁₀ , N-term LC x 1	0.76
C2 muIgG1, CR1 ₁₋₁₀ , N-term HC x 2	0.7
C2 muIgG1, CR1 ₁₋₁₀ , N-term LC x 2	0.9

[00381] Table 24: Cardiolipin EC₅₀ of C2 humanized variants on a human IgG4 backbone

Construct Description	SEQ ID No. (VH/HC)	SEQ ID No. (VL/LC)	EC ₅₀ , nM
C2 VH0Vκ0	98	45	1.51
C2 VH0Vκ1	98	266	<0.8
C2 VH1Vκ0	261	45	<0.8
C2 VH1Vκ1	261	266	<0.8
C2 VH1Vκ2	261	267	<0.8
C2 VH1Vκ3	261	268	0.50
C2 VH1Vκ4	261	269	0.59
C2 VH2Vκ1	262	266	<0.8
C2 VH2Vκ2	262	267	<0.8
C2 VH2Vκ3	262	268	0.52
C2 VH2Vκ4	262	269	0.47
C2 VH3Vκ1	263	266	<0.8
C2 VH3Vκ2	263	267	<0.8
C2 VH3Vκ3	263	268	0.47
C2 VH3Vκ4	263	269	0.59
C2 VH4Vκ1	264	266	<0.8
C2 VH4Vκ2	264	267	<0.8
C2 VH4Vκ3	264	268	0.54
C2 VH4Vκ4	264	269	0.48
C2 VH5Vκ1	265	266	<0.8
C2 VH5Vκ2	265	267	<0.8
C2 VH5Vκ3	265	268	0.48
C2 VH5Vκ4	265	269	0.41

Example 12: Evaluation of the inhibitory potency of 3d8b fusion proteins in a human microvascular endothelial cell (HMEC) injury assay

[00382] 96-well plates were coated with collagen by adding 50 μ L of 0.1 mg/ml gelatin-based coating solution (Cell Biologic) for at least 5 minutes. An HMEC cell suspension was prepared at a cell density of 320,000 cells/mL in complete culture media. Gelatin solution was removed and a 200 μ L of cell suspension was dispensed into each well of a TrueLine Cell culture plate (MedSupply Partners). Seeded cells were incubated in standard culturing conditions for at least 48 hours or until confluency was reached. Test media was prepared by mixing a solution of 0.1% dextrose (Sigma), 28 mM Trizma Base (Sigma), 0.5% BSA (Jackson Imm. Research) in HBSS media (Fisher Scientific) at pH 7.3. A solution of 100 mM H₂O₂ was prepared by diluting 30% H₂O₂ 1:100 or 10 μ M ADP (Chrono) in test media. The HMEC monolayer was gently washed with test media three times to remove residual culture media ensuring that the monolayer remains intact. After washing, 50 μ L of 100 mM H₂O₂ or 10 μ M ADP was added and

the plates were incubated at 37°C supplemented with 5% CO₂ for exactly 10 minutes. The 50 μ L of 100 mM H₂O₂ or 10 μ M ADP was removed and the HMEC monolayer was gently washed with test media three times. To assess C3 fragment (C3b/iC3b) deposition,, 50 μ L of 25% human serum (CompTech) diluted in test media (premixed with or without fusion proteins) was added to wells. The plates were incubated for 60 minutes at 37°C supplemented with 5% CO₂. Cells were washed three times with test media to remove residual serum.

[00383] Treated cells were fixed with 4% paraformaldehyde in test media at room temperature for 10 minutes. Fixed cells were washed with test media three times. Fixed cells were blocked with 5% BSA in test media at room temperature for 30 minutes and washed with test media once. For C3 fragment (C3b/iC3b) staining, cells were stained by addition of 50 μ L per well of FITC-rabbit anti-human C3c (Agilent/Dako) at a 1:200 dilution. Stained samples were incubated for 60 minutes in the dark. After incubation, samples were washed three times with test media and counterstained with addition of 50 μ L of diluted DAPI (1:10,000 DAPI in PBS) per well. Counterstained samples were incubated in the dark at room temperature for 5 minutes. The DAPI counterstain was replaced with 100 μ L of PBS. Imaging of stained samples was performed on a BioTek Cytation1 imaging station in either the FITC or PE channel at 10X magnification using Gen5 3.05 software.

[00384] **Table 25** shows IC₅₀ values for the tested CR1₁₋₁₀ constructs in the H₂O₂ HMEC injury assay. **Table 26** shows IC₅₀ values for CR1₁₋₁₇ constructs used in the H₂O₂ HMEC injury assay. **Table 27** shows IC₅₀ values for CR1₁₋₁₀ constructs tested in the ADP-HMEC injury assay. **Table 28** shows IC₅₀ values for CR1₁₋₁₇ constructs used in the ADP HMEC injury assay.

[00385] **Table 25: Targeted vs. Non-Targeted CR1₁₋₁₀ constructs in H₂O₂-HMEC assay**

Compound ID	Targeted/Non-targeted	IC ₅₀ , nM	SD
Exemplary construct 70	Non-targeted	21.11	8.93
Exemplary fusion construct 43	Targeted	6.32	2.06
Exemplary fusion construct 45	Targeted	18.2	n/a
Exemplary fusion construct 46	Targeted	2.13	1.39
Exemplary fusion construct 51	Targeted	22.9	n/a
Exemplary fusion construct 52	Targeted	6.13	5.17
Exemplary construct 58	Targeted	No Inhibition	n/a
Exemplary construct 93	Targeted	No Inhibition	n/a
Exemplary fusion construct 95	Targeted	0.58	n/a
Exemplary fusion construct 96	Targeted	2.07	0.90
Exemplary fusion construct 99	Targeted	4.8	n/a
Exemplary fusion construct 106	Targeted	1.05	0.06

[00386] Table 26: Targeted vs. Non-Targeted CR1₁₋₁₇ constructs in H₂O₂-injured HMEC assay

Compound ID	Targeted/Non-targeted	IC ₅₀ , nM	SD
Exemplary construct 72	Non-targeted	1.73	0.58
Exemplary fusion construct 62	Targeted	1.39	0.20
Exemplary fusion construct 64	Targeted	0.77	0.50
Exemplary fusion construct 65	Targeted	1.35	0.13
Exemplary fusion construct 94	Targeted	0.18	0.04
Exemplary fusion construct 107	Targeted	0.98	0.21

[00387] Table 27: Targeted vs. Non-Targeted CR1 (1-10) constructs in ADP-HMEC assay

Compound ID	Targeted/Non-targeted	IC ₅₀ , nM	SD
Exemplary construct 70	Non-targeted	8.90	2.35
Exemplary construct 93	Targeted	No Inhibition	n/a
Exemplary fusion construct 95	Targeted	1.42	0.48
Exemplary fusion construct 96	Targeted	1.75	1.44
Exemplary fusion construct 99	Targeted	2.21	0.83
Exemplary fusion construct 106	Targeted	0.62	0.4

[00388] Table 28: Targeted vs. Non-Targeted CR1 (1-17) constructs in ADP-HMEC assay

Compound ID	Targeted/Non-targeted	IC ₅₀ , nM	SD
Exemplary construct 72	Non-targeted	1.28	0.31
Exemplary construct 58	Targeted	No inhibition	n/a
Exemplary construct 93	Targeted	No Inhibition	n/a
Exemplary fusion construct 94	Targeted	0.13	0.07
Exemplary fusion construct 107	Targeted	0.12	0.02
Exemplary fusion construct 100	Targeted	0.25	0.03

Example 13: Evaluation of the effects of complement inhibitors in factor H deficient (*cfh*^{-/-}) mice

Effects of complement inhibitors in cfh^{-/-} mice 72 hours after treatment

[00389] Female *cfh*^{-/-} mice at 3-4 months of age were treated with the following: 1) PBS, n=6; 2) 3d8b – CR1₁₋₁₇, n=5; 3) 3d8b-hfH₁₋₅, n=5; 4) soluble CR1₁₋₁₇ (sCR1₁₋₁₇), n=5; or 5) soluble factor H (sfH₁₋₅), n=5. The treatment groups were given a single intravenous (IV) injection and sacrificed 72 hours later. A control group of 4 month old female *cfh*^{-/-} (n=4) was administered one IV injection of soluble 3d8b-G1 and sacrificed 72 hours later. Untreated, age-matched wildtype mice were also used as a control by following the study during the same time period.

[00390] Serum C3 levels were measured by ELISA at the start and conclusion of the study. Plasma transaminase (ALT and AST) was measured at the conclusion of the study using a Reflotron® test (The Reflotron® test uses reagent strips for specific testing of important clinical-chemistry parameters directly from whole blood, plasma or serum. The direct use of whole blood is made possible through an integrated plasma separation pad. Various tests can also be run using urine). Upon sacrifice, kidneys and livers were harvested and measured for C3 deposits by immunofluorescence (IF).

[00391] **FIG. 32A** shows the staining of glomerular C3 deposits in harvested kidneys 72 hrs after treatment measured by IF. Quantification of C3 positive staining in 10 glomeruli per tissue section was expressed as percentage of total glomerular area (ImageJ software analyses). Data are expressed as mean $\pm$ SE. * $p < 0.05$, ** $p < 0.0001$ vs WT; ° $p < 0.0001$ vs *Cfh*^{-/-} + A and + D (one-way ANOVA with Tukey's *post hoc* test). **FIG. 32B** shows the C3 deposits of harvested livers 72 hrs after treatment using IF. For liver quantification, 10 – 15 non-overlapping fields were analyzed at 400X magnification. Semiquantitative scoring for liver stainings are as follows: 0=absent; 1=faint; 2=moderate; 3=intense staining. Results are mean $\pm$ SE. * $p < 0.05$; ** $p < 0.0001$ vs WT; ° $p < 0.0001$ vs *Cfh*^{-/-} + A and + D; \$ $p < 0.0001$ vs *Cfh*^{-/-} + B and + E (one-way ANOVA with Tukey's *post hoc* test).

Effects of complement inhibitors on cfh^{-/-} mice 72 hours after treatment

[00392] Male *cfh*^{-/-} mice at age 4-5 months were treated with the following (all groups n=3): 1) 3d8b-CR1₁₋₁₇, 2) 3d8b-mfH₁₋₅, 3) 3d8b-Crry, or 4) 3d8b. Compounds were administered via IV injection on days 1 and 2. On day 9, the mice were sacrificed. Serum C3 levels were measured by ELISA at baseline (pre-treatment) and at the end of the study. Plasma transaminase (ALT and AST) were measured by a Reflotron® test. Upon sacrifice, kidneys and livers were harvested and C3 deposits were measured by IF.

[00393] **FIG. 33A** shows the staining of glomerular C3 deposits in harvested kidneys 7 days after the last injection measured by IF. Quantification of C3 positive staining in 10 glomeruli per tissue section was expressed as percentage of total glomerular area (ImageJ software analyses). Data are expressed as mean $\pm$ SE. * $p < 0.0001$ vs WT mice; ° $p < 0.001$, °° $p < 0.0001$ vs *Cfh*^{-/-} + I mice (one-way ANOVA with Tukey's *post hoc* test).

[00394] **FIG. 33B** shows the C3 deposits of harvested livers using IF. For liver quantification, 10 – 15 non-overlapping fields were analyzed at 400X magnification. Semiquantitative scoring for liver stainings are as follows: 0=absent; 1=faint; 2=moderate; 3=intense staining. Data are expressed as mean $\pm$ SE and analyzed using a one-way ANOVA test using Tukey's *post hoc* test. * $p < 0.0001$ vs WT mice; ° $p < 0.001$, °° $p < 0.0001$ vs *Cfh*^{-/-} + I mice, # $p < 0.0001$ vs *Cfh*^{-/-} mice + F.

[00395] Table 29 shows levels of serum C3 levels in tested animals. Table 30 shows the levels of measured plasma transaminase of tested animals. Table 31 shows levels of serum C3 levels in tested animals. Table 32 shows the levels of measured plasma transaminase of tested animals. .

[00396] Table 29: Evaluation of serum C3 levels in 4-month old female wild-type and *cfh*^{-/-} mice

		Baseline	72 hours after single injection
Genotype	Treatment	µg/mL	µg/mL
Wildtype	none	1020.4 +/- 49.88	929.40 +/- 34.13
<i>cfh</i> -/-	Exemplary fusion construct 64	41.75 +/- 5.94	48.5 +/- 11.58
<i>cfh</i> -/-	PBS	47.00 +/- 3.67	45.75 +/- 5.85
<i>cfh</i> -/-	Exemplary construct 72	52.5 +/- 2.90	39.25 +/- 2.95
<i>cfh</i> -/-	Exemplary fusion construct 48	50.50 +/- 5.84	57.00 +/- 2.48
<i>cfh</i> -/-	Exemplary construct 71	41.75 +/- 2.59	38.25 +/- 2.29

[00397] Table 30: Plasma transaminase levels in 4-month old female wild-type and *cfh*^{-/-} 72 hours after single injection

		ALT (GPT)	AST (GOT)
Genotype	Treatment	(U/L)	(U/L)
Wildtype	none	45.22 +/- 9.02	112.63 +/- 19.64
<i>cfh</i> -/-	Exemplary fusion construct 64	40.45 +/- 6.81	219.25 +/- 38.20
<i>cfh</i> -/-	PBS	51.98 +/- 11.10	97.95 +/- 2.38
<i>cfh</i> -/-	Exemplary construct 72	34.00 +/- 3.75	185.05 +/- 38.46
<i>cfh</i> -/-	Exemplary fusion construct 48	62.68 +/- 14.84	120.10 +/- 32.37
<i>cfh</i> -/-	Exemplary construct 71	43.05 +/- 7.31	267.25 +/- 50.62

[00398] Table 31: Evaluation of serum C3 levels in 4-5 month old male *cfh*^{-/-} mice

			day 3 24 h after 2nd injection	day 9 1 week after 2nd injection
Genotype	Treatment	(µg/ml)	(µg/ml)	(µg/ml)
<i>cfh</i> -/-	Exemplar fusion construct 64	35.00 +/- 2	46.00 +/- 2.65	47.33 +/- 9.24
<i>cfh</i> -/-	Exemplary fusion construct 118	46.33 +/- 10.87	629.00 +/- 91.90	61.00 +/- 17.04

cfh -/-	Exemplary fusion construct 116	42.33 +/- 0.67	203.00 +/- 30.92	86.67 +/- 16.02
cfh -/-	Exemplary construct 58	30.00 +/- 3.61	23.00 +/- 1.00	36.00 +/- 2.00

[00399] Table 32: Plasma transaminase levels in 4-5 month old male *cfh*^{-/-} mice 1 week after 2nd injection

Genotype	Treatment	ALT (GPT) (U/L)	AST (GOT) (U/L)
cfh -/-	Exemplary fusion construct 64	48.73 +/- 4.56	140.33 +/- 13.45
cfh -/-	Exemplary fusion construct 118	63.8.3 +/- 10.73	205.67 +/- 65.74
cfh -/-	Exemplary fusion construct 116	56.13 +/- 2.56	270.67 +/- 67.36
cfh -/-	Exemplary construct 58	42.80 +/- 1.54	184.07 +/- 96.14

Example 14: Evaluation of C3d mAb and complement inhibitors in a Middle Cerebral Artery Occlusion (MCAO) model

Study Design

[00400] Ninety-eight male Balb/c mice 8-20g (Charles River Laboratories, Wilmington, MA) were allowed free access to food and water and were housed in a room provided with filtered air at a temperature of 21 +/- 5°C and 50% +/- 30% relative humidity. The room was on an automatic timer for a light dark cycle of 12 hours on and 12 hours off with no twilight. Shepherd's ® ¼" premium corn cob was used for bedding and 2 pieces of Neslets by Ancare and crink'l Nest™ were put in each cage. Animals were fed with Lab Diet ® 5001 chow. Water was provided ad libitum. 4-5 animals were housed per cage. 9 experimental groups consisting of 8 to 10 mice each were used for this study.

Surgical Preparation

[00401] Surgeries were all performed using aseptic technique. Cefazolin (40mg/kg; Hospira) was administered intraperitoneally (IP) before Middle Cerebral Artery Occlusion (MCAO) to prevent infections. Buprenorphine was provided subcutaneously (SC) (~0.1mg/kg, Par

Pharmaceuticals) as an analgesic, prior to MCAO. Sodium chloride hypertonicity ophthalmic ointment (Muro 128 sterile ophthalmic 5% ointment), was applied to the eyes prior to surgery.

Middle Cerebral Artery Occlusion Model

[00402] The MCAO reperfusion model, a model of acute stroke, was used for this study. Mice were anesthetized using 2-3% isoflurane with N₂O:O₂ (2:1) and maintained with a breathing tube at 1.5-2.5% isoflurane in a supine position. The middle of the neck was shaved with electric clippers and cleaned with multiple applications of Hibiclens and alcohol. Using aseptic technique, a skin incision was made over the right common carotid artery (CCA), the muscle was retracted and the CCA bifurcation was exposed. The CCA was ligated and a distal segment of the external carotid artery (ECA) was temporarily clamped. A nylon suture was then inserted through the CCA and advanced into the internal carotid artery (ICA) for a predetermined distance of 8-9 mm. Using this procedure, the silicone coated tip of the suture occludes the origin of the MCA in the brain, causing lack of blood flow in the MCA territory. The ECA clip/suture was then removed. The skin incision was closed with surgical staples and the animals were allowed to awaken from anesthesia and put back to the home cage. The animals were again anesthetized after the 60 minutes ischemic period, the wound was re-opened, and the intravascular suture was removed from the VVA. The skin wound was again closed, and the animals were monitored until they had fully awaked from anesthesia at which point they were returned to their home cage. During the times of anesthesia, a self-regulating heating pad was connected to a rectal thermometer in order to maintain the core temperature at 37°C +/- 1°C.

Sham Operation of MCAO

[00403] A sham MCAO operation was also performed. Mice were anesthetized using 2-3% isoflurane with N₂O:O₂ (2:1) and maintained with a breathing tube at 1.5-2.5% isoflurane in a supine position. The middle of the neck was shaved with electric clippers and cleaned with multiple applications of Hibiclens and alcohol. Using aseptic technique, a skin incision was made over the right common carotid artery (CCA), the muscle was retracted and the CCA bifurcation was exposed. The CCA, ECA, and ICA were isolated, then the skin incision was closed with surgical staples. The animals were allowed to awaken from anesthesia and put back in their home cage. During the time of anesthesia, a self-regulating heating pad connected to a rectal thermometer was used to maintain the core temperature of 37°C +/- 1°C.

Dosing

[00404] All dosing solutions were stored at 4°C until use.

The MCAO animals received PBS, C3d mAb or C3d-CR11-17 through an IV tail vein injection 60 minutes after reperfusion. The sham operated animals received PBS 60 minutes after the operation time.

Randomization and Blinding

[00405] Treatments were randomly assigned to each animal after the surgery by a different individual who did not perform the surgery. The treatment of the dosing solution were evenly distributed each day.

Sacrifice

[00406] Forty-eight hours after MCAO, mice were anesthetized using ketamine/xylazine mixture (~100/10 mg/kg) and perfused with ice cold heparinized PBS followed by ice cold 4% paraformaldehyde (PFA). Brains were then removed and post-fixed in 4% PFA in the refrigerator for twenty-four hours.

Tissue preparation for Histology:

[00407] After 24 hours of 4% PFA post fixation, brains were changed to a 30% sucrose solution and kept in the refrigerator for 3 more days. Each brain was then cut into five 1mm thick coronal sections using a mouse brain matrix (1.1, -0.9, -1.9, -2.9, compared to bregma respectively and embedded with Tissue-Tek® O.C.T. compound in standard CryoMold. The mold was then placed in a tray filled with 2-Methyl butane among dry ice. When the OCT compound was frozen, the samples were immediately sealed in Ziplock bags and stored at -80°C until sent to a histology laboratory.

Imaging and Image Analysis

[00408] Images were captured using a digital camera fixed on a microscope using SPOT software. Volumetric analysis of the infarct area was performed using ImageJ (NIH software). The free-hand tool was used to trace the area of the un-infarcted tissue of the ipsilateral (right) hemisphere and the tissue of the contralateral (left) hemisphere. Infarct area was calculated by subtracting the un-infarcted area of the ipsilateral hemisphere from the area of the intact contralateral hemisphere. The volume of each hemisphere was then calculated by multiplying the area with section thickness (1 mm) and adding the number of sections in between each sampling (5). The infarct volume was expressed as a percentage of the intact hemispheric volume.

Data Analysis

[00409] **Table 33** summarizes the proteins tested in the MCAO study.

FIG. 34 shows the calculated percentage infarct area for study. All data were expressed as mean +/- standard error of the mean. Data was analyzed by one-way ANOVA.

[00410] **Table 33: Summary of reagents tested in the MCAO Study**

Compound ID	Dose Level (mg/kg)	Dose Volume (ml/kg)
Exemplary construct 64	67	5
Exemplary construct 58	24.8	5
Vehicle	NA	5

Example 15: Effects of complement inhibitor fusion proteins on Adriamycin induced kidney damage

[00411] Male BALB/c OLA mice received adriamycin (11 mg/kg) intravenously via the tail vein on day 0. On day 8, mice were placed in metabolic cages and urine was collected over 16 hours. Urine samples were analyzed for albumin and creatinine using a Cobas c111 analyzer. All mice exhibited renal impairment by day 8 as determined by urine albumin: creatinine ratios (uACR). Mice were randomized into groups based on uACR. On day 10, mice received a single dose IV of either PBS (n=14) or fully murine fusion proteins C3d mAb-Crry (n=14; 50 mg/kg), C3d mAb-fH₁₋₅ (n=13; 50 mg/kg), or non-targeted controls containing the fH₁₋₅ or Crry proteins. Mice were placed again in metabolic cages to collect day 22 urine over 16 hr, and urine albumin and creatinine were determined (FIG. 35).

Example 16: Study of an exemplary C3d-complement modulator protein of this disclosure in a patient with Progressive Complement 3 Glomerulonephritis

[00412] Aim: The aim of this study is to evaluate the efficacy, safety, and tolerability of treatment with the exemplary anti-C3d antibody-complement modulator fusion protein construct in a patient with a complement mediated disease or disorder, for instance and for illustration only, progressive complement 3 (C3) glomerulonephritis.

[00413] Objectives: The primary safety objective of this study is to evaluate the safety and tolerability of treatment with the exemplary anti- C3d antibody-complement modulator fusion protein construct, for instance, for complement 3 (C3) glomerulonephritis. The primary efficacy objective is to evaluate the efficacy of treatment with the exemplary anti-C3d antibody-complement modulator fusion protein construct based on change from baseline, for example, in eGFR (MDRD, Estimated Glomerular Filtration Rate) and proteinuria. The secondary objectives of this study include assessment of: 1. Change from baseline in pharmacodynamic markers in plasma and urine, *e.g.*, MCP-1, C3a, C5a, properdin, and sC5b-9; 2. Change from baseline in glomerular pathology based on renal biopsy; 3. Evaluation of the plasma concentrations of treatment with the exemplary anti-C3d antibody-complement modulator fusion protein construct in C3 glomerulonephritis.

[00414] A C3 glomerulonephritis patient receives treatment with a parenterally intravenously administered (*e.g.*, intravenously, subcutaneously) exemplary anti-C3d antibody-complement modulator fusion protein of this disclosure, following the protocol detailed below. In some cases, the patient has refractory disease despite a kidney transplant and prior treatment with the broadly immunosuppressive drugs, *e.g.*, with rituximab, cyclophosphamide, mycophenolate mofetil, tacrolimus, and steroids. In some cases, renal allograft biopsies are taken pre-dose, 2- and 7-months during therapy.

[00415] Methodology: In some cases, the patient will have biopsy proven recurrent C3GN prior to start of dosing and be deemed eligible based on the inclusion and exclusion criteria. Screening procedures will include recording of demographics, medical history, medication history, physical examination and vital signs, serum chemistry, hematology, urinalysis (including UPCR measurement), viral screening (if not performed within prior 12 weeks) and estimated glomerular filtration rate (eGFR) assessment based on serum creatinine. The baseline eGFR is, for example, about 15-25 mL/min/1.73 m² for study eligibility. On Day 1, the patient may start treatment with the exemplary anti- C3d antibody-complement modulator fusion protein construct treatment. Patients will take treatment with the exemplary anti- C3d antibody-complement modulator fusion protein construct parenterally, for an initial period of about 60-84 days. The patient will visit the study center at frequent intervals for monitoring. If the patient's clinical condition stabilizes or improves, and there are no adverse events preventing further treatment, the patient may be treated for another treatment cycle, *e.g.*, of about 60-84 days. Treatment cycles may be repeated for a total of 4 cycles under this protocol.

[00416] At the Day 1 and post-Day 1 study visits, blood and urine samples will be collected for safety, efficacy, and pharmacokinetic measurements. Physical examinations and vital signs assessments will be performed throughout the study. Concomitant medication and adverse event assessments will be made at every study visit. If possible, a renal biopsy will be performed after an appropriate follow-up period to assess the changes in kidney histology.

[00417] Results: The patient's condition is expected to improve in response to the treatment with the exemplary C3d-complement modulator fusion protein construct of this disclosure. The improvement seen with the C3d-complement modulator fusion protein construct treatment in this patient is based on the on-treatment kidney biopsy histologic findings showing clearance of glomerular endocapillary proliferation and a marked decrease in glomerular inflammatory macrophages compared to the pre-treatment biopsy. Proteinuria drops approximately 80% with the fusion protein construct treatment.

[00418] Estimated glomerular filtration rate (eGFR) can be, for example, about 80-90 mL/min/1.73 m² 14 months prior to treatment with the exemplary C3d fusion protein construct

and can deteriorate to, for example, about 30-50 mL/min/1.73 m² when treatment with the exemplary C3d fusion protein construct is started. In addition, treatment with the exemplary C3d fusion protein construct attenuates or stops the eGFR decline. After 1 month of treatment, the eGFR decline is expected to be already attenuated. Repeat biopsies show resolution of glomerular endocapillary hypercellularity and reduction in glomerular macrophages. Thus, treatment with the exemplary C3d fusion protein construct stabilizes eGFR and reduced glomerular inflammation.

Example 17: Study of efficacy of an exemplary fusion protein construct of this disclosure in treating renal ischemia/reperfusion

[00419] Ischemia-Reperfusion (I/R) injury in kidney at body temperature has relevance in several clinical conditions, including hypovolemic shock, renal artery occlusion and cross-clamping procedures.

[00420] Kidney ischemia-reperfusion (I/R) is an important cause of acute renal failure, associated with a mortality rate of up to 50% (Levy *et al.*, *JAMA* 275:1489-94, 1996; Thadhani *et al.*, *N. Engl. J. Med.* 334:1448-60, 1996). Post-transplant renal failure is a common and threatening complication after renal transplantation (Nicholson *et al.*, *Kidney Int.* 58:2585-91, 2000). Effective treatment for renal FR injury is currently not available and hemodialysis is the only treatment available. The pathophysiology of renal FR injury is complicated. Recent studies have shown that the lectin pathway of complement activation may have an important role in the pathogenesis of renal I/R injury (deVries *et al.*, *Am. J. Path.* 165:1677-88, 2004).

[00421] Renal function is assessed at 24 and 48 hours after reperfusion in a patient administered an exemplary fusion protein construct of this disclosure. Blood creatinine measurement is determined by mass spectrometry, which provides a reproducible index of renal function. The patient displays a significant reduction in the amount of blood urea at 24 and 48 hours, indicating a protective functional effect from renal damage. Overall, increased blood urea is seen in both at 24 and 48 hours following the surgical procedure and ischemic insult.

Example 18: Study of efficacy of an exemplary fusion protein construct of this disclosure in treating macular degeneration

[00422] Age-related macular degeneration (AMD) is the leading cause of blindness after age 55 in the industrialized world. AMD occurs in two major forms: neovascular (wet) AMD and atrophic (dry) AMD. The neovascular (wet) form accounts for 90% of severe visual loss associated with AMD, even though only ~20% of individuals with AMD develop the wet form. Clinical hallmarks of AMD include multiple drusen, geographic atrophy, and choroidal

neovascularization (CNV). In December 2004, the FDA approved Macugen (pegaptanib), a new class of ophthalmic drugs to specifically target and block the effects of vascular endothelial growth factor (VEGF), for treatment of the wet (neovascular) form of AMD (Ng et al., *Nat Rev. Drug Discov* 5:123-32 (2006)). Although Macugen represents a promising new therapeutic option for a subgroup of AMD patients, there remains a pressing need to develop additional treatments for this complex disease. Multiple, independent lines of investigation implicate a central role for complement activation in the pathogenesis of AMD. The pathogenesis of choroidal neovascularization (CNV), the most serious form of AMD, may involve activation of complement pathways.

[00423] A group of patients suffering from AMD are administered, intraocularly or parenterally, an exemplary fusion protein construct of this disclosure. At various time points following the administration, choroidal neovascularization is assessed. In patients administered the exemplary fusion protein construct of the disclosure, a 20% to 100% reduction in CNV area is observed, compared to patients administered a sham control.

Example 19: Study of efficacy of an exemplary fusion protein construct of this disclosure in treating atypical hemolytic uremic syndrome (aHUS)

[00424] Atypical hemolytic uremic syndrome (aHUS) is characterized by hemolytic anemia, thrombocytopenia, and renal failure caused by platelet thrombi in the microcirculation of the kidney and other organs. aHUS is associated with defective complement regulation and can be either sporadic or familial. aHUS is associated with mutations in genes coding for complement activation, including complement factor H, membrane cofactor B and factor I, and well as complement factor H-related 1 (CFHR1) and complement factor H-related 3 (CFHR3). Zipfel, P. F., et al., *PloS Genetics* 3(3):e41 (2007).

[00425] The effect of the exemplary fusion protein construct of this disclosure to treat aHUS is determined by obtaining and lysing red blood cells from aHUS patients treated with the exemplary fusion protein construct. It is observed that treatment with the exemplary fusion protein construct is effective in blocking lysis of red blood cells in the patients suffering from aHUS, compared to treatment with a sham control.

Example 20: PEPperMAP® Linear Epitope Mapping of 5 Mouse IgG1 Antibodies against C3dg_extended

[00426] The PEPperMAP® Linear Epitope Mappings of mouse IgG1 antibodies were performed against C3dg_extended translated into linear overlapping 15 amino acid peptides with a peptide-

peptide overlap of 14 amino acids as well as against 15 additional peptides. Pre-staining of a C3dg peptide microarray was performed with secondary goat anti-mouse IgG (H+L) DyLight680 antibody (1:5000) to determine background interactions with the linear C3dg peptides that could interfere with the main assays. The C3dg peptide microarrays were incubated with exemplary anti-C3d mouse IgG1 antibodies 3d29, 3d8b, 3d9a at concentrations of 1 µg/ml, 10 µg/ml or 100 µg/ml in incubation buffer (*e.g.*, washing buffer with 10% blocking buffer) followed by staining with secondary goat anti-mouse IgG (H+L) DyLight680 antibody (1:5000) and control mouse monoclonal anti-HA (12CA5) DyLight800 antibody (1:2000). The CI samples were used as negative controls. The incubation step was performed for 16 hours at 4°C with shaking at 140 rpm. The staining with secondary antibody and control antibody was performed for 45 min in incubation buffer at room temperature (RT). Read-out with a LI-COR Odyssey Imaging System was done at scanning intensities of 7/7 (red/green). The additional HA peptides framing the peptide microarrays were subsequently stained as internal quality control to confirm the assay quality and the peptide microarray integrity. **Table 34** describes the materials and methods in more detail.

[00427] Table 34: Materials and Methods

Microarray Content:	The sequence of C3dg_extended was elongated with neutral GSGSGSG linkers (SEQ ID NO: 297) at the C- and N- terminus to avoid truncated peptides and translated into 15 amino acid linear peptides with a peptide-peptide overlap of 14 amino acids. The C3dg peptide microarrays were further complemented by 15 additional peptides and contained 375 different peptides printed in duplicate (750 peptide spots) as well as additional HA (YPYDVDPYAG (SEQ ID NO: 298), 80 spots) control peptides.
Samples:	Mouse anti-C3d IgG1 antibodies 3d29, 3d8b, 3d9a, CI-00008, and CI-00009 (CI samples are negative controls)
Washing Buffer:	PBS, pH 7.4 with 0.05% Tween 20 (3 x 1 min after each assay)
Blocking Buffer:	Rockland blocking buffer MB-070 (30 min before the first assay)
Incubation Buffer:	Washing buffer with 10% blocking buffer
Assay Conditions:	Antibody concentrations of 1 µg/ml, 10 µg/ml and 100 µg/ml in incubation buffer; incubation for 16 h at 4°C and shaking at 140 rpm.
Secondary Antibody:	Goat anti-mouse IgG (H+L) DyLight680 (1:5000); 45 min staining in incubation buffer at RT
Control Antibody:	Mouse monoclonal anti-HA (12CA5) DyLight800 (1:2000); 45

	min staining in incubation buffer at RT
Scanner:	LI-COR Odyssey Imaging System; scanning offset 0.65 mm, resolution 21 μ m, scanning intensities of 7/7 (red = 680 nm/green = 800 nm).

[00428] Quantification of spot intensities and peptide annotation were based on the 16-bit gray scale tiff files at scanning intensities of 7/7 that exhibited a higher dynamic range than the 24-bit colorized tiff files. Further, microarray image analyses, quantification of spot intensities and peptide annotation were performed with PepSlide[®] Analyzer. In short, the software algorithm breaks down fluorescence intensities of each spot into raw, foreground and background signal, and calculates average median foreground intensities and spot-to-spot deviations of spot duplicates. An intensity map was generated, based on the averaged median foreground intensities, and interactions in the peptide map highlighted by an intensity color code with red for high and white for low spot intensities. A maximum spot-to-spot deviation of 40% was found to be acceptable (otherwise the corresponding intensity value was zeroed).

[00429] In addition, the averaged spot intensities of the assays with the mouse antibodies against the antigen sequence from the N- to the C-terminus of C3dg_extended were plotted to visualize overall spot intensities and signal-to-noise ratios. The intensity plots were correlated with peptide and intensity maps as well as with visual inspection of the microarray scans to identify epitopes of the mouse antibody samples. If it was not clear whether a certain amino acid contributed to antibody binding, the corresponding letters of such amino acids were underlined, as illustrated in **FIGS. 21-23**. In some cases, the baselines of the intensity plots were leveled. **FIGS. 24-25** illustrate epitope mapping studies that were carried out with negative control anti-C3d or anti-C4d antibodies at 1, 10 and 100 μ g/mL, which did not recognize the epitopes recognized by the exemplary anti-C3d antibodies 3d9a, 3d29, or 3d8b (as shown by the peaks in **FIGS. 21-23**).

[00430] Pre-staining of a C3dg peptide microarray with secondary goat anti-mouse IgG (H+L) DyLight680 antibody did not show any background interaction with the linear C3dg_extended peptides that could interfere with the main assays. Mouse anti-C3d IgG1 antibodies 3d29, 3d8b and 3d9a showed very strong monoclonal antibody responses with high spot intensities and signal-to-noise ratios against adjacent peptides with similar consensus motifs NLDVSLQLPS (SEQ ID NO: 299), NLDVSLQLPS (SEQ ID NO: 299) and NLDVSLQLPS (SEQ ID NO: 299), as illustrated in **Figs. 21-23**. The 15 additional peptides did not react with the mouse IgG1 antibodies. Specifically, when the C3dg peptide microarray was incubated with 1 μ g/ml of either

the mouse anti-C3d IgG1 antibody 3d29 or the mouse anti-C3d IgG1 antibody 3d9a, very strong monoclonal antibody responses with high signal-to-noise ratio against adjacent peptides with the consensus motif NLDVSLQLPS (SEQ ID NO: 299) were observed, as illustrated in **FIG. 21** and **FIG. 23**, respectively. Similarly, a very strong monoclonal antibody response with high signal-to-noise ratio against adjacent peptides with the consensus motif NLDVSLQLPS (SEQ ID NO: 299) was observed when the C3dg peptide microarray was incubated with the mouse anti-C3d IgG1 antibody 3d8b, at a concentration of 1 µg/ml, as illustrated in **FIG. 22**. All the data were obtained by a read-out at scanning intensities of 7/7 (red/green) after the C3dg peptide microarray was incubated with a mouse IgG1 antibody followed by staining with secondary and control antibodies. The underlined amino acids correspond to residues for which contribution to antibody binding was not clear. For all **FIGS. 21-23**, the staining of HA control peptides is shown in the control staining boxes in **FIGS. 21-23**). Further, PEPperMAP® Epitope Substitution Scans can be used to investigate proposed epitopes by, for example, underlying wild type peptides with an exchange of all amino acid positions with the 20 main amino acids.

[00431] Table 35: Exemplary protein table

Exemplary protein constructs	Polypeptide sequence of the heavy chain (HC), variable domain heavy (VH)	Polypeptide sequence of the light chain (LC) or variable domain light (VL)
Exemplary anti-C3d construct 32	SEQ ID No. 58	SEQ ID No. 59
Exemplary anti-C3d construct 33	SEQ ID No. 73	SEQ ID No. 68
Exemplary anti-C3d construct 34	SEQ ID No. 288	SEQ ID No. 287
Exemplary anti-C3d construct 35	SEQ ID No. 60	SEQ ID No. 59
Exemplary anti-C3d construct 49	SEQ ID No. 58	SEQ ID No. 68
Exemplary anti-C3d construct 53	SEQ ID No. 62	SEQ ID No. 59
Exemplary anti-C3d construct 54	SEQ ID No. 67	SEQ ID No. 68
Exemplary anti-C3d construct 55	SEQ ID No. 288	SEQ ID No. 287
Exemplary anti-C3d construct 56 (Fab)	SEQ ID No. 288	SEQ ID No. 287
Exemplary anti-C3d construct 58	SEQ ID No. 73	SEQ ID No. 68
Exemplary anti-C3d construct 73	SEQ ID No. 73	SEQ ID No. 68
Exemplary anti-C3d construct 74	SEQ ID No. 249	SEQ ID No. 258
Exemplary anti-C3d construct 75	SEQ ID No. 252	SEQ ID No. 258
Exemplary anti-C3d construct 76	SEQ ID No. 250	SEQ ID No. 258
Exemplary anti-C3d construct 77	SEQ ID No. 253	SEQ ID No. 258
Exemplary anti-C3d construct 78	SEQ ID No. 251	SEQ ID No. 258
Exemplary anti-C3d construct 79	SEQ ID No. 254	SEQ ID No. 258
Exemplary anti-C3d construct 86	SEQ ID No. 280	SEQ ID No. 279
Exemplary anti-C3d construct 87	SEQ ID No. 281	SEQ ID No. 279
Exemplary anti-C3d construct 93	SEQ ID No. 282	SEQ ID No. 279
Exemplary C2 construct 35	SEQ ID No. 98	SEQ ID No. 45
Exemplary C2 construct 36	SEQ ID No. 98	SEQ ID No. 266

Exemplary C2 construct 37	SEQ ID No. 261	SEQ ID No. 45
Exemplary C2 construct 38	SEQ ID No. 261	SEQ ID No. 266
Exemplary C2 construct 39	SEQ ID No. 261	SEQ ID No. 267
Exemplary C2 construct 40	SEQ ID No. 261	SEQ ID No. 268
Exemplary C2 construct 41	SEQ ID No. 261	SEQ ID No. 269
Exemplary C2 construct 42	SEQ ID No. 262	SEQ ID No. 266
Exemplary C2 construct 43	SEQ ID No. 262	SEQ ID No. 267
Exemplary C2 construct 44	SEQ ID No. 262	SEQ ID No. 268
Exemplary C2 construct 45	SEQ ID No. 262	SEQ ID No. 269
Exemplary C2 construct 46	SEQ ID No. 263	SEQ ID No. 266
Exemplary C2 construct 47	SEQ ID No. 263	SEQ ID No. 267
Exemplary C2 construct 48	SEQ ID No. 263	SEQ ID No. 268
Exemplary C2 construct 49	SEQ ID No. 263	SEQ ID No. 269
Exemplary C2 construct 50	SEQ ID No. 264	SEQ ID No. 266
Exemplary C2 construct 51	SEQ ID No. 264	SEQ ID No. 267
Exemplary C2 construct 52	SEQ ID No. 264	SEQ ID No. 268
Exemplary C2 construct 53	SEQ ID No. 264	SEQ ID No. 269
Exemplary C2 construct 54	SEQ ID No. 265	SEQ ID No. 266
Exemplary C2 construct 55	SEQ ID No. 265	SEQ ID No. 267
Exemplary C2 construct 56	SEQ ID No. 265	SEQ ID No. 268
Exemplary C2 construct 57	SEQ ID No. 265	SEQ ID No. 269
Exemplary construct 70	SEQ ID No. 41	
Exemplary construct 71	SEQ ID No. 72	
Exemplary construct 72	SEQ ID No. 42	

[00432] Table 36: SEQUENCE TABLE

SEQ ID NO:	DESCRIPTION	SEQUENCE
1	MCP/CD46	>sp P15529 MCP_HUMAN Membrane cofactor protein OS=Homo sapiens OX=9606 GN=CD46 PE=1 SV=3 MEPPGRRECPFPSWRFPGLLLAAMVLLLYSFSDACEEPPTFEAMELIGKPK PYYEIGERVDYKCKKGYFYIPLATHHTICDRNHTWLPVSDDACYRETCPI RDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWGK PPICEKVLCTPPPKIKNGKHTFSEVEVFEYLDVATYSCDPAPGPDPSLIG ESTIYCGDNSVWSRAAPECKVVKCRFPVVENGGQISGFGKKFYKATVMFE CDKGFYLDGSDTIVCDNSTWDPPVPKCLKVLPPSSTKPPALSHSVSTSST TKSPASSASGPRPTYKPPVSNYPGYPKPEEGILDSLVDVWVIAVIVIAVVG VAVICVVPYRYLQRRKKKGTYLTDETHREVKFTSL
2	DAF	>sp P08174 DAF_HUMAN Complement decay-accelerating factor OS=Homo sapiens OX=9606 GN=CD55 PE=1 SV=4 MTVARPSVPAALPLLGLPRLLLLVLLCLPAVWGDCGLPPDPVNAQPALEG RTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFNRSCEVPT RLNSASLKQPYITQNYFPVGTVEYECRPGYRREPSLSPKLTCLQNLKWT AVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFC LISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNK GFTMIGEHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPTTVNVPT TEVSPTSQKTTTKTTPNAQATRSTPVSRTTKHFHETTPNKGSGTTSSTGTR LLSGHTCFTLTGLLGLTVMGLLT
3	DAF1_mouse	>sp Q61475 DAF1_MOUSE Complement decay-accelerating factor, GPI-anchored OS=Mus musculus OX=10090 GN=Cd55 PE=1 SV=2

		MIRGRAPRTRPSPPPPLLPILLSLSLLLLSPTVRGDCGPPPDIPNARPIILGR HSKF AEQSKVAYSCNNGFKQVPDKSNIVVCLENGQWSSHETFC E KSCVAPE RLSFASLKKEYLNMNFFPVGTIVEYECRPGFRKQPPPLPGKATCLEDLVWSP VAQFCKKKKSCPNPKDLNNGHINIPTGILFGSEINFSCNPGYRLVGVSTFC SVTGNTVDWDDEFPVCTEIHCEPPKINNGIMRGESDSYYSQVVTYS CDK GFILVGNASIYCTVSKSDVGQWSSPPPRCIEKSKVPTTKPTINVPSTGTPS TPQKPTTESVNPNGDQPTPQKPSTVKVSATQHVPVTKTTVRHPIRTSTDKG EPNTGGDRYIYGHTCLITLTVLHVMLSLIGYLT
4	CD59	>sp P13987 CD59_HUMAN CD59 glycoprotein OS=Homo sapiens OX=9606 GN=CD59 PE=1 SV=1 MGIQGGSVLFGLLLVLAVFCHSGHSLQCYNCPNPTADCKTAVNCSSDFDAC LITKAGLQVYNKCWKFEHCNFNDVTTTLRENELTYCYCKKDL CNFNEQLEN GGTSLSEKTVLLLVTPLAAAWSLHP
5	CD59_mouse isoform A	>sp O55186 CD59A_MOUSE CD59A glycoprotein OS=Mus musculus OX=10090 GN=Cd59a PE=2 SV=1 MRAQRGLILLLLLLLAVFCSTAVSLTCYHCFQPVVSSCNMNSTCSPDQDSCL YAVAGMQVYQRCWKQSDCHGEIIMDQLEETKLKFRCCQFNLCNKSDGSLGK TPLLGTSVLVAILNLCFLSHL
6	CD59_mouse isoform B	>sp P58019 CD59B_MOUSE CD59B glycoprotein OS=Mus musculus OX=10090 GN=Cd59b PE=2 SV=2 MRAQRGLILLLLLLLAVFCSTAVSLKCYNCLDPVSSCKINTTCSPNLDSCLY AVAGRQVYQQCWKLSDCNSNYIMSRLDVAGIQSKCCQWDL CNKNLDGLEEP NNAETSSLRKTALLGTSVLVAILKFCF
7	Crly	>sp Q64735.1 CR1L_MOUSE Complement component receptor 1-like protein MEVSSRSSEPLDPVWLLVAFGRGGVKLEVL LLLFLLPFTLGELRGGLGKHGH TVHREPAV NRLCADSKRWSGLPVSAQRPFPMGHCPAPSQLP SAKPINLTDESMFPIGT LLYECLPGYIKRQFSITCKQDSTWTS AEDKCIKQCKTPSDPENGLVHVHT GIQFGSRINYTCNQGYRLIGSSSAVCVITDQSV DWDTEAPICEWIPCEIPP GIPNGDFFSSTREDFHYGMVVTYRCNTDARGKALFNLVGEPSLYCTSN DGE IGVWSGPPPQCIELNKCTPPPYVENAVMLSENRSLSLRDIVEFRCHPGEI MKGASSVHCQSLNKWEPELPSCFKGVICRLPQEMSGFQKGLGMKKEYYYGE NVTLECEDGYTLEGSSQSQCQSDGSWNPLLAKCVSRISGLIVGIFIGIIV FILVIVFIWMILKYKKRNTTDEKYKEVGIHLNLYKEDSCVRLQSL L TSQEN SSTTSPARNSLTQEV S
8	CR1	>sp P17927 CR1_HUMAN Complement receptor type 1 OS=Homo sapiens OX=9606 GN=CR1 PE=1 SV=3 MGASSPRSPEPVGPAPGLPFCCGGSL LAVVLLALPVAWGQCNAPEWL P ARPTNL TDEFEP IGT YLNYECRPGYSGRPF SII CLKNSVW TGAKDR CRK SCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKG YRLIGSSSATCII S GDTVI WDNETPICDRIPCGLPPTITNGDFISTNRENFHYG SVV TYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSL FSLNEVVEFRCPGFVMKGPRRVK CQALNKWEPELPSCSRVCQPPPDVLHA ERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESL WNSSVPVCEQIFCPSPPIVNGRHTGKPLEVFPFGKTVNYTCDPHDRGTS FDLIGESTIRCTSDPQGNVWSSPAPRCGILGH CQAPDHFLFAKLKTQ TNA SDFPIGTS LKRYECRPEYYGRPF SITCLDNLVWSSPKDVCKRKSCKTPPDV NGMVHVITDIQVGRINYSCTTGHR LIGHSSAECILSGNAAHWSTKPPICQ RIPCGLPPTIANGDFISTNRENFHYG SVV TYRCNPGSGGRKVFELVGEPSI YCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSLNEVVEF RCQPGFVMKGPRRVK CQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDN FSPGQEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKS CDDFMGQLL NGRVLFVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCE QIFCPSPPIVNGRHTGKPLEVFPFGKAVNYTCDPHDRGTSFDLIGESTI RCTSDPQGNVWSSPAPRCGILGH CQAPDHFLFAKLKTQ TNASDFPIGTS L KYECRPEYYGRPF SITCLDNLVWSSPKDVCKRKSCKTPPDVNGMVHVITD IQVGRINYSCTTGHR LIGHSSAECILSGNTAHWSTKPPICQ RIPCGLPPT

		IANGDFISTNRENFHYGSVVITYRCNLGSRGRKVFELVGEPSIYCTSNDDQV GIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRQCQPGFVMK GPRRVKQALNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFY SCEPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRVLFPLN LQLGAKVSFVCDEGFRLKGSSSVSHCVLVGMRSLLWNSVVPVCEHIFCPNPFA ILNGRHTGTPSGDIPYGKEISYTCDPHPDRGMTFNLIgestIRCTSDPHGN GVWSSPAPRCELSVRAGHCKTPEQFPFASPTIPINDFEFFVGTSLNYECP GYFGKMFSISCLENLVWSSVEDNCRKSCGPPPEPFNGMVHINTDTQFGST VNYSCNEGFRLLIGSPSTTCLVSGNNVTWDDKAPICEIISCEPPPTISNGDF YSNNRTSFHNGTVVITYQCHTGPDEQLFELVGERSIYCTSKDDQVGVWSSP PPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIRFRCQPGFVMVGSHTVQ CQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQDNFSPGQEVFYSCPSY DLRGAASLHCTPQGDWSPEAPRCTVKSCDDFLGQLPHGRVLLPLNLQLGAK VSFVCDEGFRLKGRSASHCVLAGMKALWNSVVPVCEQIFCPNPFAILNGRH TGTPFGDIPYGKEISYACDTHPDRGMTFNLIgestIRCTSDPQNGVWSSP APRCELSVPAACPHPPKIQNGHYIGGHVSLYLPGMTISYICDPGYLLVGKG FIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHYGDYVTLKC EDGYTLEGSPWSQCQADDRWDPPLAKCTSRTHDALIVGTLSGTIFFILLII FLSWIILKHRKGNNAHENPKEVAIHLHSQGGSSVHPRTLQTNEENSRLVP
9	Factor H	>sp P08603 CFAH_HUMAN Complement factor H OS=Homo sapiens OX=9606 GN=CFH PE=1 SV=4 MRLLAIIICMLWAICVAEDCNELPPRRNTEILTGWSWDQTYPEGTQAIYK CRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTGNG VFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAP NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKKPK CVEISCKSPDVINGSPIISQKIIYKENERFQYKCNMGYEYSERGDVCTESG WRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNT AKCTSTGWIPAPRCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYQ DEHFETPSGSYWDHIHCTQDGWSPAVPCLRKCYFPYLENGYNQNYGRKFVQ GKSIDVACHPGYALPKAQTTVTCMENGWSPTPRCIRVKTCSSKSIDIENG ISESQYTYALKEKAKYQCKLGYYVTADGETSGSITCGKDGWSAQPTICKSCD IPVFMNARTKNDFTWFKLNDTLDYECHEGYESNTGSTTGSIVCGYNGWSDL PICYERECLEPKIDVHLVLPDRKKDQYKVGEVLKFSCKPGFTIVGPNVQCY HFGLSPDLPICKEQVQSCGPPPELLNGNVKEKTKEEYGHSEVVEYCNPRF LMKGPNKIQCVDEWTTLPVCIVEESTCGDIPLEHGWALSSPPYYYGDS VEFNCSSEFTMIGHRSITCIHGVTQLPQCVADKLKKCKSSNLIILEEHL KNKKEFDHNSNIYRCRGKEGWIHTVCINGRWDPEVNCSMAQIQLCPPPPQ IPNSHNMTTTTLNRYDGEKVSVLCQENYLIQEGEEITCKDGRWQSIPLCEK IPCSQPPQIEHGTINSSRSQESYAHGTKLSYTCGGFRISEENETTCYMG KWSSPPQCEGLPCKSPPEISHGVVAHMSDSYQYGEVYKCFEGFGIDGPA IAKCLGEKWSHPPSCIKTDCLSLPSFENAI PMGEKKDVYKAGEQVYTCAT YYKMDGASNVTCINSRWTGRPTCRDTSVNPPTVQNAIYVSRQMSKYPSGE RVRYQCRSPYEMFGDEEVMCLNGNWTPEPPQCKDSTGKCGPPPPIDNGDITS FPLSVYAPASSVEYQCQNLQYQLEGNKRITCRNGQWSEPPKCLHPCVISREI MENYNIALRWTAQKLYSRTGESVEFVCKRGYRLSSRSHTLRTTCWDGKLE YPTCAKR
10	Factor H_mouse	>sp P06909 CFAH_MOUSE Complement factor H OS=Mus musculus OX=10090 GN=Cfh PE=1 SV=2 MRLSARIIWLLILWTVCAAEDCKGPPPRENSEILSGSWSEQLYPEGTQATYK CRPGYRTLGTIVKVKNGKWVASNPSRICRKKPCGHPGDTFPGSFRLAVGS QFEFGAKVVYTCDDGYQLLGEIDYRECGADGWINDIPLCEVVKCLPVTLE NGRIVSGAAETDQEYFYGQVVRFECSGFKIEGHKEIHCSENGLWSNEKPR CVEILCTPPRVENGGINVKPVYKENERYHYKCKHGYVPKERGDVCTGSG WSSQPFCEEKRCSPPIILNGIYTPHRIIHRSDDEIRYECNYGYFPVTGSTV SKCTPTGWIPVPRCTLKPCFEPQFKYGRLYEESLRPNFPVSI GNKYSYK DNGFSPPSGYSWYDLRCTAQGWEPVPCVRKCVFHYVENGDSAYWEKVYVQ GQSLKVQCYNGYSLQNGQDTMTCTENGWSPPPKCIRIKTCSASDIHIDNGF LSESSSIYALNRETSYRCKQGYVTNTGEISGSITCLQNGWSPQPSICKSCD MPVFENSITKNTRTWFKLNDKLDYECLEGVFENEYKHTKGSITCTYYGWSDT PSCYERECVPTLDRKLVVSPRKEKYRVGDLLEFSCHSGHRVGPDSVQCYH

		FGWSPGFPTCKGQVASCAPPLEILNGEINGAKKVEYSHGEVVKYDCKPRFL LKGPNKIQCVDGNWTTLPVCIIEERTCGDIPELEHGS AKCSVPPYHHGDSV EFICEENFTMIGHGSVSCISGKWTQLPKCVATDQLEKCRVLKSTGIEAIKP KLTEFTHNSTMDYKCRDKQEYERSICINGKWDPEPNCTSKTSCPPPPQIPN TQVIETTVKYLDGEKLSVLCQDNYLTQDSEEMVCKDGRWQSLPRCIEKIPC SQPPTIEHGSINLPRSSEERRDSIESSSHEHGTTFSYVCDGDFRIPEENRI TCYMGKWSTPPRCVGLPCGPPPSIPLGTVSLELESYQHGEVVTYHCSTGFG IDGPAFIICEGGKWS DPPKCIKTDCDVLPTVKNAIIRGKSKSYRTGEQVT FRCQSPYQMNGSDTVTCVNSRWIGQPVCKDNSCVDPHPVPNATIVTRTKNK YLHGDRVRYECNKPLELFGQVEVMCENGIWTEKPKCRDSTGKCGPPPPIDN GDITSLSLPVYEPLSSVEYQCQKYLLKGKKTITCRNGKWSEPTCLHACV IPENIMESHNIILKWRHTEKIYSHSGEDIEFGCKYGYKARDSPPFR TKCI NGTINYPTCV
11	Exemplary B4 CDRH1 sequence	GYTFTDYY
12	Exemplary B4 CDRH2 sequence	INPNNGGT
13	Exemplary B4 CDRH3 sequence	ARYDYAWYFDV
14	Exemplary B4 CDRL1 sequence	QSIVHSNGNTY
15	Exemplary B4 CDRL2 sequence	KVS
16	Exemplary B4 CDRL3 sequence	FQGSHPYPT
17	Exemplary C2 CDRH1 sequence	GYTFTSYW
18	Exemplary C2 CDRH2 sequence	INPSNGGT
19	Exemplary C2 CDRH3 sequence	ARRGIRLRHFDY
20	Exemplary C2 CDRL1 sequence	QDVGTA
21	Exemplary C2 CDRL2	WAS

	sequence	
22	Exemplary C2 CDRL3 sequence	QQYSSYPLT
23	Exemplary C3d (3d9a) CDRH1 sequence	GYTFTAYY
24	Exemplary C3d (3d9a) CDRH2 sequence	INPYNGGT
25	Exemplary C3d (3d9a) CDRH3 sequence	SSPY
26	Exemplary C3d (3d9a) CDRL1 sequence	QSLDSDGKTY
27	Exemplary C3d (3d9a) CDRL2 sequence	LVS
28	Exemplary C3d (3d9a) CDRL3 sequence	WQGFHFPRT
29	Exemplary C3d (3d8b) CDRH1 sequence	GYTFTNYY
30	Exemplary C3d (3d8b) CDRH2 sequence	INPYNGGT
31	Exemplary C3d (3d8b) CDRH3 sequence	SSPY
32	Exemplary C3d (3d8b)	QSLDSDGKTY

	CDRL1 sequence	
33	Exemplary C3d (3d8b) CDRL2 sequence	LVS
34	Exemplary C3d (3d8b) CDRL3 sequence	WQGTHFPRT
35	Exemplary C3d (3d29) CDRH1 sequence	GYTFTDYY
36	Exemplary C3d (3d29) CDRH2 sequence	INPYNGGT
37	Exemplary C3d (3d29) CDRH3 sequence	SRGGPY
38	Exemplary C3d (3d29) CDRL1 sequence	QSLDSDGKTY
39	Exemplary C3d (3d29) CDRL2 sequence	LVS
40	Exemplary C3d (3d29) CDRL3 sequence	WQGTHFPRT
41	CR1 (1- 10)	QCNAPewLPfARPTNLTDEFEEFPIGTYLNYECRPGYSGRPFSIICLKNSVW TGAKDRCCRKSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNP GSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPGFVMKGPRRVKQCALNKWEPELPSCSRV CQPPDVLHAERTQRDKDNFS PGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLPVNLQLGAKVDFVCDDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPVPIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECPREYYGRPFSITCLDNLVWSSPKDVCKR KSCKTPDPVNGMVHVITDIQVGSRLNYSCTTGHRLLIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNP GSGGRK

		VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNK
42	CR1 (1-17)	QCNAPEWLPFARPTNLTDDEFEPPIGTYLNYECRPGYSGRPFSSIICLKNSVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNPSSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSFLFSLNEVVEFRCQPGFVMKGPRRVKQCQALNKWEPFLPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLPVNLQLGAKVDFVCDDEGFQKLGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPVPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRTGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHF FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPNPSSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRS LFSLNEVVEFRCQPGFVMKGPRRVKQCQALNKWEPFLPSCSRVCQPPPDVLH AERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVK SCDDFMGQLLNGRVLPVNLQLGAKVDFVCDDEGFQKLGSSAS YCVLAGMES LWNSSVPVCEQIFCPSPVPVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRTG TSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHF LFAKLKTQTN ASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTTPDP VNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNTAHWSTKPPIC QRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPS IYCTSNDDQVGIWSGPAPQCIIPNK
43	C2 scFv- CR1 (1-10)	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSGGGGSGGGSGGGGSDIVMTQSHKFMSTSVGDRV SITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTD FTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELKGSGGGSGGGGSCNA PEWLPFARPTNLTDDEFEPPIGTYLNYECRPGYSGRPFSSIICLKNSVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCII SGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPNP SGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILV SDNRSFLFSLNEVVEFRCQPGFVMKGPRRVKQCQALNKWEPFLPSCSRVCQPP PDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAA TCEVKSCDDFMGQLLNGRVLPVNLQLGAKVDFVCDDEGFQKLGSSAS YCVL AGMESLWNSSVPVCEQIFCPSPVPVIPNGRHTGKPLEVFPFGKTVNYTCDPH PDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHF LFAKL KTQTNASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSC KTTPDPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAAHWST KPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPNPSSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNK
44	C2 scFv- Crry	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSGGGGSGGGSGGGGSDIVMTQSHKFMSTSVGDRV SITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTD FTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELKGSGGGSGGGGSCPAP SQLPSAKPINLTDESMFPIGTYLLEYECLPGYIKRQFSITCKQDSTWTS AEDKCIRKQCKTPSDPENGLVHVHTGIQFGSRINYSCTTGHRILIGHSSAECILSGNAAHWST DQSVWDWTEAPICEWIPCEIPPGIPNGDFFSSTREDFHYGMVVTYRCNTDA RGKALFNLVGEPSLYCTSNDDGEIGVWSGPPPPQCIELNKCTPPPYVENAVML SENRSFLSLRDIVEFRCHPGFIMKGASSVHCQSLNKWEPFLPSCFKGVICR LPQEMSGFQKGLGMKKEYYYGENVTLECEDGYTLEGSSQSQCQSDGSWNPL LAKCVSRSI
45	C2-kappa light chain	DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWA STRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGT KLELKRADAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVWKIDGS ERQNGVLNSWTDQDSKDSTYSMSSTLTLTKEDEYERHNSYTCEATHKSTSTSP IVKSFNRNEC
46	C2 IgG1 Fab Heavy	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLGLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA

	chain- Crry	HPASSTKVDKKIVPRDCGGGGGSGGGGSCPAPSQLPSPAKPINLTDESMFPI GTYLLYECLPGYIKRQFSITCKQDSTWTS AEDKCIKQCKTPSPDENGVLVH VHTGIQFGSRINYTCNQGYRLIGSSSAVCVITDQSVWDTEAPICEWIPCE IPPGIPNGDFFSSTREDFHYGMVVTYRCNTDARGKALFNLVGEPSLYCTSN DGEIGVWSGPPPQCIELNKCTPPPYVENAVMLSENRSLSLRLDIVEFRCHP GFIMKGASSVHCQSLNKWEPELPSCFKGVICRLPQEMSGFQKGLGMKKEYY YGENVTLECEDGYTLEGSSQSQCQSDGSGWNPLLAKCVSRSI
47	C2 Fab heavy chain-CR1 (1-10)	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLCLVKGYFP EPVTVTNWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWVSETVTCNVA HPASSTKVDKKIVPRDCGGGGGSGGGGSCQNAPEWLPFARPTNLTDEFEPF IGTYLNYECRPGYSGRPFSSIIICLNKSVWTGAKDRCCRKSCRNPPDPVNGMV HVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVIWDNETPICDRIPC GLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTS NDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCPQ GFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPG QEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRV LFPVNLQLGAKVDFVCDEGFQLKGSSASVCVLAGMESLWNSSVPVCEQIFC PSPVPVINGRHTGKPLEVFPFGKTVNYTCDPHPDRGTSFDLIGESTIRCTS DPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYEC RPEYYGRPFSSITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVG SRINYSCTTGHRLLIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANG DFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWS GPAPQCIIPNK
48	C2 Fab heavy chain-CR1 (1-17)	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLCLVKGYFP EPVTVTNWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWVSETVTCNVA HPASSTKVDKKIVPRDCGGGGGSGGGGSCQNAPEWLPFARPTNLTDEFEPF IGTYLNYECRPGYSGRPFSSIIICLNKSVWTGAKDRCCRKSCRNPPDPVNGMV HVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVIWDNETPICDRIPC GLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTS NDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCPQ GFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPG QEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRV LFPVNLQLGAKVDFVCDEGFQLKGSSASVCVLAGMESLWNSSVPVCEQIFC PSPVPVINGRHTGKPLEVFPFGKTVNYTCDPHPDRGTSFDLIGESTIRCTS DPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYEC RPEYYGRPFSSITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVG SRINYSCTTGHRLLIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANG DFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWS GPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCPQGFVMKGPRR VKQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPGQEVFYSCEP GYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLG AKVDFVCDEGFQLKGSSASVCVLAGMESLWNSSVPVCEQIFCPSPPVING RHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWS SPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPF SITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRINYSCTT GHRLLIGHSSAECILSGNTAHWSTKPPICQRI PCGLPPTIANGDFISTNREN FHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIP NK
49	CR1 (1- 10) - C2 Fab heavy chain	QNAPEWLPFARPTNLTDEFEPF IGTYLNYECRPGYSGRPFSSIIICLNKSVW TGAKDRCCRKSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPQGFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQORDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVINGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRINYSCTTGHRLLIGHSSAECILSGNAA

		HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSSVVTYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGSGGGGSQVQLQQP GTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNINPNSNGGT NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIRLRHFDYW GQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTK VDKKIVPRDCG
50	CR1 (1- 17) - C2 Fab heavy chain	QCNAPWLPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSSIICLNKNSVW TGAKDRCCRKSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVWDNETPICDRI PCGLPPTITNGDFISTNRENFHYGSSVVTYR CNP GSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHDRGTSFDLIGESTIRCTSDPQGNVWSSPAPRCGILGHCAQPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSSVVTYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDVLH AERTQRDKNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVK SCDDFMGQLLNGRVLFVPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMES LWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKAVNYTCDPHDRGT SFDLIGESTIRCTSDPQGNVWSSPAPRCGILGHCAQPDHFLFAKLKTQTN ASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSKCTPPDP VNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNTAHWSTKPPIC QRI PCGLPPTIANGDFISTNRENFHYGSSVVTYRCNLGSRGRKV FELVGEPS IYCTSNDDQVGIWSGPAPQCIIPNKGGGSGGGGSQVQLQQPGTELVKPGA SVKLSCASGYTFTSYWMHWVKQRPQGQLEWIGNINPNSNGGTNYNEKFKSK ATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIRLRHFDYWGQGTTLTVS SAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGV HTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD CG
51	C2-IgG1 heavy chain	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS LTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVN QKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPG
52	C2-IgG1- CR1 (1- 10), HC C-term x 2	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS LTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVN QKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGGGGSGGGGSQCNAPW LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSSIICLNKNSVWTGAKDR RRKSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIISGD TVIWDNETPICDRI PCGLPPTITNGDFISTNRENFHYGSSVVTYRCNPGSGG RKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDN RSLFSLNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDV LHAERTQRDKNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCE VKSCDDFMGQLLNGRVLFVPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGM ESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDR GTSFDLIGESTIRCTSDPQGNVWSSPAPRCGILGHCAQPDHFLFAKLKTQ TNASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSKCTPP DPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAAHWSTKPP

		ICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGPAPQCIIPNK
53	C2 IgG1 heavy chain (hole) - CR1 1-10	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDDKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD KVSLSCAITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVS KLNV QKSNWEAGNTFTCSVLHEGLHNHHTTEKSLSHSPGGGGGSGGGGSGCNAPEW LPFARPTNLTDEFEFFPIGTLYLNYECRPGYSGRPFSIICLKNSVWTGAKDR RRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGD TVIWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGG RKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDN RSLFSLNEVVEFRCPGPFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDV LHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCE VKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDGEFQLKGSSASYCVLAGM ESLWNSSVPVCEQIFCPSPPIPNGRHTGKPLEVFPFGKTVNYTCDPHPD GTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQ TNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKCKTTP DPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAAHWSTKPP ICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGPAPQCIIPNK
54	C2 IgG1 heavy chain (knob)	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDDKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD KVS LWCMTDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVS KLNV QKSNWEAGNTFTCSVLHEGLHNHHTTEKSLSHSPG
55	CR1 1-10- IgG1 Fc (hole)	QCNAPEWLFPFARPTNLTDEFEFFPIGTLYLNYECRPGYSGRPFSIICLKNSVW TGAKDRCCRKRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIIISGDTV IWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS L FSLNEVVEFRCPGPFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDGEFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPIPNGRHTGKPLEVFPFGKTVNYT CDPHPD RGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KCKTTPDPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGGGSGGGGSGCKPCIC TVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE VHTAQTQPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIE KTISKTKGRPKAPQVYTIPPPKEQMAKD KVSLSCAITDFFPEDITVEWQWNG QPAENYKNTQPIMDTDGSYFVVS KLNVQKSNWEAGNTFTCSVLHEGLHNH TEKSLSHSPG
56	CR1 1-10 - C2 IgG1 heavy chain (hole)	QCNAPEWLFPFARPTNLTDEFEFFPIGTLYLNYECRPGYSGRPFSIICLKNSVW TGAKDRCCRKRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIIISGDTV IWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS L FSLNEVVEFRCPGPFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDGEFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPIPNGRHTGKPLEVFPFGKTVNYT CDPHPD RGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KCKTTPDPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRK

		VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGSGSGSGSGSQVQLQQP GTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGGLWIGNINPSNGGT NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIRLRHFDYW GQGTTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTK VDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDI SKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIHQDWLNGK EFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLSCA ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVSKLNVQKSNWEA GNTFTCSVLHEGLHNHTEKSLSHSPG
57	CR1 1-10 - C2 kappa light chain	QCNAPEWLPFARPTNLTDEFEFFPIGTLYLNYECPGYSGRPFSSIICLNKNSVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNPSSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKTTPNVEN GILVSDNRSLSLNEVVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCEDEGQQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRTGSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECPREYYGRPFISITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPSSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGSGSGSGSGSDIVMTQS HKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGV PDRFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELKRA DAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEQRNGVL NSWTDQDSKSTYSMSSTLTLTKEDEYERHNSYTCEATHKTSTSPIVKSFNR NEC
58	3d29 IgG1 Fab heavy chain	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCG
59	3d29 kappa light chain	DVVMQTPTLTLSVTIGQPASISCKSSQSLLDSGKTYLNLWLLQRPQGQSPKR LIYLVSKLESQVDPDRFTGSGSGTDFTLEISRVEAEDLGYYCQWQTHFPRT FGGGTKLEIKRADAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW KIDGSEQRNGVLNSWTDQDSKSTYSMSSTLTLTKEDEYERHNSYTCEATHK TSTSPIVKSFNRNEC
60	3d29 IgG1 Fab heavy chain - Crry	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGGGGSGGGGSCAPSPQLPSAKPINLTDESMFPIGTLYLLY ECLPGYIKRQFSITCKQDSTWTS AEDKCIKQCKTPSPDENGVLHVHTGIQ FGSRINYTCNQGYRLIGSSSAVCVITDQSVWDTEAPICEWIPCEIPPGIP NGDFFSSTREDFHYGMVVTYRCNTDARGKALFNLVGEPSLYCTSNDEIGV WSGPPPQCIELNKCTPPPYVENAVMLSENRSLSLRDIVEFRCHPGFIMKG ASSVHCQSLNKWEPELPSCFKGVICRLPQEMSGFQKGLGMKKEYYYYGENVT LECEDGYTLEGSSQSQCSQSDGSWNPLLAACVSRSI
61	3d29 IgG1 Fab heavy chain - CR1 1-10	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGGGGSGGGGSCNAPEWLPFARPTNLTDEFEFFPIGTLYL NYECPGYSGRPFSSIICLNKNSVWTGAKDRCCRKSCRNPDPVNGMVHVIKGI QFGSQIKYSCTKGYRLIGSSSATCIISGDTVWDNETPICDRIPCGLPPTI TNGDFISTNRENFHYGSVVTYRCNPSSGGRKVFELVGEPSIYCTSNDDQVG IWSGPAPQCIIPNKTTPNVENGILVSDNRSLSLNEVVEFRCPQPGFVMKG PRRVKQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYS CEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNL

		QLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPPVI PNGRHTGKPLEVFPFGKTVNYTCDPHPDRTGSFDLIGESTIRCTSDPQNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYG RPFSITCLDNLVWSSPKDVCKRKCKTTPDPVNGMVHVITDIQVGSRINYS CTTGHRLLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTN RENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQC IIPNK
62	3d29 IgG1 heavy chain murine IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWVSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFIFFPKPKDVLTTITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPTPPKEQMAKDQVSLTC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTKSLSHSPG
63	3d29 heavy chain murine IgG1 - CR1 1-10	EVQLQQSGPVLVKPGASVKMSCKASGYTFDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWVSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFIFFPKPKDVLTTITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPTPPKEQMAKDQVSLTC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTKSLSHSPGGGGGSGGGGSGCNAPEWLPFARP TNLTDEFEFPIGTLYLNYECRPGYSGRPFSIIICLKNVWVTGAKDRCCRKSCR NPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVIWDN ETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLEFSL NEVVEFRCQPGFVMKGPRRVKCALNKWEPELPSCSRVCQPPDVLHAERT QRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKSDD FMGQLLNGRVLPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWN SSVPVCEQIFCPSPPPVI PNGRHTGKPLEVFPFGKTVNYTCDPHPDRTGSFDL IGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDF PIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKCKTTPDPVNGM VHVITDIQVGSRINYSCTTGHRLLIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCT SNDDQVGIWSGPAPQCIIPNK
64	3d29 heavy chain (hole) murine IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWVSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFIFFPKPKDVLTTITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPTPPKEQMAKDQVSLSC AITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTKSLSHSPG
65	3d29 heavy chain (knob) murine IgG1 - CR1 1-10	EVQLQQSGPVLVKPGASVKMSCKASGYTFDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWVSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFIFFPKPKDVLTTITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPTPPKEQMAKDQVSLWC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTKSLSHSPGGGGGSGGGGSGCNAPEWLPFARP TNLTDEFEFPIGTLYLNYECRPGYSGRPFSIIICLKNVWVTGAKDRCCRKSCR NPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVIWDN ETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLEFSL NEVVEFRCQPGFVMKGPRRVKCALNKWEPELPSCSRVCQPPDVLHAERT

		QRDKDNFSPGQEVFYSCFPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD FMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNS SVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDFHPDRGTSFDL IGESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDF PIGTSKYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSCKTPDPVNGM VHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPICQRIIP CGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCT SNDDQVGIWSGPAPQCIIPNK
66	3d29 IgG1 heavy chain - CR1 1-10	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAQAQTNMVTGLGLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFIFFPKPKDVLITITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAFAFPAPIEKTISKTKGRPKAPQVYTIPTPKQMAKDKVSLTC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTEKSLSHSPGGGGGSGGGGSGCNAPEWLPFARF TNLTDEFEPPIGTLYLNYECRPGYSGRPFISIICLKNVSWTGAKDRCCRKSCR NPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDN ETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSL NEVVEFRCPQPGFVMKGPRRVKCAALNKWEPELPSCSRVCQPPDPVLAERT QRDKDNFSPGQEVFYSCFPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD FMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNS SVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDFHPDRGTSFDL IGESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDF PIGTSKYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSCKTPDPVNGM VHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPICQRIIP CGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCT SNDDQVGIWSGPAPQCIIPNK
67	3d8b Fab heavy chain murine IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAQAQTNMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCG
68	3d8b kappa light chain	DVMTQTPLTSLVSTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKR LIYLVSKLDSGVPRDFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHTFPRT FGGGTKLEIRRADAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW KIDGSEKQNGVLNSWTDQDSKSTYSMSSTLTLTKEDEYERHNSYTCEATHK TSTSPIVKSFNREK
69	3d8b Fab heavy chain murine IgG1 - Crry	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAQAQTNMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGGGGGSGGGGSCPAPSQLPKAPINLTDESMFPIGTLYLLYEC LPGYIKRQFSITCKQDSTWTSADKCIKQCKTPSPDENGLVHVHTGIQFG SRINYTCNQGYRLIGSSSAVCVITDQSVWDTEAPICEWIPCEIPPGIPNG DFFSSTREDFHYGMVVTYRCNTDARGKALFNLVGEPSLYCTSDNGEIGVWS GPPPQCIELNKCTPPPYVENAVMLSENRSLSLRDIVEFRCHPGFIMKGAS SVHCQSLNKWEPELPSCFKGVICRLPQEMSGFQKGLGMKKEYYYYGENVTLE CEDGYTLEGSSQSQCSQSDGSWNPLAKCVSRSI
70	3d8b Fab heavy chain	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAQAQTNMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGGGGGSGGGGSGCNAPEWLPFARPTNLTDEFEPPIGTLYLNYE CRPGYSGRPFISIICLKNVSWTGAKDRCCRKSCRNPPDPVNGMVHVIKGIQF

	murine IgG1 - CR1 1-10	GSQIKYSCTKGYRLIGSSSATCIIISGDTVWDNETPICDRIPCGLPPTITN GDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIW SGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCPGFVMMKGPR RVKQCQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCE PGYDLRGAASMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRVLFVNLQL GAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSVVPVCEQIFCPSPPVIPN GRHTGKPLEVFPFGKTVNYTCDPHPDRTGSFDLIGESTIRCTSDPQNGVW SSPAPRCGILGHCAQPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRP FSITCLDNLVWSSPKDVCKRKSCKTPDPVNGMVHVIITDIQVGSRIYNSCT TGHRLIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFISTNRE NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNK
71	3d8b Fab heavy chain murine IgG1 - fH 1-5	EVQLQQSGPVLVKPGASVKMSCKASGYTFITNYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGGGGSGGGGSEDCNELPPRRNTEILTGWSWDQTYPEGTQAI YKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTG GNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVT PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEK PKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTE SGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRG NTAKCTSTGWIPAPRCTLK
72	Control soluble factor H 1-5	EDCNELPPRRNTEILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRK EWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG QAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS QKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP NGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLK
73	3d8b heavy chain murine IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFITNYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS L T C M I T D F F P E D I T V E W Q W N G Q P A E N Y K N T Q P I M D T D G S Y F V Y S K L N V Q K S N W E A G N T F T C S V L H E G L H N H H T E K S L S H S P G
74	3d8b heavy chain murine IgG1 (knob)	EVQLQQSGPVLVKPGASVKMSCKASGYTFITNYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS L W C M I T D F F P E D I T V E W Q W N G Q P A E N Y K N T Q P I M D T D G S Y F V Y S K L N V Q K S N W E A G N T F T C S V L H E G L H N H H T E K S L S H S P G
75	3d8b heavy chain murine IgG1 (hole) - CR1 1-10	EVQLQQSGPVLVKPGASVKMSCKASGYTFITNYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS L S C A I T D F F P E D I T V E W Q W N G Q P A E N Y K N T Q P I M D T D G S Y F V V S K L N V Q K S N W E A G N T F T C S V L H E G L H N H H T E K S L S H S P G G G G G S G G G G S Q C N A P E W L P F A R P T N L T D E F E F P I G T Y L N Y E C R P G Y S G R P F S I I C L K N S V W T G A K D R C R R K S C R N P P D P V N G M V H V I K G I Q F G S Q I K Y S C T K G Y R L I G S S S A T C I I S G D T V I W D N E T P I C D R I P C G L P P T I T N G D F I S T N R E N F H Y G S V V T Y R C N P G S G G R K V F E L V G E P S I Y C T S N D D Q V G I W S G P A P Q C I I P N K C T P P N V E N G I L V S D N R S L S L N E

	[pairs with knob]	VVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRVCQPPDVLHAERTQR DKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWSPAAPTCEVKSDDFM GQLLNGRVLFVPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSV PVCEQIFCPSPPVIPNGRHTGKPLEVFPPFGKTVNYTCDPHPDRGTSFDLIG ESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPI GTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAAHWSTKPPICQRIPCG LPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSSIYCTSN DDQVGIWSGPAPQCIIIPNK
76	3d8b heavy chain murine IgG1 - CR1 1-10	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAQTNMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFIFFPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPTPKQMAKDKVSLTCMI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHTEKSLSHSPGGGGGSGGGGSQCNAPEWLPFARPTN LTDEFEFPIGTLYLNYECRPGYSGRPFSIIICLKNSVWTGAKDRCCRKSCRNP PDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWDNET PICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVG EPSIYCTSNDDQVGIWSGPAPQCIIIPNKCTPPNVENGILVSDNRSLSLNE VVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRVCQPPDVLHAERTQR DKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWSPAAPTCEVKSDDFM GQLLNGRVLFVPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSV PVCEQIFCPSPPVIPNGRHTGKPLEVFPPFGKTVNYTCDPHPDRGTSFDLIG ESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPI GTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH VITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAAHWSTKPPICQRIPCG LPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSSIYCTSN DDQVGIWSGPAPQCIIIPNK
77	3d8b kappa light chain - CR1 1-10	DVVMQTPTLTLSTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGQSPKR LIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGYYICWQGTHTFPRT FGGGTKLEIRRAADAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW KIDGSEKQNGVLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCEATHK TSTSPIVKSFNRECEGGGGSGGGGSQCNAPEWLPFARPTNLTDEFEFPIGT YLNYECRPGYSGRPFSIIICLKNSVWTGAKDRCCRKSCRNPDPVNGMVHVI KGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWDNETPICDRIPCGLP PTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSSIYCTSNDD QVGIWSGPAPQCIIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFV MKGPRRVKQALNKWEPELPSCSRVCQPPDVLHAERTQRDKDNFSPGQEV FYSCPEGYDLRGAASMRCTPQGDWSPAAPTCEVKSDDFMGQLLNGRVLF VNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPS PVIPIPNGRHTGKPLEVFPPFGKTVNYTCDPHPDRGTSFDLIGESTIRCTSDPQ GNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPE YYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHITDIQVGSRI NYSCTTGHRILIGHSSAECILSGNAAHWSTKPPICQRIPCGLPPTIANGDFI STNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSSIYCTSNDDQVGIWSGPA PQCIIIPNK
78	CR1 1-10 - 3d8b heavy chain murine IgG1	QCNAPEWLPFARPTNLTDEFEFPIGTLYLNYECRPGYSGRPFSIIICLKNSVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNPGSGGRKVFELVGEPSSIYCTSNDDQVGIWSGPAPQCIIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRV CQPPDVLHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWS PAAPTCEVKSDDFMGQLLNGRVLFVPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSCKTPPDPVNGMVHITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRK VFELVGEPSSIYCTSNDDQVGIWSGPAPQCIIIPNKGGGGSGGGGSEVQLQQS GPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVINPYNGGT

		SYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWGQGTSTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
79	CR1 1-10 - 3d8b kappa light chain	QCNAPewLPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGyRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPQPGFVMKGPRRVKQALNKWEPPELPSCSR V CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRTGSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNP GSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGSGGGGSDVMTQT PLTSLVTIGQPASISCKSSQSLDSDGKTYLNLWLQRPQGS PKRLIYLVS K LD SGVPDRFTGSGSGTDFTLKI SRVEAEDLGVIYCWQGTHTFPRTFGGG TKL EIRRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE R QNGVLNSWTDQDSKSTYSMSSTLTITLTKDEYERHNSYTCEATHKTSTSP IV KSFNRNEC
80	CR1 1-10- murine IgG1 Fc (knob)	QCNAPewLPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGyRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPQPGFVMKGPRRVKQALNKWEPPELPSCSR V CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRTGSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNP GSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGSGGGGSGCKPCIC TVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIE K TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLWCMITDFFPEDITVEWQWNG QPAENYKNTQPIMDTDGSYFVYSKLVQKSNWEAGNTFTCSVLHEGLHNH H TEKSLSHSPG
81	3d8b heavy chain murine IgG1 (hole)	EVQLQQSGPVLVKPGASVKMSCKASGYTFITNYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLSCAI T DFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPG
82	3d8b heavy chain murine	EVQLQQSGPVLVKPGASVKMSCKASGYTFITNYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLSCAI T DFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVQKSNWEAG

	IgG1 (hole) - fH 1-5	NTFTCSVLHEGLHNHHTTEKSLSHSPGGGGGSGGGGSEDCNELPPRRNTEIL TGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRP CGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWT NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEG DEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKC NMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGD EITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLK
83	3d8b heavy chain murine IgG1 - fH 1-5	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDDEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTTEKSLSHSPGGGGGSGGGGSEDCNELPPRRNTEIL TGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRP CGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWT NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEG DEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKC NMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGD EITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLK
84	3d8b kappa light chain - fH 1-5	DVVMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKR LIYLVSKLDSGVPDRFTGSGSGTDFTLTKISRVEAEDLGYYCWQGTHTFPRT FGGGTKLEIRRADAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW KIDGSEKQNGVLNSWTDQDSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHK TSTSPIVKSFNRECEGGGGSGGGGSEDCNELPPRRNTEILTGSWSDQTYPE GTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRP CGHPGDTFPGT FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKC LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGF WSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERG DAVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGDEITYQCRNGFY PATRGNTAKCTSTGWIPAPRCTLK
85	fH 1-5 - 3d8b heavy chain murine IgG1	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG QAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS QKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPIYP NGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKG GGGSGGGGSEVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHG KSLEWIGVINPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAV YFCSSPYWGQGTSTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYF PEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNV AHPASSTKVDDKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPK VTCVVVDISKDDPEVQFSWFVDDDEVHTAQTQPREEQFNSTFRSVSELPIM HQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAK DKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLN VQKSNWEAGNTFTCSVLHEGLHNHHTTEKSLSHSPG
86	fH 1-5 - 3d8b kappa light chain	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG QAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS QKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPIYP NGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKG GGGSGGGGSDVVMQTPTLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLL QRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLTKISRVEAEDLGYYC WQGTHTFPRTFGGGTKLEIRRADAAPTVISIFPPSSEQLTSGGASVVCFLNNF YPKDINVKWKIDGSEKQNGVLNSWTDQDSKDSTYSMSSTLTTLTKDEYERHN SYTCEATHKTSTSPIVKSFNRECE
87	fH 1-5 - murine	EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG QAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS

	IgG1 Fc (knob)	QKIIYKENERFQYKCNMGYEYSERGDVCTESGWRPLPSCEEKSCDNPYIP NGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKG GGSGGGSGGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVT CVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD KVS LWCMI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLN VQKSNWEAG NTFTCSVLHEGLHNHHTTEKSLSHSPG
88	3d8b heavy chain murine IgG1 Fc (hole)	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAQAQTNMVTLGCLVKGYFPEPVTVTN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVT CVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD KVS LSCAI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVS KLN VQKSNWEAG NTFTCSVLHEGLHNHHTTEKSLSHSPG
89	3d8b VH- IgG1 with T366S/M36 8A/Y407V hole Fc	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAQAQTNMVTLGCLVKGYFPEPVTVTN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVT CVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD KVS LSCAI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVS KLN VQKSNWEAG NTFTCSVLHEGLHNHHTTEKSLSHSPG
90	CR1 (1-10) -linker- IgG1 with T366W knob Fc	QCNAPEWLPFARPTNLTDEFEFPIGTLYLNYECRPGYSGRPFSSIICLN SVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKG YRLIGSSSA TCIISGDTV IWDNETPICDRIPCGLPPTITNGDFISTNRENFHYG SVVTYR CNP GSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEP ELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLPVNLQLGAKVDFVCD EGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPD RGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPF SITCLDNLVWSSPKDVCKR KSCKT PDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYG SVVTYRCNP GSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGSGGGSGGCKPCIC TVPEVSSVFI FPPKPKDVLTTITLTPKVT CVVVDISKDDPEVQFSWFVDDVE VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKD KVS LWCMI TDFFPEDITVEWQWNG QPAENYKNTQPIMDTDGSYFVYSKLN VQKSNWEAGNTFTCSVLHEGLHNH TEKSLSHSPG
91	CR1 (1- 10)-His with TEV cleavage site	QCNAPEWLPFARPTNLTDEFEFPIGTLYLNYECRPGYSGRPFSSIICLN SVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKG YRLIGSSSA TCIISGDTV IWDNETPICDRIPCGLPPTITNGDFISTNRENFHYG SVVTYR CNP GSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEP ELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLPVNLQLGAKVDFVCD EGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPD RGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPF SITCLDNLVWSSPKDVCKR KSCKT PDPVNGMVHVITDIQVGS RINYSCTTGHR LIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYG SVVTYRCNP GSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKENLYFQGH HHHHHH
92	CR1 (1- 17)-His with TEV	QCNAPEWLPFARPTNLTDEFEFPIGTLYLNYECRPGYSGRPFSSIICLN SVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKG YRLIGSSSA TCIISGDTV IWDNETPICDRIPCGLPPTITNGDFISTNRENFHYG SVVTYR CNP GSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEP ELPSCSRV

	cleavage site	CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCEGFLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFFPGKTVNYT CDPHPDRTGSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRS LFSLENEVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDVLH AERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWS PAAPTCEVK SCDDFMGQLLNGRVLFVNLQLGAKVDFVCEGFLKGSSAS YCVLAGMES LWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFFPGKAVNYTCDPHPDRTG SFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTN ASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSKCTPPDP VNGMVHVITDIQVGSRIYNSCTTGHRILGHSSAECILSGNTAHWSTKPPIC QRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPS IYCTSNDDQVGIWSGPAPQCIIPNKENLYFQGHHHHHH
93	Construct : #1aC2 C2scFv- CR1 (1- 10)-His with TEV cleavage site	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSGGGGSGGGSGGGGSDIVMTQSHKFMSTSVGDRV SITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTD FTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELKGSGGGSGGGGSCNA PEWLPFARPTNLTDEFEFPIGTLYLNYECRPGYSGRPFSIICLNKSVWTGAK DRCRRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCII SGD TVIWDNETPICDRI PCGLPPTITNGDFISTNRENFHYGSVVTYRCNPG SGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILV SDNRS LFSLENEVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPP PDVLHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWS PAA TCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCEGFLKGSSAS YCVL AGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFFPGKTVNYTCDPH PDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKL KTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSK CTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILGHSSAECILSGNAAHWST KPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNKENLYFQGHHHHHH
94	Construct : #3C2 C2scFv- Crry-His with TEV cleavage site	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSGGGGSGGGSGGGGSDIVMTQSHKFMSTSVGDRV SITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTD FTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELKGSGGGSGGGGSCPAP SQLPSAKPINLTDESMFPIGTLYLLYECLPGYIKRQFSITCKQDSTWTS AED KCIRKQCKTPSDPENGLVHVHTGIQFGSRINYTCNQGYRLIGSSSAVCVIT DQSVWDWTEAPICEWIPCEIPPGIPNGDFFSSTREDFHYGMVVITYRCNTDA RGKALFNLVGEPSLYCTSNDDGEIGVWSGPPPQCIELNKCTPPPYVENAVML SENRS LFSLRDIVEFRCHPGFIMKGASSVHCQSLNKWEPELPSCFKGVICR LPQEMSGFQKGLGMKKEYYYGENVTLECEDGYTLEGSSQSQCQSDGSWNPL LAKCVSRSIENLYFQGHHHHHH
95	Construct : #5C2 C2 IgG1 heavy chain - CR1 1-10	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWVSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLITITLTPKV TCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS LTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVN QKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGGGGSGGGGSCNAPEW LPFARPTNLTDEFEFPIGTLYLNYECRPGYSGRPFSIICLNKSVWTGAKDRC RRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGD TVIWDNETPICDRI PCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGG RKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDN RSLFSLNEVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDV LHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWS PAAPTCE

		VKSCDDFMGQLLNGRVLFPPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGM ESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDPDR GTSFDLIGESTIRCTSDPQGNVWSSPAPRCGILGHCAQPDHFLFAKLKTQ TNASDFPIGTSKLYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSKCTPP DPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAAHWSTKPP ICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGPAPQCIIPNK
96	Construct : #5C2 C2 IgG1 heavy chain - CR1 1-10	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLCLVKGYFP EPVTVTNWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDDEVHTAQTPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS LTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVN QKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGGGGGSGGGGSCQNAPEW LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFISIICLNKSVWTGAKDRC RRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGD TVIWDNETPICDRI PCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGG RKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDN RSLFSLNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDV LHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWSPAAPTCE VKSCDDFMGQLLNGRVLFPPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGM ESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDPDR GTSFDLIGESTIRCTSDPQGNVWSSPAPRCGILGHCAQPDHFLFAKLKTQ TNASDFPIGTSKLYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSKCTPP DPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAAHWSTKPP ICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGPAPQCIIPNK
97	Construct : #5C2 (hole) C2 IgG1 heavy chain (hole) - CR1 1-10 [pairs with #6C2 (knob)]	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLCLVKGYFP EPVTVTNWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDDEVHTAQTPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS LSCAITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVN QKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGGGGGSGGGGSCQNAPEW LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPFISIICLNKSVWTGAKDRC RRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGD TVIWDNETPICDRI PCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGG RKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDN RSLFSLNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDV LHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWSPAAPTCE VKSCDDFMGQLLNGRVLFPPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGM ESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDPDR GTSFDLIGESTIRCTSDPQGNVWSSPAPRCGILGHCAQPDHFLFAKLKTQ TNASDFPIGTSKLYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSKCTPP DPVNGMVHVITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAAHWSTKPP ICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGPAPQCIIPNK
98	Construct : #6C2 C2 IgG1 heavy chain	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLCLVKGYFP EPVTVTNWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDDEVHTAQTPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVS LTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVN QKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPG
99	Construct	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLCLVKGYFP

	: #6C2 (knob) C2 IgG1 heavy chain (knob) [pairs with #5C2 hole)]	EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKD KVSLWCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVN QKSNWEAGNTFTCSVLHEGLHNNHTEKSLSHSPG
100	Construct : #7C2 C2 IgG1 Fab heavy chain - Crry	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGGGGGSGGGGSCPAPSQLP SAKPINLTDESMFPI GTYLLYECLPGYIKRQFSITCKQDSTWTS AEDKCIRKQCKTPSPDENGLVH VHTGIQFGSRINYTCNQGYRLIGSSSAVCVITDQSV DWDTEAPICEWIPCE IPPGIPNGDFFSSTREDFHYGMVVTYRCNTDARGKALFNLVGEPSLYCTSN DGEIGVWSGPPPQCIELNKCTPPPYVENAVMLSENRSLSLRDIVEFRCHP GFIMKGASSVHCQSLNKWEPELPSCFKGVICRLPQEMSGFQKGLGMKKEYY YGENVTLECEDGYTLEGSSQSQCSQSDGSWNPLLAACVSRSI
101	Construct : #8aC2 C2 IgG1 Fab heavy chain - CR1 1-10	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGGGGGSGGGGSCQNAPEWLPFARPTNLTDDEFEP IGTYLNYECRPGYSGRPFSSII CLKNSVWTGAKDRCKRKS CRNPPDPVNGMV HVIKGIQFGSQIKYSCTKGYRLIGSSSATCII S GDTVWDNETPICDRIPC GLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTS NDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLSNEVVEFRCP GFVMKGPRRVKQALNKWEPELPSCSRVCQPPDPVLHAERTQRDKDNFSPG QEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRV LFPVNLQLGAKVDFVCDEGFQLKGSSASVCVLAGMESLWNSSVPVCEQIFC PSPVPIPNGRHTGKPLEVFPFGKTVNYTCDPHPD RGTSFDLIGESTIRCTS DPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTS LKYEC RPEYYGRPF SITCLDNLVWSSPKDVCKRKSCKTPPDVNGMVHVITDIQVG SRINYSCTTGHR LIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANG DFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDQVGIWS GPAPQCIIPNK
102	Construct : #8bC2 C2 IgG1 Fab heavy chain - CR1 1-17	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGGGGGSGGGGSCQNAPEWLPFARPTNLTDDEFEP IGTYLNYECRPGYSGRPFSSII CLKNSVWTGAKDRCKRKS CRNPPDPVNGMV HVIKGIQFGSQIKYSCTKGYRLIGSSSATCII S GDTVWDNETPICDRIPC GLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTS NDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLSNEVVEFRCP GFVMKGPRRVKQALNKWEPELPSCSRVCQPPDPVLHAERTQRDKDNFSPG QEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRV LFPVNLQLGAKVDFVCDEGFQLKGSSASVCVLAGMESLWNSSVPVCEQIFC PSPVPIPNGRHTGKPLEVFPFGKTVNYTCDPHPD RGTSFDLIGESTIRCTS DPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTS LKYEC RPEYYGRPF SITCLDNLVWSSPKDVCKRKSCKTPPDVNGMVHVITDIQVG SRINYSCTTGHR LIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANG

		DFISTNRENFHYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWS GPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCPQPGFVMKGPRR VKCQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEP GYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFVNLQLG AKVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNG RHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWS SPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPF SITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVHVITDIQVGSRIYNSCTT GHRILIGHSSAECILSGNTAHWSTKPPICQRI PCGLPPTIANGDFISTNREN FHYGSVVITYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIP NK
103	Construct : #10C2 (hole) CR1 1-10- IgG1 Fc (hole) [pairs with #6C2 (knob)]	QCNAPewLPfARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSIICLNsvw TGAKDRcRRKScRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVITYR CNPgSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPQPGFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVITYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGSGGGSGCKPCIC TVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDISKDDPEVQFSWFVDDVE VHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLSCAITDFFPEDITVEWQWNG QPAENYKNTQPIMDTDGSYFVVS KLVNQKSNWEAGNTFTCSVLHEGLHNHH TEKSLSHSPG
104	Construct : #11C2 (hole) CR1 1-10 - C2 IgG1 heavy chain (hole) [pa irs with #6C2 (knob)]	QCNAPewLPfARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSIICLNsvw TGAKDRcRRKScRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVITYR CNPgSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPQPGFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVITYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGSGGGSGVQLQQP GTELKPGASVKLSCKASGYTFTSYWMHWVKQRPQGGLWIGNINPNSGGT NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIRLRHFDYW GQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWSETVTCNVAHPASSTK VDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDI SKDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGK EFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLSCA ITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVS KLVNQKSNWEA GNTFTCSVLHEGLHNHTEKSLSHSPG
105	Construct : #12aC2 CR1 1-10 - C2 IgG1 Fab heavy chain	QCNAPewLPfARPTNLTDEFEFPIGTYLNYECRPGYSGRPFSIICLNsvw TGAKDRcRRKScRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVITYR CNPgSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPQPGFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVITYRCNPGSGGRK

		VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGGSGGGGSQVQLQQP GTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGT NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIRLRHFDYW GQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW NSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTK VDKKIVPRDCG
106	Construct : #12bC2 CR1 1-17 - C2 IgG1 Fab heavy chain	QCNAPewLPFARPTNLTDEFEEFPIGTYLNYECRPGYSGRPFSSIICLNKNSVW TGAKDRCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGyRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVPVNLQLGAKVDFVCDGEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTS LKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVIITDIQVGS RINYSCTTGHR LIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRVCQPPPDVLH AERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVK SCDDFMGQLLNGRVLFVPVNLQLGAKVDFVCDGEGFQLKGSSAS YCVLAGMES LWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGT SFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTN ASDFPIGTS LKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSCKTTPDP VNGMVHVIITDIQVGS RINYSCTTGHR LIGHSSAECILSGNTAHWSTKPPIC QRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPS IYCTSNDDQVGIWSGPAPQCIIPNKGGGGSGGGGSQVQLQQP GTELVKPGA SVKLSCASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTNYNEKFKSK ATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIRLRHFDYW GQGTTLTVS SAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGV HTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD CG
107	Construct : #13C2 CR1 1-10 - C2 kappa light chain	QCNAPewLPFARPTNLTDEFEEFPIGTYLNYECRPGYSGRPFSSIICLNKNSVW TGAKDRCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGyRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNP GSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRS LFS LNEVVEFRCQPGFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVPVNLQLGAKVDFVCDGEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTS LKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVIITDIQVGS RINYSCTTGHR LIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGGSGGGGS DIVMTQS HKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGV PDRFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELKRA DAAPT VSI FPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE RQNGVL NSWTDQDSKDYSTYSMSSTLTLT KDEYERHNSYTC EATHKTSTSPIVKS FNR NEC
108	Factor H (1-5)-His with TEV cleavage site	EDCNELPPRRNTEILTGSWS DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRK CQKRPCGHPGDT PFGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG QAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKVEISCKSPDVINGSPIS QKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP NGDYSPLRIKHRTGDEITYQCRNGFY PATRGNTAKCTSTGWIPAPRCTLKE NLYFQGHHHHHH
109	3d29 Fab	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYIMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY

	heavy chain murine IgG1 - Crry-His with TEV cleavage site	WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGGGGGSGGGGSCPAPSQLPSPAKPINLTDESMFFIGTYLLY ECLPGYIKRQFSITCKQDSTWTS AEDKCIKQCKTPSDPENGLVHVHTGIQ FGSRINYTCNQGYRLIGSSSAVCVITDQSVWDWTEAPICEWIPCEIPPGIP NGDFFSSTREDFHYGMVVITYRCNTDARGKALFNLVGEPSTYCTSNDDGEIGV WSGPPQCIELNKCTPPPYVENAVMLSENRSLSFLRDIVEFRCHPGFIMKG ASSVHCQSLNKWEPELPSCFKGVICRLPQEMSGFQKGLGMKKEYYYYGENVT LECEDGYTLEGSSQSQSQSDGSWNPLAKCVSRSIENLYFQGHHHHHH
110	3d29 Fab heavy chain murine IgG1 - CR1 1-10- His with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGGGGGSGGGGSCNAPEWLPFARPTNLTDEFEPPIGTYN YECRPGYSGRPFSIICLKNSVWTGAKDRCCRKSCRNPDPVNGMVHVIKGI QFGSQIKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPPTI TNGDFISTNRENFHYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVG IWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSFLNEVVEFRCPQPGFVMKG PRRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYS CEPGYDLRGAASMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRVLFVN QLGAKVDFVCDGEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVI PNGRHTGKPLEVFPPFGKTVNYTCDPHPDGRGTSFDLIGESTIRCTSDPQNG VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYG RPFSTITCLDNLVWSSPKDVCKRKSCKTPDPVNGMVHVITDIQVGSRI CTTGHRLLIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTN RENFHYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSNDDQVG IWSGPAPQC IIPNKENLYFQGHHHHHH
111	3d29 Fab heavy chain murine IgG1 - fH 1-5 with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGGGGGSGGGGSEDCNELP PRRNTEILTGWSWDQTYPEGTQ AIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTL TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPV TAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSK EKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVC TESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGDEITYQCRNGFYPAT RGNTAKCTSTGWIPAPRCTLKENLYFQGHHHHHH
112	3d29 heavy chain murine IgG1 (knob)	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLITITLTPKVT CVVD ISKDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLWC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTEKSLSHSPG
113	3d29	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI

	heavy chain murine IgG1 (hole) - fH 1-5- His with TEV cleavage site	NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWTPSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLSC AITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVS KLVNQKSNWE AGNTFTCSVLHEGLHNNHTEKSLSHSPGGGGGSGGGGSEDCNELPPRRNTE ILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQK RPCGHPGDTFFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKI EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQY KCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRT GDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKENLYFQGHHHHHH
114	3d29 heavy chain murine IgG1 - fH 1-5-His with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYIMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWTPSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVS KLVNQKSNWE AGNTFTCSVLHEGLHNNHTEKSLSHSPGGGGGSGGGGSEDCNELPPRRNTE ILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQK RPCGHPGDTFFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKI EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQY KCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRT GDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKENLYFQGHHHHHH
115	3d8b Fab heavy chain murine IgG1 - Crry with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWTPSETVTCNVAHPASSTKV DKKIVPRDCGGGGGSGGGGSCPAPSQLP SAKPINLTDESMFPIGTYYLLYEC LPGYIKRQFSITCKQDSTWTS AEDKCIKQCKTPSPDENGLVHVHTGIQFG SRINYTCNQGYRLIGSSSAVCVITDQSDVDWTEAPICEWIPCEIPPGIPNG DFFSSTREDFHYGMVVTYRCNTDARGKALFNLVGEPSLYCTSNDGEIGVWS GPPPQCIELNKCTPPPYVENAVMLSENRLSFLRDIVEFRCHPGFIMKGAS SVHCQSLNKWEPELPSCFKGVICRLPQEMSGFQKGLGMKKEYYYGENVTLE CEDGYTLEGSSQSQSQSDGSWNPLLAKCVSRSIENLYFQGHHHHHH
116	3d8b Fab heavy chain murine IgG1 - CR1 1-10-	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWTPSETVTCNVAHPASSTKV DKKIVPRDCGGGGGSGGGGSCNAPEWLFPARPTNLTDEFEPPIGTYYLNYE CRPGYSGRPFSIICLKNSVWTGAKDRCCRKSCRNPDPVNGMVHVIKGIQF GSQIKYSCTKGYRLIGSSSATCIIISGDTVWDNETPICDRIPCGLPPTITN GDFISTNRENFHYGSVVTYRCNPNPGSGGRKVFELVGEPSIYCTSNDDQVGIW SGPAPQCIIPNKCTPPNVENGILVSDNRLSFLNEVVEFRCPQPGFVMKGPR RVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCE PGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFVNLQL

	His with TEV cleavage site	GAKVDFVCDEGFQ ¹ LKGSSASYCVLAGMESLWNSSVPVCEQ ¹ IFCPSPFVIPN GRHTGKPLEVF ¹ FPFGKTVNYTCDPHPD ¹ RGTSFDLIGESTIRCTSDPQ ¹ QNGVW SSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRP FSITCLDNLVWSSPKDVCKRK ¹ SCKTPPDPVNGMVHVITDIQVGS ¹ RINYSCT TGHRLIGHSSAECILSGNAAHWSTKPPICQ ¹ RIPCGLPPTIANGDFISTNRE NFHYGSVV ¹ TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQ ¹ CII PNKENLYFQ ¹ GHHHHHH
117	3d8b Fab heavy chain murine IgG1 - fH 1-5-His with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGGGGSGGGGSEDCNELPPRRNTEILTGSWSDQTYPEGTQAI YKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTFPGTFTLTG GNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVT PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEK PKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSE ¹ RGDAVCTE SGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGDEITYQCRNGFYPATRG NTAKCTSTGWIPAPRCTLKENLYFQ ¹ GHHHHHH
118	3d8b kappa light chain - CR1 1-10- His with TEV cleavage site	DVVMQTPTLTLSTIGQPASISCKSSQSLLDSGKTYLNWLLQRPQGSPKR LIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCQWQTHFPRT FGGGTKLEIRRADAAPT ¹ VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW KIDGSE ¹ RQNGVLNSWTDQDSKDSTYSMSSTLTLTKEDEYERHNSYTCEATHK TSTSPIVKSFN ¹ RNECGGGSGGGGSCNAPEWLPFARPTNLTDEFEFFIGT YLN ¹ YECRPGYSGRPFSIIICLKNSVWTGAKDR ¹ CRRKSCRNPDPVNGMVHVI KGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVIWDNETPICDRI ¹ PCGLP PTITNGDFISTNREN ¹ FHYGSVV ¹ TYRCNPGSGGRKVFELVGEPSIYCTSNDD QVGIWSGPAPQ ¹ CIIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFV MKGPRRVK ¹ CQALNKWEPEL ¹ PSCSRVCQPPDPVLHAERTQ ¹ RDKDNFSPGQEV FYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLN ¹ GRVLF VNLQLGAKVDFVCDEGFQ ¹ LKGSSASYCVLAGMESLWNSSVPVCEQ ¹ IFCPSP PVI ¹ PNGRHTGKPLEVF ¹ FPFGKTVNYTCDPHPD ¹ RGTSFDLIGESTIRCTSDPQ GNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPE YYGRPFSITCLDNLVWSSPKDVCKRK ¹ SCKTPPDPVNGMVHVITDIQVGS ¹ R NYSCTTGHRLIGHSSAECILSGNAAHWSTKPPICQ ¹ RIPCGLPPTIANGDFI STNREN ¹ FHYGSVV ¹ TYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPA PQCIIIPNKENLYFQ ¹ GHHHHHH
119	3d8b heavy chain murine IgG1 (hole) - CR1 1-10 (pairs with #17) with TEV cleavage	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI ¹ FPKPKDVLTTITLTPKVT ¹ CVVVDIS KDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSA ¹ AFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD ¹ VSLSCAI TDFFPEDITVEWQWNGQPAENYKNTQPI ¹ MDTDGSYFVVS ¹ KLNVQKSNWEAG NTFTCSVLHEGLHNHHT ¹ TEKSLSHSPGGGGSGGGGSCNAPEWLPFARPTN LTDEFEFFIGTYLN ¹ YECRPGYSGRPFSIIICLKNSVWTGAKDR ¹ CRRKSCRNP PDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVIWDNET PICDRI ¹ PCGLPPTITNGDFISTNREN ¹ FHYGSVV ¹ TYRCNPGSGGRKVFELV EPSIYCTSNDDQVGIWSGPAPQ ¹ CIIIPNKCTPPNVENGILVSDNRSLSLNE VVEFRCQPGFVMKGPRRVK ¹ CQALNKWEPEL ¹ PSCSRVCQPPDPVLHAERTQ ¹ R DKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFM GQLLN ¹ GRVLF ¹ PNLQLGAKVDFVCDEGFQ ¹ LKGSSASYCVLAGMESLWNSSV PVCEQ ¹ IFCPSPFVIPNGRHTGKPLEVF ¹ FPFGKTVNYTCDPHPD ¹ RGTSFDLIG ESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPI GTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRK ¹ SCKTPPDPVNGMVH VITDIQVGS ¹ RINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPICQ ¹ RIPC

	site	LPPTIANGDFISTNRENFHYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSN DDQVGIWSGPAPQCIIIPNKENLYFQGHHHHHH
120	3d8b heavy chain murine IgG1 – CR1 1-10 with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTNW SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTSEKSLSHSPGGGGGSGGGGSQCNAPEWLPFARPTN LTDEFEFPITGYLNYECRPGYSGRPFSIIICLKNSVWTGAKDRCCRKSCRNP PDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWIDNET PICDRIPCGLPPTITNGDFISTNRENFHYGSVVITYRCNPGSGGRKVFELVGE EPSIYCTSNDDQVGIWSGPAPQCIIIPNKTTPNVENGILVSDNRSLSFSLNE VVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQR DKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSDDFM GQLLNGRVLFPPVNLQLGAKVDFVCDGEGQLKGSSASYCVLAGMESLWNSSV PVCEQIFCPSPPIVINGRHTGKPLEVFPFGKTVNYTCDPHDPDRGTSFDLIG ESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLLFAKLKTPQNASDFPI GTSCLKYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSCKTPDPVNGMVH VITDIQVGSRINYSCTTGHRILIGHSSAECILSGNAAHWSTKPPICQRI PCG LPPTIANGDFISTNRENFHYGSVVITYRCNPGSGGRKVFELVGEPSIYCTSN DDQVGIWSGPAPQCIIIPNKENLYFQGHHHHHH
121	3d8b heavy chain murine IgG1 – (hole) – fH 1-5 (pairs with 3d8b heavy chain murine IgG1 (knob)) with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTNW SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLSCAI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTSEKSLSHSPGGGGGSGGGGSEDCNELPPRRNTEIL TGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRP CGHPGDTPTFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWT NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEG DEEMHCSDDGFWSKEKPKCIVEISCKSPDVINGSPISQKIIYKENERFQYKC NMGYEYSERGDVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGD EITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKENLYFQGHHHHHH
122	3d8b heavy chain murine	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTNW SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMI

	IgG1 - fH 1-5 with TEV cleavage site	TDDFFEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTTEKSLSHSPGGGGGSGGGGSEDCNELPPRRNTEIL TGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKQKRP CGHPGDTFPGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWT NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCSNGYKIEG DEEMHCSDDGFWSEKPKCIVEISCKSPDVINGSPISQKLIYKENERFQYKC NMGYEYSERGDVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGD EITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKENLYFQGHHHHHH
123	CR1 1-10 - 3d8b heavy chain murine IgG1-His with TEV cleavage site	QCNAPWELPFARPTNLTDDEFEPPIGTYLNYECRPGYSGRPFSIICLNKSNVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNPSSGGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPGPFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLPVNLQLGAKVDFVCDDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGGSGGGGSEVQLQOS GPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVINPYNGGT SYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWGQTSVTV SSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSG VHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPR DCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDISKDDPEVQ FSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS AAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPED ITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSV LHEGLHNHHTTEKSLSHSPGENLYFQGHHHHHH
124	CR1 1-10 - 3d8b kappa light chain-His with TEV cleavage site	QCNAPWELPFARPTNLTDDEFEPPIGTYLNYECRPGYSGRPFSIICLNKSNVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVIWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNPSSGGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPGPFVMKGPRRVKQALNKWEPELPSCSRV CQPPPDVLHAERTQRDKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLPVNLQLGAKVDFVCDDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKR KSKCTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKGGGGSGGGGSDVMTQT PLTSLVTIGQPASISCKSSQSLDSDGKTYLNLWLLQRPQGQSPKRLIYLVSK LDGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHTFPRFTGGGTKL EIRRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVWKIDGSER QNGVLNSWTDQDSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKSTSTPIV KSFNRNECENLYFQGHHHHHH
125	3d29 heavy chain murine IgG1 - CR1 1-10	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTTEKSLSHSPGGGGGSGGGGSGCNAPEWELPFAR TNLTDEFEPPIGTYLNYECRPGYSGRPFSIICLNKSNVWTGAKDRCCRKSCR NPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVIWDN ETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSL

		NEVVEFRCQPGFVMKGPRRVKQCQALNKWEPELPSCSRVCQPPPDVLHAERT QRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD FMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNS SVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDRGTSFDL IGESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDF PIGTSCLKYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSCKTPPDPVNGM VHVITDIQVGSRINYSCTTGHRILGHSSAECILSGNAAHWSTKPPICQRIIP CGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCT SNDDQVGIWSGPAPQCIIPNK
126	3d29 heavy chain murine IgG1 - CR1 1-10 +His tag	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAQAQTNMSMTLGLCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHTEKSLSHSPGGGGGSGGGGSQCNAPEWLPFARP TNLTDEFEFPIGTLYLNYECRPGYSGRPFSIIICLKNSVWTGAKDRCCRKSCR NPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWDN ETPICDRI PCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSL NEVVEFRCQPGFVMKGPRRVKQCQALNKWEPELPSCSRVCQPPPDVLHAERT QRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD FMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNS SVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDRGTSFDL IGESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDF PIGTSCLKYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSCKTPPDPVNGM VHVITDIQVGSRINYSCTTGHRILGHSSAECILSGNAAHWSTKPPICQRIIP CGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCT SNDDQVGIWSGPAPQCIIPNKHSHHHHH
127	3d29 heavy chain murine IgG1 (knob) - CR1 1-10 +His tag	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAQAQTNMSMTLGLCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLWC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHTEKSLSHSPGGGGGSGGGGSQCNAPEWLPFARP TNLTDEFEFPIGTLYLNYECRPGYSGRPFSIIICLKNSVWTGAKDRCCRKSCR NPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWDN ETPICDRI PCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEL VGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSL NEVVEFRCQPGFVMKGPRRVKQCQALNKWEPELPSCSRVCQPPPDVLHAERT QRDKDNFSPGQEVFYSCPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDD FMGQLLNGRVLFPVNLQLGAKVDFVCDEGFQLKGSSASYCVLAGMESLWNS SVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDRGTSFDL IGESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDF PIGTSCLKYECRPEYYGRPFISITCLDNLVWSSPKDVCKRKSCKTPPDPVNGM VHVITDIQVGSRINYSCTTGHRILGHSSAECILSGNAAHWSTKPPICQRIIP CGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCT SNDDQVGIWSGPAPQCIIPNKHSHHHHH
128	3d8b kappa light chain - fH 1-5-	DVVMQTPLTSLVSTIGQPASISCKSSQSLLDSGKTYLNLWLLQRPQGSPKR LIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCQWQGHFPRT FGGGTKLEIRRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKW KIDGSEKQNGVLNSWTDQDSKDSTYSMSSTLTLTKEDEYERHNSYTCEATHK TSTSPIVKSFNRECGGGGSGGGGSEDCNELPPRRNTEILTGSWSDDQTYPE GTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCKQKRCGHPGDTFPFGT FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKC LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGF WSKEKPKVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSEKRGD AVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGDEITYQCRNGFY

	His with TEV cleavage site	PATRGNTAKCTSTGWIPAPRCTLKENLYFQGHHHHHH
129	fH 1-5 - 3d8b kappa light chain-His with TEV cleavage site	EDCNELPPRRNTEILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFFGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG QAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEISCKSPDVINGSPIS QKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP NGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKG GGSGGGGSDVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLL QRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKRVEAEDLGYYC WQGTHTFPRTFGGGTKLEIRRADAAPTIVSIFPPSSEQLTSGGASVVCFLNMF YPKDINVKKIDGSEKQNGVLNSWTDQDSKSTYSMSSTLTTLTKDEYERHN SYTCEATHKTSTSPIVKSFNNECENLYFQGHHHHHH
130	CR1 1-10- murine IgG1 Fc (knob)	QCNAPWELPFARPTNLTDDEFEPFIGTYLNYECRPGYSGRPFSIICLNKNSVW TGAKDRCCRKSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGVSVTYR CNPFGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIIPNKCTPPNVEN GILVSDNRSLSFSLNEVVEFRCPQPGFVMKGPRRVKQALNKWEPELPSCSRVC QPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSDDDFMGQLLNGRVLFVNLQLGAKVDFVCEGFLQKGSAS YCVLAGMESLWNSSVPVCEQIFCPSPVPIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRTGSFDLIGESTIRCTSDPQNGVWSSPAPRCGLGHQCAPDHFL FAKLKTQTNASDFPIGTSKYECPREYGRPFSITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVITDIQVGSRIYNSCTTGHRILGHSSAECILSGNAA HWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGVSVTYRCNPFGSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIIPNKGSGGGGSGGCKPCIC TVPEVSSVFIFFPKPKDVLITITLTPKVTCVVVDISKDDPEVQFSWFVDDVE VHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLWCMITDFFPEDITVEWQWNG QPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVLHEGLHNHH TEKSLSHSPG
131	fH 1-5 - murine IgG1 Fc (knob)	EDCNELPPRRNTEILTGWSWDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG EWVALNPLRKCQKRPCGHPGDTFFGTFTLTGGNVFEYGVKAVYTCNEGYQL LGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFG QAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCWEISCKSPDVINGSPIS QKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP NGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKG GGSGGGGSGCKPCICTVPEVSSVFIFFPKPKDVLITITLTPKVTCVVVDIS KDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLWCMIT DFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTKSLSHSPG
132	3d8b Fab heavy chain murine IgG1 - CR1 1-17	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTVSSAKTTPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTN SGSLSSGVHTFPAVLQSDLYTLSSSVTPSSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGGGGGSGGGGSCNAPEWLPFARPTNLTDDEFEPFIGTYLNYE CRPGYSGRPFSIICLNKNSVWTGAKDRCCRKSCRNPPDPVNGMVHVIKGIQF GSQIKYSCTKGYRLIGSSSATCIISGDTVWDNETPICDRIPCGLPPTITN GDFISTNRENFHYGVSVTYRCNPFGSGGRKVFELVGEPSIYCTSNDDQVGIW SGPAPQCIIIPNKCTPPNVENGILVSDNRSLSFSLNEVVEFRCPQPGFVMKGPR RVKQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCE PGYDLRGAASMRCTPQGDWSAPAPTCEVKSDDDFMGQLLNGRVLFVNLQL

	with TEV cleavage site	GAKVDFVCDEGFQ ¹ LGSSAS ² YCVLAGMESLWNSSVPVCEQ ³ IFCPSP ⁴ PPVIPN GRHTGKPLEVFPFGKTVNYTCDPHDRGTSFDLIGESTIRCTSDPQNGVW SSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRP FSITCLDNLVWSSPKDVCKRK ⁵ SCKT ⁶ PPDPVNGMVHVITDIQVGS ⁷ RINYSCT TGHRLIGHSSAECILSGNAAHWSTKPPICQ ⁸ RIPCGLPPTIANGDFISTNRE NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQ ⁹ CII PNKCTPPNVENGILVSDNRS ¹⁰ LFSLNEVVEFRCQPGFVMKGPRRVK ¹¹ CQALNK WEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSC ¹² EPGYDLRGA SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLF ¹³ FPVNLQLGAKVDFVCD EGFQ ¹⁴ LGSSAS ¹⁵ YCVLAGMESLWNSSVPVCEQ ¹⁶ IFCPSP ¹⁷ PPVIPNGRHTGKPLE VFPFGKAVNYTCDPHDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGI LGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSITCLDNL VWSSPKDVCKRK ¹⁸ SCKT ¹⁹ PPDPVNGMVHVITDIQVGS ²⁰ RINYSCTTGHRLIGH SAECILSGNTAHWSTKPPICQ ²¹ RIPCGLPPTIANGDFISTNREN ²² FHYGSVV TYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQ ²³ CII ²⁴ PNKENLYFQ GHHHHHH
133	3d8b heavy chain murine IgG1 (hole) - CR1 1-17 (pairs 3d8b heavy chain murine IgG1 (knob)) with TEV cleavage site	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTW ²⁵ SETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI ²⁶ FPKPKDVLTTITLTPKVT ²⁷ CVVDIS KDDPEVQFSWFVDDVEVHTAQ ²⁸ TQPREEQFNSTFRSVSELPI ²⁹ MHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP ³⁰ PPKEQMAKD ³¹ KVSLSCAI TDFFPEDITVEWQWNGQPAENYKNTQ ³² PIMDTDGSYFV ³³ VSKLN ³⁴ VQKSNWEAG NTFTCSVLHEGLHNHHT ³⁵ TEKSLSHSPGGGGGSGGGGSQCNAPEWLPFARPTN LTDEFEFPIGT ³⁶ YLN ³⁷ YECRPGYSGRPFSII ³⁸ CLKNSVWTGAKDR ³⁹ CRRKSCRNP PDPVNGMVHVIKGIQFGS ⁴⁰ QIKY ⁴¹ SCTKGYRLIGSSSATCII ⁴² SGD ⁴³ TVIWDNET PICDRI ⁴⁴ PCGLPPTITNGDFISTNREN ⁴⁵ FHYGSVVTYRCNPGSGGRKVFELV EPSIYCTSNDDQVGIWSGPAPQ ⁴⁶ CII ⁴⁷ PNKCTPPNVENGILVSDNRS ⁴⁸ LFSLNE VVEFRCQPGFVMKGPRRVK ⁴⁹ CQALNKWEPELPSCSRVCQPPPDVLHAERTQR DKDNFSPGQEVFYSC ⁵⁰ EPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFM GQLLNGRVLF ⁵¹ FPVNLQLGAKVDFVCDEGFQ ⁵² LGSSAS ⁵³ YCVLAGMESLWNSSV PVCEQ ⁵⁴ IFCPSP ⁵⁵ PPVIPNGRHTGKPLEVFPFGKTVNYTCDPHDRGTSFDLIG ESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPI GTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRK ⁵⁶ SCKT ⁵⁷ PPDPVNGMVH VITDIQVGS ⁵⁸ RINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPICQ ⁵⁹ RIPC GLPPTIANGDFISTNREN ⁶⁰ FHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSN DDQVGIWSGPAPQ ⁶¹ CII ⁶² PNKCTPPNVENGILVSDNRS ⁶³ LFSLNEVVEFRCQPG FVMKGPRRVK ⁶⁴ CQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQ EVFYSC ⁶⁵ EPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVL FPVNLQLGAKVDFVCDEGFQ ⁶⁶ LGSSAS ⁶⁷ YCVLAGMESLWNSSVPVCEQ ⁶⁸ IFCP SPPVIPNGRHTGKPLEVFPFGKAVNYTCDPHDRGTSFDLIGESTIRCTSD PQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYECR PEYYGRPFSITCLDNLVWSSPKDVCKRK ⁶⁹ SCKT ⁷⁰ PPDPVNGMVHVITDIQVGS RINYSCTTGHRLIGHSSAECILSGNTAHWSTKPPICQ ⁷¹ RIPCGLPPTIANGD FISTNREN ⁷² FHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSG PAPQ ⁷³ CII ⁷⁴ PNKENLYFQ ⁷⁵ GHHHHHH
134	3d8b heavy chain murine IgG1 - CR1 1-17 with TEV cleavage	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTW ⁷⁶ SETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI ⁷⁷ FPKPKDVLTTITLTPKVT ⁷⁸ CVVDIS KDDPEVQFSWFVDDVEVHTAQ ⁷⁹ TQPREEQFNSTFRSVSELPI ⁸⁰ MHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP ⁸¹ PPKEQMAKD ⁸² KVSLTCMI TDFFPEDITVEWQWNGQPAENYKNTQ ⁸³ PIMDTDGSYFV ⁸⁴ YSKLN ⁸⁵ VQKSNWEAG NTFTCSVLHEGLHNHHT ⁸⁶ TEKSLSHSPGGGGGSGGGGSQCNAPEWLPFARPTN LTDEFEFPIGT ⁸⁷ YLN ⁸⁸ YECRPGYSGRPFSII ⁸⁹ CLKNSVWTGAKDR ⁹⁰ CRRKSCRNP PDPVNGMVHVIKGIQFGS ⁹¹ QIKY ⁹² SCTKGYRLIGSSSATCII ⁹³ SGD ⁹⁴ TVIWDNET PICDRI ⁹⁵ PCGLPPTITNGDFISTNREN ⁹⁶ FHYGSVVTYRCNPGSGGRKVFELV EPSIYCTSNDDQVGIWSGPAPQ ⁹⁷ CII ⁹⁸ PNKCTPPNVENGILVSDNRS ⁹⁹ LFSLNE VVEFRCQPGFVMKGPRRVK ¹⁰⁰ CQALNKWEPELPSCSRVCQPPPDVLHAERTQR DKDNFSPGQEVFYSC ¹⁰¹ EPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFM GQLLNGRVLF ¹⁰² FPVNLQLGAKVDFVCDEGFQ ¹⁰³ LGSSAS ¹⁰⁴ YCVLAGMESLWNSSV

	site	PVCEQIFCPSPPPVIPNGRHTGKPLEVFPPFGKTVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQKLGSSASVCVLAGMESLWNSSVPVCEQIFCPSPPPVIPNGRHTGKPLEVFPPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNTAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKENLYFQGHHHHHH
135	3d8b kappa light chain - CR1 1-17 with TEV cleavage site	DVVMQTQPLTSLVTIGQPASISCKSSQSLLDSGKTYLNLWLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLTKISRVEAEDLGYYCQWQTHFPRTFGGGTKLEIRRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLNSWTDQDSKSTYSMSSTLTLTKEDEYERHNSYTCEATHKTSTSPIVKSFNNECGGGGSGGGGSCNAPEWLPFARPTNLTDDEFEPPIGTYLNYECRPGYSGRPFSSICLKNSVWTGAKDRCKRKRSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQKLGSSASVCVLAGMESLWNSSVPVCEQIFCPSPPPVIPNGRHTGKPLEVFPPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQKLGSSASVCVLAGMESLWNSSVPVCEQIFCPSPPPVIPNGRHTGKPLEVFPPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNTAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKENLYFQGHHHHHH
136	CR1 1-17 - 3d8b heavy chain murine IgG1 with TEV cleavage site	QCNAPWLPFARPTNLTDDEFEPPIGTYLNYECRPGYSGRPFSSICLKNSVWTGAKDRCKRKRSCRNPPDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQKLGSSASVCVLAGMESLWNSSVPVCEQIFCPSPPPVIPNGRHTGKPLEVFPPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQORDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDEGFQKLGSSASVCVLAGMESLWNSSVPVCEQIFCPSPPPVIPNGRHTGKPLEVFPPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSCLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNTAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKENLYFQGHHHHHH

		IYCTSNDDQVGIWSGPAPQCIIPNKGGGGSGGGGSEVQLQQSGPVLVKPGA SVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVINPYNGGTSYNQKFKGK ATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWGQGTSTVTSSAKTTPPS VYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQ SDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIVPRDCGCKPCIC TVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDISKDDPEVQFSWFVDDVE VHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNG QPAENYKNTQPIMDTDGSYFVYSKLVNQKSNWEAGNTFTCSVLHEGLHNNHH TEKSLSHSPGENLYFQGHNNHHH
137	CR1 1-17 - 3d8b kappa light chain-His with TEV cleavage site	QCNAPWELPFARPTNLTDEFEFPIGTLYLNYECRPGYSGRPFSSIICLNKSVW TGAKDRCCRKSCRNPDPVNGMVHVIKGIQFGSQIKYSCTKGRLIGSSSA TCIISGDTVWDNETPICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYR CNPSSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVEN GILVSDNRSLSLNEVVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRV CQPPDPVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVKSCDDFMGQLLNGRVLFVNLQLGAKVDFVCDDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYT CDPHPDRGTSFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFL FAKLKTQTNASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKR KSCKTTPDPVNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNAA HWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNPNSSGGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRS LFSLSNEVVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPDPVLH AERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDWS PAAPTCEVK SCDDFMGQLLNGRVLFVNLQLGAKVDFVCDDEGFQLKGSSAS YCVLAGMES LWNSSVPVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGT SFDLIGESTIRCTSDPQNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTN ASDFPIGTSLKYECRPEYYGRPFSSITCLDNLVWSSPKDVCKRKSCKTTPDP VNGMVHVITDIQVGSRIYNSCTTGHRILIGHSSAECILSGNTAHWSTKPPIC QRI PCGLPPTIANGDFISTNRENFHYGSVVTYRCNLGSRGRKVFELVGEPS IYCTSNDDQVGIWSGPAPQCIIPNKGGGGSGGGGSDVVMVTQPTLTLSTVIG QPASISCKSSQSLLDSDGKTYLNLWLLQRPGQSPKRLIYLVS KLDSGVDPDRF TGSGSGTDFTLKI SRVEAEDLGYYCQWQGTHTFRTFGGGTKLEIRADAAP TVSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVLNSWT DQDSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNECE NLYFQGHNNHHH
138	Exemplary linker	GGGGSGGGGS
139	Heavy chain: VH-IgG1 with T366S/M36 8A/Y407V hole Fc- linker- factor H	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLSCAI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVNQKSNWEAG NTFTCSVLHEGLHNNHTEKSLSHSPGGGGSGGGGSEDCNELPPRRNTEIL TGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRP CGHPGDTFFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWT NDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEG DEEMHCSDDGFWFSKEKPKCEVISCKSPDVINGSPISQKIIYKENERFQYKC NMGYEYSERGDVCTESGWRPLPSCEEKSCDNPIYPNGDYSPLRIKHRTGD EITYQCRNGFYF PATRGNTAKCTSTGWIPAPRCTLK
140	Heavy Chain: VH-IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS

	with T366W knob Fc- linker- CR1 (1- 10)	KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLWCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPGGGGGSGGGGSGCNAPEWLPFARPTNLTDEFEFPITGYLNYECPGYSGRPFSSIIICLNKSNVWTGAKDRCCRKSCRNP PDPVNGMVHVIKGIQFGSQIKYSCTKGYRLIGSSSATCIIISGDTVWDNET PICDRIPCGLPPTITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVG EPSIYCTSNDDQVGIIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSFLSNE VVEFRCPQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQR DKDNFSPGQEVFYSCPEGYDLRGAASMRCTPQGDWSPAAPTCEVKSDDDFM GQLLNGRVLFPVNLQLGAKVDFVCDGEGFQLKGSSASYCVLAGMESLWNSSV PVCEQIFCPSPPVIPNGRHTGKPLEVFPFGKTVNYTCDPHPDRTGTSFDLIG ESTIRCTSDPQGNVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPI GTSLSKYECRPEYYGRPFSSITCLDNLVWSSPKDVCCKRKSCTPPDPVNGMVH VITDIQVGSRIYNSCTTGHRLLIGHSSAECILSGNAAHWSTKPPICQRIPCG LPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSN DDQVGIIWSGPAPQCIIPNK
141	Heavy Chain: VH- muIgG1- linker- DAF (1-4)	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMI TDDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPGGGGGSGGGGSDCGLPDPVNAQPAL EGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEV PTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKW STAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSS FCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYAC NKGFTMIGEHSIYCTVNNDGEWEGSPPPECRG
142	Heavy Chain: VH- muIgG1- linker- CD59	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMI TDDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPGGGGGSGGGGSLQCYNCNPNTADCKT AVNCSSDFDACLITKAGLQVYNKCWKFEHCNFDVTTTLRENELTYCCKK DLCNFNEQLEN
143	Heavy Chain: VH- muIgG1- linker- Map44	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS KDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMI TDDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNHHTEKSLSHSPGGGGGSGGGGSHTELNNMFGQIQSP GYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQ VLATFCGRETTDTEQTPGQEVVLSPGSFMSITFRSDFSNEERFTGFDAYM AVDVDECKEREDEELSCDHYCHNYIGGYCSCRFGYILHTDNRTCRVECS DLFTQRTGVITSPDFPNPYPKSSECLYTIIELEEGFMVNLQFEDIFDIEDHP EVPCPYDIKIKVGPVKVLGPFCEGEKAPEISTQSHSVLILFHSNDNSGENRG WRLSYRAAGNECPQLPPVHGKIEPSQAKYFFKQVVLVSCDTGYKVLKDNV EMDTFQIECLKDGTSWNKIPTCKKNEIDLESELKSEQVTE
144	Heavy Chain:	EVQLQQSGPVLVKPGASVKMSCKASGYTFTNYYINWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWG QGTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTGLGLVKGYFPEPVTVTWN SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKV DKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVDIS

	VH-muIgG1 - linker - MCP 1-4	KDDPEVQFSWFVDDVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKE FKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMI TDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAG NTFTCSVLHEGLHNNHTEKSLSHSPGGGGGSGGGGSCEEPPTFEAMELIGK PKPYEIGERVDYKCKKGYFYIPPLATHHTICDRNHTWLPVSDDACYRETCP YIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWS GKPPICEKVLCTPPPKIKNGKHTFSEVEVFEYLDVITYSCDPAPGDPFSL IGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGGKQISGFGKKFYKATVM FECDKGFYLDGSDTIVCDNSTWDPPVPKCLK
145	Exemplary anti-C3d antibody, C8D3, heavy chain sequence	QAYLQQSGAELVRPGASVKMSCKASGYTFTSYMHVVKQTPRQGLEWIGAI YPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCAKGFY WGQGTTVTVSS
146	Exemplary anti-C3d antibody, C8D3, light chain sequence	DVVMQTPLSLPVSLGDQASISCRSSQSLVYSNGNTYLHWYLOKPGQSPKL LIYKVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYT FGGGTKLEIKR
147	Exemplary anti-C3d antibody, C8D3, CDRH1	GYTFTSYY
148	Exemplary anti-C3d antibody, C8D3, CDRH2	IYPGNGDT
149	Exemplary anti-C3d antibody, C8D3,	AKGFYD

	CDRH3	
150	Exemplary anti-C3d antibody, C8D3, CDRL1	QSLVYSNGNTY
151	Exemplary anti-C3d antibody, C8D3, CDRL2	KVS
152	Exemplary anti-C3d antibody, C8D3, CDRL3	SQSTHVPYT
153	Exemplary anti-C3d antibody, C6, heavy chain sequence	QAYLQQSGAELVRPGASVKMSCKASGYTFTSYMHVVKQTTPRQGLEWIGAI YPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCAKYGSG YWGQGTITVTVSS
154	Exemplary anti-C3d antibody, C6, light chain sequence	DVVMQTQTPSLPVSLGDAQASISCRSSQSLVYSNGNTYLHWYLQKPGQSPKL LIYKVSNRFGVPDRFSGSGGTDFTLKISRVEAEDLGVIYFCSQSTHVPYT FGGGTKLEIKR
155	Exemplary anti-C3d antibody, C6, CDRH1	GYTFTSYY
156	Exemplary	IYPGNGDT

	anti-C3d antibody, C6, CDRH2	
157	Exemplary anti-C3d antibody, C6, CDRH3	AKYGSGY
158	Exemplary anti-C3d antibody, C6, CDRL1	QSLVYSNGNTY
159	Exemplary anti-C3d antibody, C6, CDRL2	KVS
160	Exemplary anti-C3d antibody, C6, CDRL3	SQSTHVPYT
161	Linker	(G) _n
162	Linker	KESGSVSSEQLAQFRSLD
163	Linker	EGKSSSGSGSESKST
164	Linker	(GGGGS) _n
165	Linker	(EAAAK) _n
166	Linker	A(EAAAK) _n A
167	Linker	GSAGSAAGSGEF
168	Linker	(XP) _n
169	Linker	A(EAAAK) ₄ ALEA(EAAAK) ₄ A
170	Linker	(PAS) _n
171	Linker	(GS) _n
172	Linker	GGGGSLVPRGSGGGGS

173	Linker	GGSGGHMGSGG
174	Linker	(GGS) _n
175	Linker	GGSGGGGG
176	Linker	GGGSEGGGSEGGGSE
177	Linker	AAGAATAA
178	Linker	GGSSG
179	Linker	(GT) _n
180	Linker	GSSSG
181	Linker	GSGGGTGGGSG
182	Linker	GSGGSGGSGGSGS
183	Linker	GSGSGSGSGGSG
184	DAF 1-4	DCGLPPDVPNAQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGS QWSDIEEFNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRRE PSLSPKLTCLQNLKWSSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATIS FSCNTGYKLFGSTSSFCCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQG ERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPPECRG
185	CD59	LQCYNCPNPTADCKTAVNCSSDFDACLITKAGLQVYNKCWKFEHCNFDVT TRLRENELTYCCKKDLNCFNEQLEN
186	Map44	HTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESS YLCEYDYVKVETEDQVLATFCGRETDTDEQTPGQEVVLSPGSFMSTIFRSD FSNEERFTGFDAHYMAVDVDECKEREDEELSCDHYCHNYIGGYCSCRFGY ILHTDNRTCRVECDNLFTQRTGVITSPDFPNYPKSSECLYTIELEEGFM VNLQFEDIFDIEDHPEVPCPYDIKIKVGPVKVLGPFCEKAPEPISTQSHS VLILFHSDNSGENRGWRLSYRAAGNECPQLQPPVHGKIEPSQAKYFFKDQV LVSCDTGYKVLKDNVEMDTFQIECLKDGTWSNKIPTCKKNEIDLESELKSE QVTE
187	MCP 1-4	CEEPPTFEAMELIGKPKPYEIGERVDYKCKKGYFYIPPLATHITICDRNHT WLPVSDDACYRETCPIYIRDPLNGQAVPANGTYEFGYQMHFICNEGYLIGE EILYCELKGSVAIWGKPPICEKVLCTPPPDKNGKHTFSEVEVFEYLDVAV TYSKDPAGPDPFSLIGESTIYCGDNSVWSRAAPECKVVKCRFPVVENGGKQ ISGFGKKFYKATVMFECDKGFYLDGSDTIVCDNSNSTWDPPVPKCLK
188	Exemplary anti-C3d antibody 3d3, CDRH1	GHSFTNYL
189	Exemplary anti-C3d antibody 3d3, CDRH2	INPGSGGT
190	Exemplary anti-C3d antibody 3d3, CDRH3	ASYYSNSYAMDY

191	Exemplary anti-C3d antibody 3d3, CDRL1	ENIYSY
192	Exemplary anti-C3d antibody 3d3, CDRL2	KAK
193	Exemplary anti-C3d antibody 3d3, CDRL3	QHHYGIPYT
194	Exemplary anti-C3d antibody 3d3, Heavy chain variable region	QVQLQQSGAELVRPGTSVKVSCKASGHSFTNYLIEWVKQRPQGQLEWIGVI NPGSGGTNYNEKFKVKATLTADKSSSTAYMQLSSLTSEDSAVYFCASYYSN SYAMDYWGQGTSVTVSS
195	Exemplary anti-C3d antibody 3d3, Light chain variable region	DIQMTQSPASLSASVGETVTIACRASENIYSYLAWYLQKEGKSPQLLVSKA KTLADGVPSRFSGGSGTQFSLKINSLQPEDFGTFYCQHHYGIPYTFGGGT KLEIK
196	Exemplary anti-C3d antibody 3d10, CDRH1	GYAFAHYL
197	Exemplary anti-C3d antibody 3d10, CDRH2	INPGTDGT
198	Exemplary anti-C3d antibody 3d10, CDRH3	AREELGFAY
199	Exemplary	QDISNH

	anti-C3d antibody 3d10, CDRL1	
200	Exemplary anti-C3d antibody 3d10, CDRL2	YIS
201	Exemplary anti-C3d antibody 3d10, CDRL3	QQGDTLPYT
202	Exemplary anti-C3d antibody 3d10, Heavy Chain variable region	QVQLQQSGAELVRPGTSVKVSCASGYAFAHYLIEWVKQRPQGQLEWIGVI NPGTDGTNYNEKFKGKATLTADKSSSTAYMHLSSLTSEDSAVYFCAREELG FAYWGQGTLLTVSA
203	Exemplary anti-C3d antibody 3d10, Light chain variable r	DIQMTQSTSSLSASLGDRVTISCRASQDISNHLNHWYQQRPDGTVKLLIYYI SRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGDTLPYTFGGGT TLEIR
204	Exemplary anti-C3d antibody 3d11, CDRH1	GYTFTSY
205	Exemplary anti-C3d antibody 3d11, CDRH2	SDPSDTYT
206	Exemplary anti-C3d antibody 3d11, CDRH3	ARPGRVAYYFDY
207	Exemplary anti-C3d antibody	QSLVHSNGNTY

	3d11, CDRL1	
208	Exemplary anti-C3d antibody 3d11, CDRL2	KVS
209	Exemplary anti-C3d antibody 3d11, CDRL3	FQGSHPPT
210	Exemplary anti-C3d antibody 3d11, Heavy chain variable region	QVQLQQPGAELVRPGTSVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGVS DPSDTYTKNNQKFTGKATLTVDTSSTAYMQLSSLTSEDSAVYYCARPGRV AYYFDYWGQGTTTLTVSS
211	Exemplary anti-C3d antibody 3d11, Light chain variable region	DVLMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLEWYLQKPGQSPKL LIYKVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPPT FGGGTKLEIK
212	Exemplary anti-C3d antibody 3d15, CDRH1	GYAFTNYL
213	Exemplary anti-C3d antibody 3d15, CDRH2	INPGSGGT
214	Exemplary anti-C3d antibody 3d15, CDRH3	ATYYSNSFAMDY
215	Exemplary anti-C3d antibody	QSLNSSNQKNY

	3d15, CDRL1	
216	Exemplary anti-C3d antibody 3d15, CDRL2	FAS
217	Exemplary anti-C3d antibody 3d15, CDRL3	QQYYSIPFT
218	Exemplary anti-C3d antibody 3d15, Heavy chain variable region	QVQLQQSGAELVRPGTSVKVSKASGYAFTNYLIEWIKQRPQGQLEWIGVINPGSGGTNYNEKFKGKATLTADKSSNTAYMHLSSLTSEDSAVYFCATYYNSFAMDYWGQGTSTVTVSS
219	Exemplary anti-C3d antibody 3d15, Light chain variable region	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNSSNQKNYLAWYQQKPGQCPKVLVYFASTRESGVPDRFIGSGSGTDFTLTISVQAEDLADYFCQQYYSIPFTFGSGTKLEIK
220	Exemplary anti-C3d antibody 3d16, CDRH1	GYAFAHYL
221	Exemplary anti-C3d antibody 3d16, CDRH2	INPGTDGT
222	Exemplary anti-C3d antibody 3d16, CDRH3	AREELGFAY
223	Exemplary anti-C3d antibody	QDISNH

	3d16, CDRL1	
224	Exemplary anti-C3d antibody 3d16, CDRL2	YIS
225	Exemplary anti-C3d antibody 3d16, CDRL3	QQGDTLPYT
226	Exemplary anti-C3d antibody 3d16, Heavy chain variable region	QVQLQQSGAELVRPGTSVKVSKASGYAFAHYLIEWVKQRPGQGLEWIGVINPGTDGTNYNEKFKGKATLTADKSSSTAYMHLSSLTSEDSAVYFCAREELGFAYWGQGTLLTVSA
227	Exemplary anti-C3d antibody 3d16, Light chain variable region	DIQMTQSTSSLSASLGDRVTISCRASQDISNHLNHWYQQRPDGTVKLLIYYISRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGDTLPYTFGGGT TLEIR
228	Exemplary anti-C3d antibody 3d31, CDRH1	GYSFTDYN
229	Exemplary anti-C3d antibody 3d31, CDRH2	INPNYGGT
230	Exemplary anti-C3d antibody 3d31, CDRH3	ARNDY
231	Exemplary anti-C3d antibody	QSIVHSNGNTY

	3d31, CDRL1	
232	Exemplary anti-C3d antibody 3d31, CDRL2	KVS
233	Exemplary anti-C3d antibody 3d31, CDRL3	FQGSHPFT
234	Exemplary anti-C3d antibody 3d31, Heavy chain variable region	EFQLQQSGPELVKPGASVKLSCKASGYSFTDYNMNWVKQSNKGKLEWIGVI NPNYGTTFYNQKFKGKATLTVDQSSSTAYMQLNSLTSEDSAVYYCARNDYW GRGTTTLTVSS
235	Exemplary anti-C3d antibody 3d31, Light chain variable region	DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLDWYLQRPQGSPKL LIYKVSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHVPFT FGSGTKLEIK
236	Kabat EU C222S muIgG1 Fc	VPRDSGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCTVVVDI SKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQD WLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQM AKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSY FVYSKLVNQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
237	Kabat EU S228P/ L235E huIgG4	ESKYGPCCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSLG
238	C2 IgG1 heavy chain (hole)	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAQAQTNMVTGLCLVKGYFP EPVTVTWNSSGLSSGVHTFPAVLQSDLYTLSSSVTPSSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKV TCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMH QDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKD KVSLSCAITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVVSCLNV QKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
239	C2 scFv	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPQGQLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGQGTTLTVSSGGGGSGGGSGGGGSDIVMTQSHKFMSTSVGDRV SITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTD

		FTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELK
240	C2 Fab	QVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNI NPSNGGTNYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARRGIR LRHFDYWGGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPE EPVTVTNWNSGLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVA HPASSTKVDKKIVPRDCG
241	Exemplary linker	GGGGSGGGSGGGGS
242	Exemplary linker	GGGGSGGGGS
243	3d29 heavy chain (knob) IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLITITLTPKVTCTVVD ISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNG KEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLWC MITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWE AGNTFTCSVLHEGLHNHHTTEKSLSHSPG
244	3d29 Fab heavy chain	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYMNWVKQSHGKSLEWIGVI NPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSAVYYCSRGGPY WGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASST KVDKKIVPRDCG
245	murine IgG1 Fc (knob)	CKPCICTVPEVSSVFI FPPKPKDVLITITLTPKVTCTVVDISKDDPEVQFSW FVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAF PAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLWCMITDFFPEDITV EWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVLHE GLHNHHTTEKSLSHSPG
246	Exemplary humanized- AMX02_3d8b _VH1_aa	EVQLVQSGPVVVKPGASVKMSCKASGYTFTNYYINWVKQAHGQGLE WIGVINPYNGGTSYNQKFKGRATLTVDKSSSTAYMELSSLRSEDTA VYFCSSPYWGQGTTLTVSS
247	Exemplary humanized- AMX02_3d8b _VH2_aa	EVQLVQSGAVVKKPGASVKMSCKASGYTFTNYYINWVKQAPGQGLE WIGVINPYNGGTSYNQKFKGRATLTVDKSSSTAYMELSSLRSEDTA VYFCSSPYWGQGTTLTVSS
248	Exemplary humanized- AMX02_3d8b _VH3_aa	EVQLVQSGAEVKKPGASVKVSCASGYTFTNYYINWVRQAPGQGLE WIGVINPYNGGTSYNQKFKGRATLTVDKSSSTAYMELSSLRSEDTA VYFCSSPYWGQGTTLTVSS
249	Exemplary humanized- AMX02_3d8b _VH4_aa	QVQLVQSGAEVKKPGASVKVSCASGYTFTNYYINWVRQAPGQGLE WIGVINPYNGGTSYNQKFKGRATLTVDSTSTAYMELSSLRSEDTA VYFCSSPYWGQGTTLTVSS
250	Exemplary humanized- AMX02_3d8b _VH4_N54H	QVQLVQSGAEVKKPGASVKVSCASGYTFTNYYINWVRQAPGQGLE WIGVINPYHGGTSYNQKFKGRATLTVDSTSTAYMELSSLRSEDTA VYFCSSPYWGQGTTLTVSS

	aa	
251	Exemplary humanized-AMX02_3d8b_VH4_N54S_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYINWVRQAPGQGLEWIGVINPYSGGTSYNQKFKGRATLTVDSTSTAYMELSSLRSEDTAVYFCSSPYWGQGTLLTVSS
252	Exemplary humanized-AMX02_3d8b_VH5_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYINWVRQAPGQGLEWMGVINPYNGGTSYNQKFKGRVTMTVDSTSTAYMELSSLRSEDTAVYFCSSPYWGQGTLLTVSS
253	Exemplary humanized-AMX02_3d8b_VH5_N54H_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYINWVRQAPGQGLEWMGVINPYHGGTSYNQKFKGRVTMTVDSTSTAYMELSSLRSEDTAVYFCSSPYWGQGTLLTVSS
254	Exemplary humanized-AMX02_3d8b_VH5_N54S_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYINWVRQAPGQGLEWMGVINPYSGGTSYNQKFKGRVTMTVDSTSTAYMELSSLRSEDTAVYFCSSPYWGQGTLLTVSS
255	Exemplary humanized-AMX02_3d8b_VH6_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYINWVRQAPGQGLEWMGVINPYNGGTSYNQKFKGRVTMTTRDTSTSTVYMELSSLRSEDTAVYFCSSPYWGQGTLLTVSS
256	Exemplary humanized-AMX02_3d8b_VK1_aa	DVVMTQSPLSLPVTLGQPASISCKSSQSLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLD SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPRTFGGGTKLEIK
257	Exemplary humanized-AMX02_3d8b_VK2_aa	DVVMTQSPLSLPVTLGQPASISCKSSQSLDSDGKTYLNWLQQRPGQSPRRLIYLVSKLD SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPRTFGGGTKVEIK
258	Exemplary humanized-AMX02_3d8b_VK3_aa	DVVMTQSPLSLPVTLGQPASISCKSSQSLDSDGKTYLNWFQQRPGQSPRRLIYLVSKLD SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPRTFGGGTKVEIK
259	Exemplary CDRH2_3d8b	INPYHGGT
260	Exemplary CDRH2_3d8b	INPYSGGT
261	Exemplary humanized-AMX01_C2_VH1_aa	QVQLQQPGTELKKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTNYNEKFKSRATLTVDKSTSTAYMELSSLRSEDSA VYYCARRGIRLRHFDYWGQGT TTVTVSS
262	Exemplary humanized-	QVQLVQSGAEVKKPGASVKLSCKASGYTFTSYWMHWVKQRPGQGLEWIGNINPSNGGTNYNEKFKSRATLTVDKSTSTAYMELSSLRSEDTA

	AMX01_C2_V H2_aa	VYYCARRGIRLRHFDYWGQGTTVTVSS
263	Exemplary humanized- AMX01_C2_V H3_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQGLE WIGNINPSNGGTNYNEKFKSRATLTVDKSTSTAYMELSSLRSED TA VYYCARRGIRLRHFDYWGQGTTVTVSS
264	Exemplary humanized- AMX01_C2_V H4_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQGLE WIGNINPSNGGTNYNEKFKSRVTMTVDKSTSTAYMELSSLRSED TA VYYCARRGIRLRHFDYWGQGTTVTVSS
265	Exemplary humanized- AMX01_C2_V H5_aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQGLE WIGNINPSNGGTNYNEKFQGRVTMTVDKSTSTAYMELSSLRSED TA VYYCARRGIRLRHFDYWGQGTTVTVSS
266	Exemplary humanized- AMX01_C2_V K1_aa	DIVMTQSPSFLSASVGDRVITITCKASQDVGTA VAWYQQKPGKAPKL LIYWASTRHTGV PDRFTGSGSGTDF TLTISSLQSEDFAD YFCQQYS SYPLTFGQGTKLEIK
267	Exemplary humanized- AMX01_C2_V K2_aa	DIVMTQSPSFLSASVGDRVITITCKASQDVGTA VAWYQQKPGKAPKL LIYWASTRHTGV PDRFSGSGSGTDF TLTISSLQPEDFAD YFCQQYS SYPLTFGQGTKLEIK
268	Exemplary humanized- AMX01_C2_V K3_aa	DIQMTQSPSFLSASVGDRVITITCKASQDVGTA VAWYQQKPGKAPKL LIYWASTRHTGV PSRFGSGSGTEFT LTISSLQPEDFAD YFCQQYS SYPLTFGQGTKLEIK
269	Exemplary humanized- AMX01_C2_V K4_aa	DIQLTQSPSFLSASVGDRVITITCKASQDVGTA VAWYQQKPGKAPKL LIYWASTRHTGV PSRFGSGSGTEFT LTISSLQPEDFAD YFCQQYS SYPLTFGQGTKLEIK
270	Exemplary humanized- AMX01_B4_V H1_aa	EVQLQQSGPELKKPGASVKISCKASGYTFTD YIMNWVKQAHGQGLE WIGDINPNNGGTSYNQKFKGRATLTVDKSSSTAYMELRSLTSE DSA VYYCARYDYAWYFDVWGQGTTVTVSS
271	Exemplary humanized- AMX01_B4_V H2_aa	EVQLVQSGAEVKKPGASVKISCKASGYTFTD YIMNWVKQAHGQGLE WIGDINPNNGGTSYNQKFKGRATLTVDKSSSTAYMELSSLRSED TA VYYCARYDYAWYFDVWGQGTTVTVSS
272	Exemplary humanized- AMX01_B4_V H3_aa	EVQLVQSGAEVKKPGASVKVSCKASGYTFTD YIMNWVRQAPGQGLE WIGDINPNNGGTSYNQKFKGRATLTVDKSSSTAYMELSSLRSED TA VYYCARYDYAWYFDVWGQGTTVTVSS
273	Exemplary humanized- AMX01_B4_V H4_aa	EVQLVQSGAEVKKPGASVKVSCKASGYTFTD YIMNWVRQAPGQGLE WIGDINPNNGGTSYNQKFKGRVTMTVDKSSSTAYMELSSLRSED TA VYYCARYDYAWYFDVWGQGTTVTVSS

274	Exemplary humanized-AMX01_B4_V H5_aa	EVQLVQSGAEVKKPGASVKVSCKASGYTFTDYMNWVRQAPGQGLE WIGDINPNNGGTSYNQKFQGRVTMTVDKSSSTAYMELSSLRSEDTA VYYCARYDYAWYFDVWGQGTTVTVSS
275	Exemplary humanized-AMX01_B4_V K1_aa	DVLMTQSPLSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYQQRPG QSPRLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYY CFQGSHPVPTFGQGTKLEIK
276	Exemplary humanized-AMX01_B4_V K2_aa	DVVMTQSPLSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYQQRPG QSPRLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYY CFQGSHPVPTFGQGTKLEIK
277	Exemplary humanized-AMX01_B4_V K3_aa	DVVMTQSPLSLPVTLGQPASISCRSSQSIVHSNGNTYLEWFQQRPG QSPRLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYY CFQGSHPVPTFGQGTKLEIK
278	Exemplary humanized-AMX01_B4_V K4_aa	DVVMTQSPLSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYQQRPG QSPRLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYY CFQGSHPVPTFGQGTKLEIK
279	LC1 Light Chain Sequence (Vk3), humanized IgG4 kappa	DVVMTQSPLSLPVTLGQPASISCKSSQSLDSDGKTYLNWFQQRPG QSPRLIYLVSKLDSGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYY CWQGTHTFPRTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTL TLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC
280	HC1 Heavy Chain Sequence (VH5), humanized IgG4 with hinge stabilizing/effector function (S228P/L235E)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYINWVRQAPGQGLE WMGVINPYNGGTSYNQKFQGRVTMTVDTSTSTAYMELSSLRSEDTA VYFCSSPYWGQGLTLTVSSASTKGPSVFPLAPCSRSTSESTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SSLGKTITYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLGLG
281	HC2 Heavy Chain Sequence (VH5), humanized IgG4 with hinge stabilizing/effector function (S228P/L235E), enhanced	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYINWVRQAPGQGLE WMGVINPYNGGTSYNQKFQGRVTMTVDTSTSTAYMELSSLRSEDTA VYFCSSPYWGQGLTLTVSSASTKGPSVFPLAPCSRSTSESTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SSLGKTITYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVLHEALHSHYTQKSLSLGLG

	FcRn binding (M428L/N434S)	
282	HC3 Heavy Chain Sequence (VH5), humanized IgG4 with hinge stabilizing/effector function (S228P/L235E), enhanced FcRn binding (M428L/N434S), deamidation (N54S)	QVQLVQSGAEVKKPGASVKVSKASGYTFTNYYINWVRQAPGQGLEWMGVINPYSGGTSYNQKFKGRVTMTVDTSTSTAYMELSSLRSEDVAVYFCSSPYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSLSLSLG
237	HC4 Heavy Chain Sequence, humanized IgG4 Fc with hinge stabilizing/effector function (S228P/L235E)	ESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSLSLSLG
283	HC5 Heavy Chain Sequence, humanized IgG4 Fc with hinge stabilizing/effector function (S228P/L235E), enhanced FcRn binding (M428L/N434S)	ESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSLSLSLG
284	HC6 Heavy Chain Sequence (VH5), humanized IgG4 VH1 (N54S) +	QVQLVQSGAEVKKPGASVKVSKASGYTFTNYYINWVRQAPGQGLEWMGVINPYSGGTSYNQKFKGRVTMTVDTSTSTAYMELSSLRSEDVAVYFCSSPYWGQGLTVTVSSASTKGPSVFPLAPCSRSTSESTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYG

	CH1	
285	HC7 Heavy Chain Sequence (VH5), humanized IgG4 with hinge stabilizing/effector function (S228P/L235E), deamidation (N54S)	QVQLVQSGAEVKKPGASVKVSCKASGYTFNYYINWVRQAPGQGLEWMGVINPYSGGTSYNQKFKGRVTMTVDSTSTAYMELSSLRSEDTAVYFCSSPYWGQGLTLVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGLG**
286	HC8 Heavy Chain Sequence (VH5), humanized IgG4 with hinge stabilizing/effector function (S228P/L235E), enhanced FcRn binding (M428L/N434S), deamidation (N54S), triple histidine (V2H/T30H/T73H)	QHQLVQSGAEVKKPGASVKVSCKASGYTFHNYINWVRQAPGQGLEWMGVINPYSGGTSYNQKFKGRVTMTVDHSTSTAYMELSSLRSEDTAVYFCSSPYWGQGLTLVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSLSLGLG**
68	muLC1 Light Chain Sequence, murine kappa	DVVMQTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNLWLLQRPQQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHTFPRTFGGGTKLEIRRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVWKIDGSEKQNGVLNSWTDQDSKDSTYSMSSTLTLTKEDEYERHNSYTCEATHKSTSTSPIVKSFNRECC**
73	muHC1 Heavy Chain Sequence, murine IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFNYYINWVKQSHGKSLEWIGVINPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYFCSSPYWGQGSTVTSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLITITLTPKVTCTVVVDISKDDPEVQFSWFVDDEVHTAQ TQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMDTDGSYFVYSKLVNQKSNWEAGNTFTCS VLHEGLHNHHTESLSHSPG**
287	muLC2 Light Chain	DVVMQTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNLWLLQRPQQSPKRLIYLVSKVDGVPDRFTGSGSGTDFTLKINRVEAEDLGVYYCWQGTHTFPRTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVV

	Sequence, murine kappa	CFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSTYSMSSTL TLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC**
288	muHC2 Heavy Chain Sequence, murine IgG1	EVQLQQSGPVLVKPGASVKMSCKASGYTFTAYYMNWVRQSHGKSLE WIGVINPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSA VYYCSSPYWGQGTSTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLG LVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPS TWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFI FPPKPKDVLTTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQ TQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK TISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVE WQWNGQPAENYKNTQPIMDTDGSYFVYSKLVNQKSNWEAGNTFTCS VLHEGLHNHHTTEKSLSHSPG**
59	muLC3 Light Chain Sequence, murine kappa	DVVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNLWLLQRP QSPKRLIYLVSKLESGVPDRFTGSGSGTDFTLEISRVEAEDLGYY CWQGTHTFPRTFGGGKTLEIKRADAAPTVSIFPPSSEQLTSGGASV CFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSTYSMSSTL TLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC**
244	muHC3 Heavy Chain Sequence, murine IgG1 Fd (VH1 + CH1 + partial hinge) (truncated hinge contains VPRDCG (SEQ ID NO: 300))	EVQLQQSGPVLVKPGASVKMSCKASGYTFTDYIMNWVKQSHGKSLE WIGVINPYNGGTSYNQKFKGKATLTVDKSSRTAYMELNSLTSEDSA VYYCSRGGPYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVT GCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTV SSTWPSETVTCNVAHPASSTKVDKKIVPRDCG**
289	muLC4 Light Chain Sequence, murine kappa	NIMMTQSPSSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKP GQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISVQAEDLAVY YCHQYLSSRTFGGGKTLEIKRADAAPTVSIFPPSSEQLTSGGASV CFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSTYSMSSTL TLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC**
290	muHC4 Heavy Chain Sequence, murine IgG1	QVQLQQPGAELVRPGTSVKLSCKASGYTFTSSWMHWVKQRPQG WIGVIDPSDSYTNYNQKFKGKATLTVDTSSTAYMQLSSLTSEDSA VYYCARGGGSSYNRYFDVWGTGTTVTVSSAKTTPPSVYPLAPGSAA QTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYT LSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCIC TVPEVSSVFIFFPPKPKDVLTTITLTPKVTCVVVDISKDDPEVQFSWF VDDVEVHTAQTTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVN SAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMIT DFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLVNQKSN WEAGNTFTCSVLHEGLHNHHTTEKSLSHSPG**
291	E3m murine Factor H (1-5), Short Consensus Repeats 1- 5: fh1-5	EDCKGPPPRENSEILSGSWSEQLYPEGTQATYKCRPGYRTLTGTIVK VCKNGKWVASNPSRICRKPCGHPGDTFFGSFRLAVGSQFEFGAKV VYTCDDGYQLLGEIDYRECGADGWINDIPLCEVVKCLPVTLENGR IVSGAAETDQEYYFGQVVRFECSGFKIEGHKEIHCSENGLWSNEK PRCVEILCTPPRVENGDGINVKPVYKENERYHYKCKHGYVPKERGD AVCTGSGWSSQPFCEEKRCSPPYILNGIYTPHRIIHRSDDEIRYEC NYGFYPVTGSTVSKCTPTGWIPVPRCTLK**

	sequence	
301	Exemplary epitope sequence	GSGSGSGRLGREGVQ
302	Exemplary epitope sequence	GREGVQKEDI PPADL
303	Exemplary epitope sequence	IPPADLSDQVPDTE
304	Exemplary epitope sequence	VPDTESETRILLQGT
305	Exemplary epitope sequence	ILLQGTPVAQMTEDA
306	Exemplary epitope sequence	QMTEDAVDAERLKHL
307	Exemplary epitope sequence	ERLKHLIVTPSGCGE
308	Exemplary epitope sequence	PSGCGEQNMIGMTPT
309	Exemplary epitope sequence	IGMTPTVIAVHYLDE
310	Exemplary epitope sequence	VHYLDETEQWEKFGL
311	Exemplary epitope sequence	WEKFGLQKRGAL
312	Exemplary epitope sequence	QGALELIKKGYTQQL
313	Exemplary epitope sequence	GYTQQLAFRQPSAF
314	Exemplary epitope sequence	QPSAFAAFVKRAPS
315	Exemplary epitope sequence	VKRAPSTWLTAYVVK
316	Exemplary epitope sequence	TAYVVKVFS LAVNLI
317	Exemplary epitope sequence	LAVNLI AID SQVLCG
318	Exemplary epitope sequence	SQVLCG AVKWLILEK
319	Exemplary epitope sequence	WLILEK QKPDGVFQE
320	Exemplary epitope sequence	DGVFQEDAPVIHQEM
321	Exemplary	VIHQEMIGGLRNNNE

	epitope sequence	
322	Exemplary epitope sequence	LRNNNEKDMALTAFV
323	Exemplary epitope sequence	ALTAFVLISLQEAKD
324	Exemplary epitope sequence	LQEAKDICEEQVNSL
325	Exemplary epitope sequence	EQVNSLPGSITKAGD
326	Exemplary epitope sequence	ITKAGDFLEANYMNL
327	Exemplary epitope sequence	ANYMNLQRSYTVAIA
328	Exemplary epitope sequence	YTVAIAGYALAQMG
329	Exemplary epitope sequence	LAQMGRLLKGPLLNKF
330	Exemplary epitope sequence	PLLNKFLTTAKDKNR
331	Exemplary epitope sequence	AKDKNRWEDPGKQLY
332	Exemplary epitope sequence	PGKQLYNVEATSYAL
333	Exemplary epitope sequence	ATSYALLALLQLKDF
334	Exemplary epitope sequence	LQLKDFDFVPPVVRW
335	Exemplary epitope sequence	PPVVRWLNEQRYYG
336	Exemplary epitope sequence	QRYYG GYGSTQATF
337	Exemplary epitope sequence	STQATFMVFQALAQY
338	Exemplary epitope sequence	QALAQYQKDAPDHQE
339	Exemplary epitope sequence	APDHQELNLDVSLQL
340	Exemplary epitope sequence	DVSLQLPSRSSKITH
341	Exemplary epitope sequence	IVTPSGSGEQNMIGM

342	<i>mu</i> HC7 Heavy Chain Sequence, murine IgG2b	EVQLQQSGPVLVKPGASVKMSCKASGYTFTAYYMNWVRQSHGKSLE WIGVINPYNGGTSYNQKFKGKATLTVDKSSSTAYMELNSLTSEDSA VYYCSSPYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGC LVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPS TWPSQTVTCVAHPASSTTVDDKLEPSGPISTINPCPPCKECKCP APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVRIS WVFNNEVHTAQTQTHREDYNSTIRVVSALPIQHQQDWMMSGKEFKCK VNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCL VVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLDIKT SKWEKTDSFSCNVRHEGLKNYYLKKTI SRSPGK* *
343	Exemplary anti-C3d antibody 3d11, CDRH1	GYTFETSYW

Key= In SEQ ID Nos.: 161, 164, 165, 166, 168, 170, 171, 174, and 179 n ranges from 0 to 17, 1 to 8, 1 to 5, at least 4, or 5 to 17.

In the claims which follow and in the preceding description of the invention, except where the context requires otherwise due to express language or necessary implication, the word “comprise” or variations such as “comprises” or “comprising” is used in an inclusive sense, i.e. to specify the presence of the stated features but not to preclude the presence or addition of further features in various embodiments of the invention.

It is to be understood that, if any prior art publication is referred to herein, such reference does not constitute an admission that the publication forms a part of the common general knowledge in the art, in Australia or any other country.

CLAIMS

WHAT IS CLAIMED IS:

1. A fusion protein construct comprising:
 - (1) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
 - (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
 - (2) a complement modulator polypeptide, wherein the complement modulator polypeptide comprises factor H, or a biologically active fragment thereof.
2. A fusion protein construct comprising:
 - (1) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
 - (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the

- amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
- (2) a complement modulator polypeptide, wherein the complement modulator polypeptide comprises CR1 or a biologically active fragment thereof.
3. The fusion protein construct of claim 1 or 2, wherein the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258.
4. The fusion protein construct of claim 3, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
5. The fusion protein construct of any one of claims 1 to 4, wherein the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254.
6. The fusion protein construct of claim 5, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
7. The fusion protein construct of claim 6, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 282.
8. The fusion protein construct of claim 6, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 285.
9. The fusion protein construct of any one of claims 1 to 8, wherein:
- (a) the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258; and,
- (b) the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254.
10. The fusion protein construct of claim 9, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
11. The fusion protein construct of claim 10, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
12. The fusion protein construct of claim 11, wherein the fusion protein construct further

- comprises a linker linking the antibody or antigen binding fragment thereof to the complement modulator polypeptide.
13. The fusion protein construct of claim 12, wherein the linker comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, and SEQ ID NO: 241.
 14. The fusion protein construct of claim 12, wherein the linker is bound to the C-terminus of the heavy chain and comprises the amino acid sequence of SEQ ID NO: 138.
 15. The fusion protein construct of any one of claims 1 or 3 to 14, wherein the complement modulator polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108.
 16. The fusion protein construct of any one of claims 2 to 14, wherein the complement modulator polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
 17. The fusion protein construct of claim 15, wherein the complement modulator polypeptide comprises an amino acid sequence of SEQ ID NO: 72.
 18. The fusion protein construct of claim 16, wherein the complement modulator polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 41 and SEQ ID NO: 42.
 19. The fusion protein construct of any one of claims 1 to 18, wherein the antibody or antigen binding fragment thereof comprises:
 - (a) a first heavy chain and a second heavy chain, wherein each of the first and the second heavy chain comprises three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence

- of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
- (b) a first light chain and a second light chain, wherein each of the first and the second light chain comprises three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34.
20. The fusion protein construct of claim 19, wherein each of the first and the second heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254, and wherein each of the first and the second light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258.
21. The fusion protein construct of claim 20, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 284, and wherein the first and the second light chain each comprises the amino acid sequence of SEQ ID NO: 279.
22. The fusion protein construct of claim 21, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 282.
23. The fusion protein construct of claim 21, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 285.
24. The fusion protein construct of claim 21, wherein the fusion protein further comprises a linker linking the antibody or antigen binding fragment thereof to one of the complement modulator polypeptides.
25. The fusion protein construct of claim 24, wherein the linker comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, and SEQ ID NO: 241.

26. The fusion protein construct of claim 24, comprising:
- (c) a first linker bound to the C-terminus of the first heavy chain and comprising the amino acid sequence of SEQ ID NO: 138; and
 - (d) a second linker bound to the C-terminus of the second heavy chain and comprising the amino acid sequence of SEQ ID NO: 138.
27. The fusion protein construct of claim 26, wherein the complement modulator polypeptide that comprises Factor H or a biologically active fragment thereof comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108.
28. The fusion protein construct of claim 26, wherein the complement modulator polypeptide that comprises CR1 or a biologically active fragment thereof comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
29. The fusion protein construct of any one of claims 1 to 28, wherein the fusion protein construct is selected from the group consisting of:
- (1) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (2) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (3) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41;

- (4) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279;
 - (5) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (6) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (7) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and,
 - (8) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279.
30. An antibody or antigen-binding fragment thereof comprising:
- a heavy chain comprising: three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3) comprising the following set of amino acid sequences: SEQ ID NOs: 29, 260, and 31, and
 - a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3) comprising the following set of amino acid sequences: SEQ

ID NOs: 32, 33, and 34.

31. The antibody or antigen-binding fragment thereof of claim 30, wherein:
 - (a) the heavy chain comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 254; and
 - (b) the light chain comprises a light chain variable region comprising the amino acid sequence of SEQ ID NO: 258.
32. The antibody or antigen-binding fragment thereof of claim 31, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
33. The antibody or antigen-binding fragment thereof of claim 32, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
34. The antibody or antigen-binding fragment thereof of claim 33, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 282.
35. The antibody or antigen-binding fragment thereof of claim 33, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 285.
36. A pharmaceutical composition comprising the fusion protein of any one of claims 1 to 29 or the antibody or antigen-binding fragment thereof of any one of claims 30 to 35.
37. A method of treating a complement mediated disease characterized by an increased deposition of C3d, the method comprising administering to a subject a fusion protein construct comprising:
 - (i) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
 - (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a light chain comprising three light chain complementarity determining

- regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
- (ii) a complement modulator polypeptide comprising a complement protein selected from the group consisting of: CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, factor H, and a biologically active fragment thereof.
38. Use of a fusion protein construct in the manufacture of a medicament for treating a complement mediated disease characterized by an increased deposition of C3d, wherein the fusion protein construct comprises:
- (1) an antibody or an antigen-binding fragment thereof that specifically binds to a complement protein 3d (c3d), wherein the antibody or antigen-binding fragment thereof comprises:
- (a) a heavy chain comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
- (b) a light chain comprising three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34; and
- (2) a complement modulator polypeptide comprising a complement protein selected from the group consisting of: CR1, DAF, MCP, Crry, MAp44, MAp19, CD59, factor H, and a biologically active fragment thereof.
39. The method of claim 37, or use of claim 38, wherein the complement mediated disease is a complement mediated kidney disease.
40. The method or use of claim 39, wherein the complement mediated kidney disease is selected from the group consisting of: focal segmental glomerulosclerosis,

glomerulonephritis, complement 3 glomerulopathy (C3G), membranoproliferative glomerulonephritis, C3 glomerulonephritis, type II membranoproliferative glomerulonephritis (MPGN II), membranous nephropathy (MN), IgA nephropathy (IgAN), lupus nephritis (LN), hemolytic uremic syndrome (HUS), atypical hemolytic uremic syndrome (aHUS), and diabetic retinopathy.

41. The method of claim 37, or the use of claim 38, wherein the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258, or wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279.
42. The method of claim 37, or the use of claim 38, wherein the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254, or wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 282, 284, or 285.
43. The method of claim 37, or the use of claim 38, wherein:
 - (a) the light chain comprises a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 258; and,
 - (b) the heavy chain comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 254.
44. The method or use of claim 43, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 279, and wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 284.
45. The method or use of claim 44, wherein the fusion protein construct further comprises a linker linking the antibody or antigen binding fragment thereof to the complement modulator polypeptide, wherein the linker is bound to the C-terminus of the heavy chain and comprises the amino acid sequence of and one of SEQ ID NO: 138, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, SEQ ID NO: 177, SEQ ID NO: 178, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 182, SEQ ID NO: 183, and SEQ ID NO: 241.

46. The method of claim 37, or the use of claim 38, wherein the complement modulator polypeptide comprises:
- (a) an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108, or,
 - (b) an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
47. The method or use of claim 46, wherein the complement modulator polypeptide comprises:
- (a) an amino acid sequence of SEQ ID NO: 72, or,
 - (b) an amino acid sequence selected from the group consisting of: SEQ ID NO: 41 and SEQ ID NO: 42.
48. The method of claim 37, or the use of claim 38, wherein the antibody or antigen binding fragment thereof comprises:
- (a) a first heavy chain and a second heavy chain, wherein each of the first and the second heavy chain comprises three heavy chain complementarity determining regions (CDR-H1, CDR-H2, CDR-H3), wherein the CDR-H1 comprises the amino acid sequence of SEQ ID NO: 29, the CDR-H2 comprises the amino acid sequence of SEQ ID NO: 260, and the CDR-H3 comprises the amino acid sequence of SEQ ID NO: 31, and
 - (b) a first light chain and a second light chain, wherein each of the first and the second light chain comprises three light chain complementarity determining regions (CDR-L1, CDR-L2, CDR-L3), wherein the CDR-L1 comprises the amino acid sequence of SEQ ID NO: 32, the CDR-L2 comprises the amino acid sequence of SEQ ID NO: 33, and the CDR-L3 comprises the amino acid sequence of SEQ ID NO: 34.
49. The method or use of claim 48, wherein the first and the second heavy chain each comprises the amino acid sequence of SEQ ID NO: 282.
50. The method or use of claim 49, comprising:
- (c) a first linker bound to the C-terminus of the first heavy chain and comprising the amino acid sequence of SEQ ID NO: 138; and
 - (d) a second linker bound to the C-terminus of the second heavy chain and comprising

the amino acid sequence of SEQ ID NO: 138.

51. The method or use of claim 50, wherein the complement modulator polypeptide comprises:
 - (a) an amino acid sequence selected from the group consisting of: SEQ ID NO: 72 and SEQ ID NO: 108, or,
 - (b) an amino acid sequence selected from the group consisting of: SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 91, and SEQ ID NO: 92.
52. The method of claim 37, or the use of claim 38, wherein the fusion protein construct is selected from the group consisting of:
 - (1) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (2) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
 - (3) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41;
 - (4) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72 or 41; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279;
 - (5) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID

- NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
- (6) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 285, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, two light chain-containing polypeptides each comprising the amino acid sequence of SEQ ID NO: 279;
- (7) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 279, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and,
- (8) a heavy chain-containing polypeptide comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 284, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 108 or 42; and, a light chain comprising the amino acid sequence of SEQ ID NO: 279.
53. The method of claim 37, or the use of claim 38, wherein the fusion protein construct comprises:
- (i) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 72; and,
- (ii) two light chain-containing polypeptides, each comprising the amino acid sequence of SEQ ID NO: 279.
54. The method of claim 37, or the use of claim 38, wherein the fusion protein construct comprises:
- (i) two heavy chain-containing polypeptides, each comprising, from N- to C-terminal, the amino acid sequence of SEQ ID NO: 282, the amino acid sequence of SEQ ID NO: 138, and the amino acid sequence of SEQ ID NO: 41; and,

- (ii) two light chain-containing polypeptides, each comprising the amino acid sequence of SEQ ID NO: 279.
55. The method or use of claim 53, wherein the complement mediated disease is a complement mediated kidney disease.
56. The method or use of claim 55, wherein the complement mediated kidney disease is selected from the group consisting of: focal segmental glomerulosclerosis, glomerulonephritis, complement 3 glomerulopathy (C3G), membranoproliferative glomerulonephritis, C3 glomerulonephritis, type II membranoproliferative glomerulonephritis (MPGN II), membranous nephropathy (MN), IgA nephropathy (IgAN), lupus nephritis (LN), hemolytic uremic syndrome (HUS), atypical hemolytic uremic syndrome (aHUS), and diabetic retinopathy.
57. The method or use of claim 55, wherein the complement mediated kidney disease is IgA nephropathy (IgAN), complement 3 glomerulopathy (C3G), or lupus nephritis (LN).

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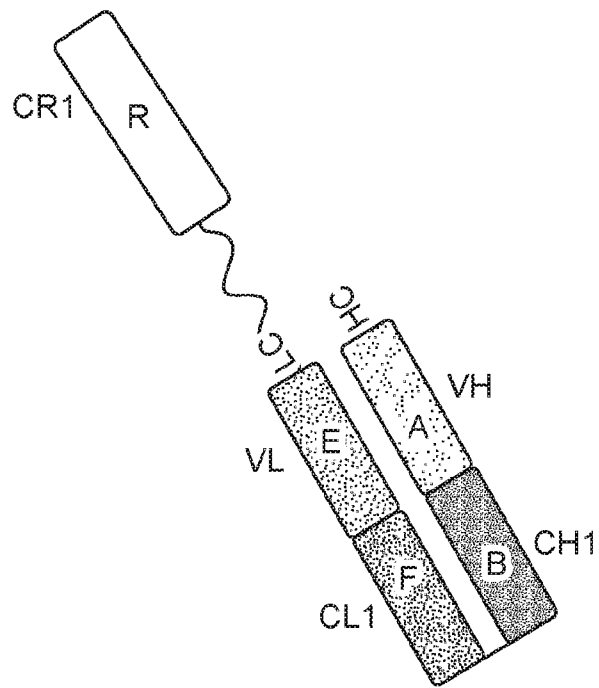


FIG. 1

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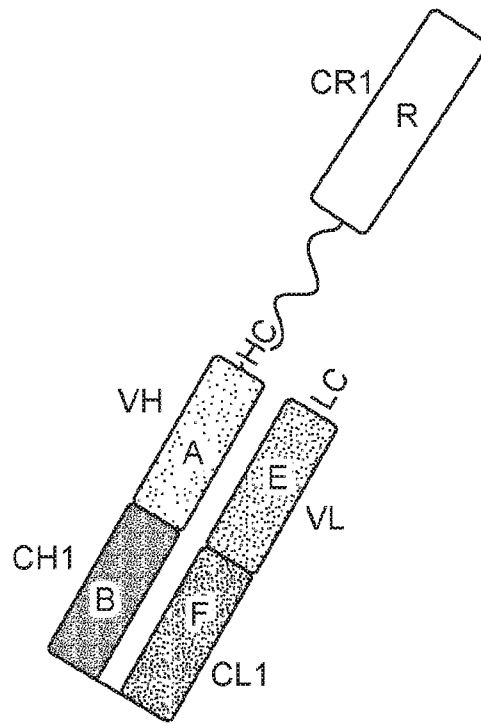


FIG. 2

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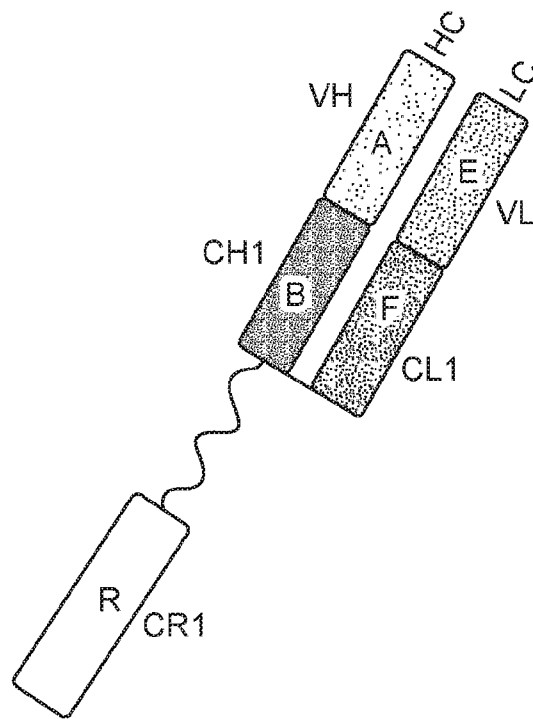


FIG. 3

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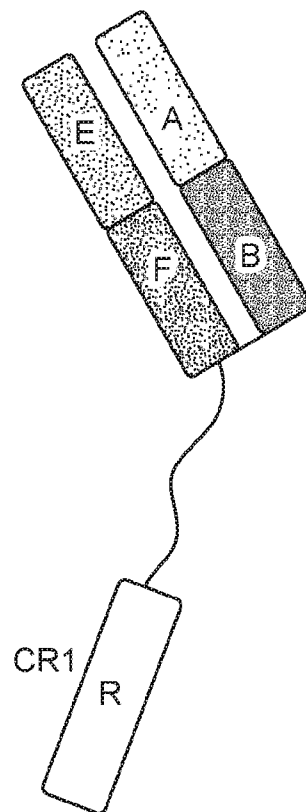


FIG. 4

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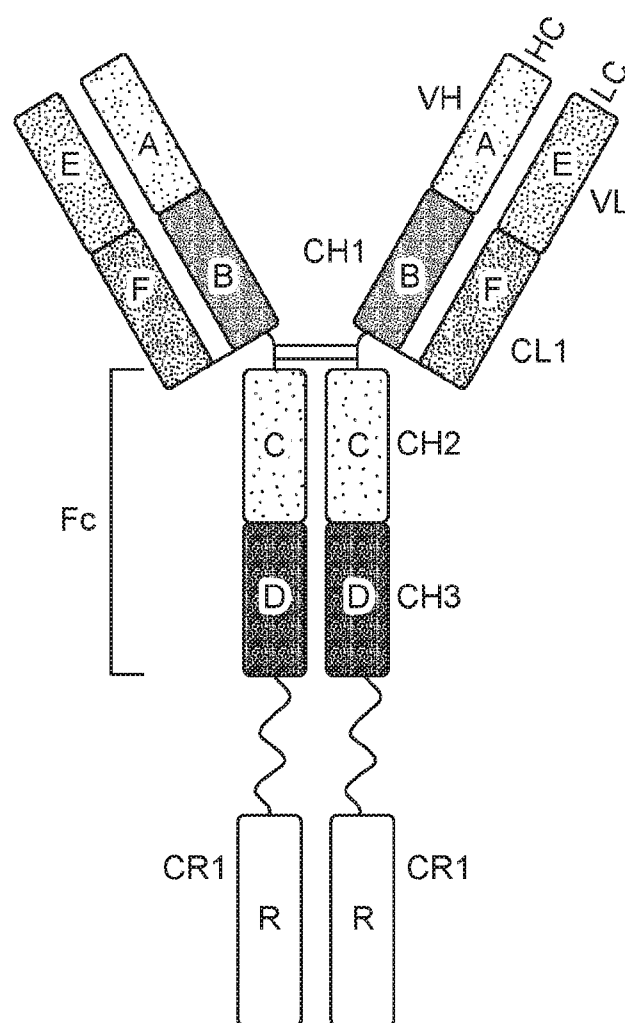


FIG. 5

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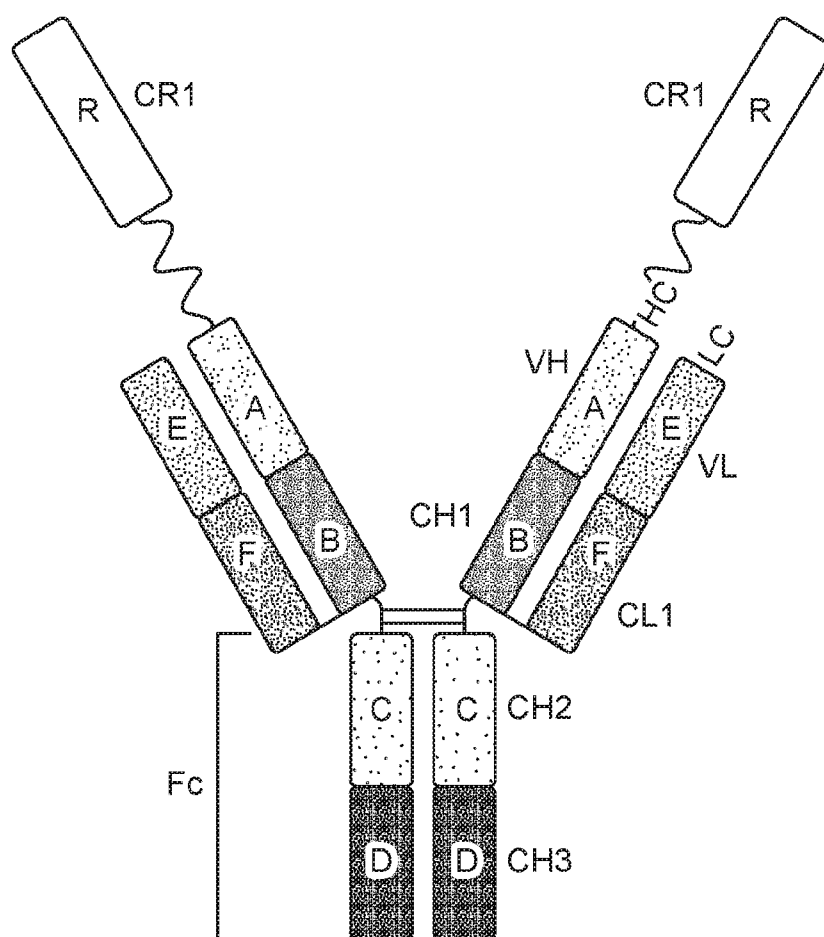


FIG. 6

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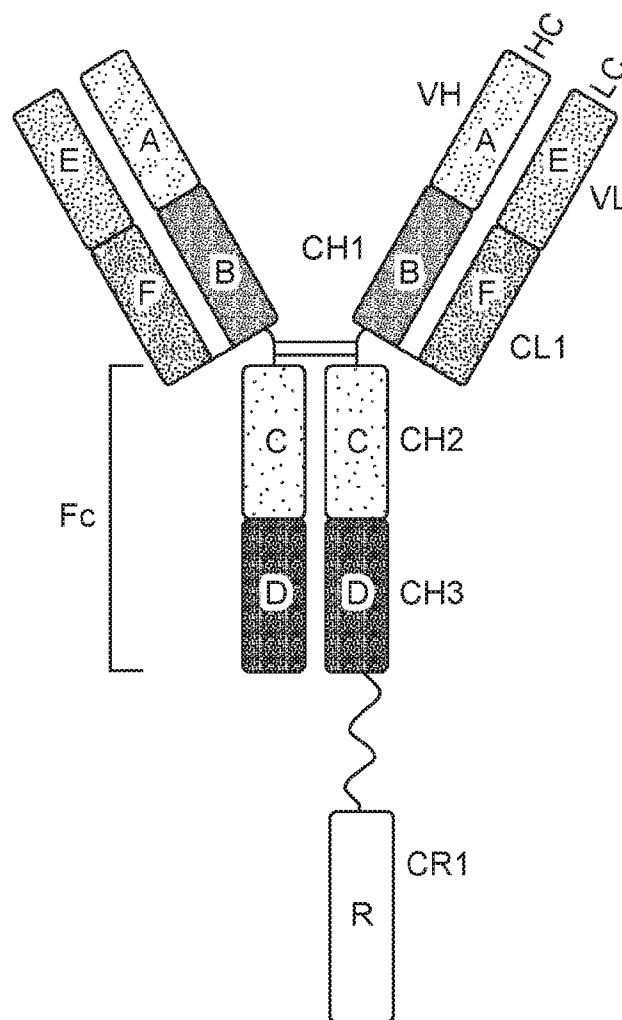


FIG. 7

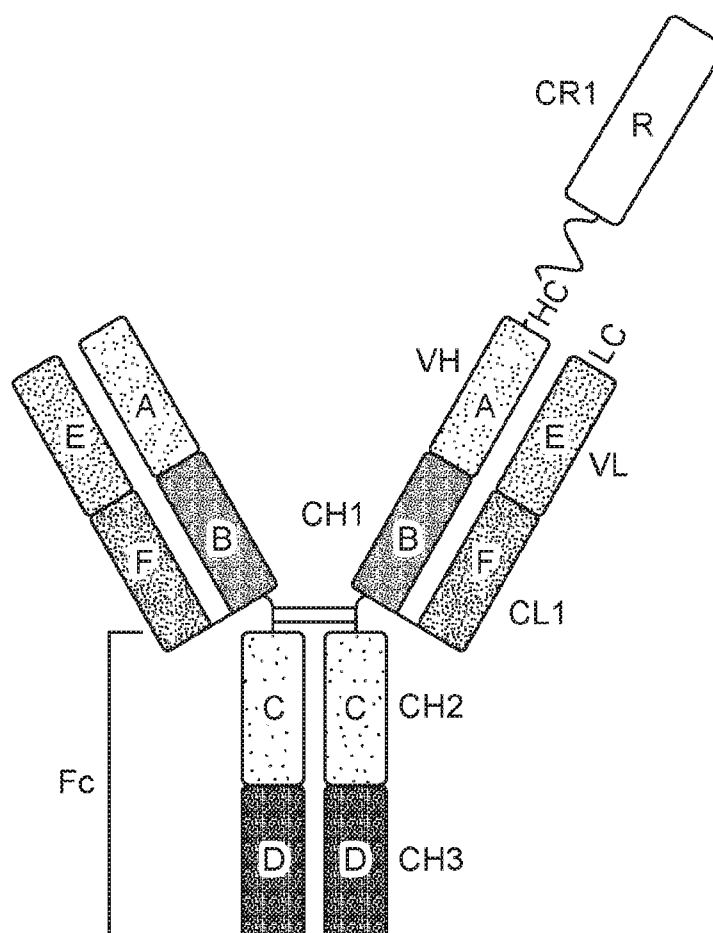


FIG. 8

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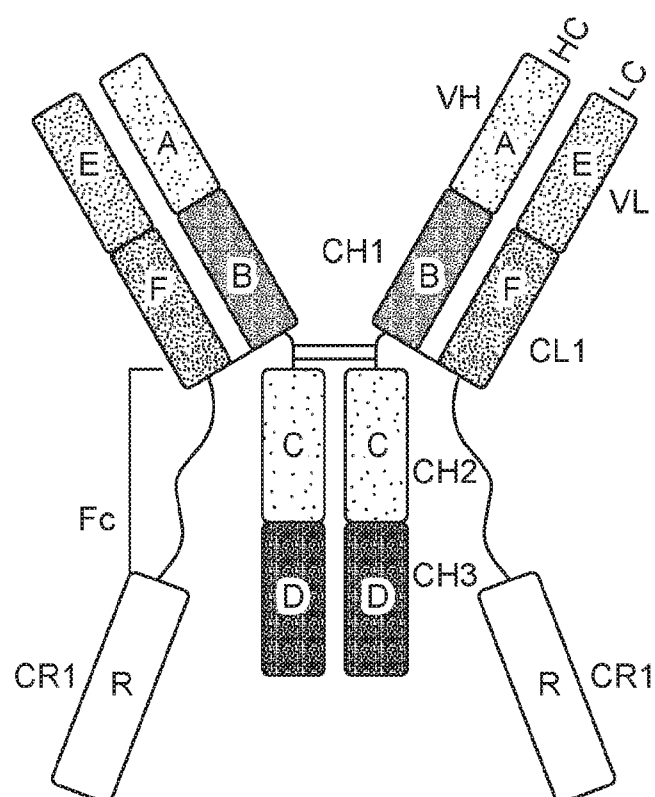


FIG. 9.

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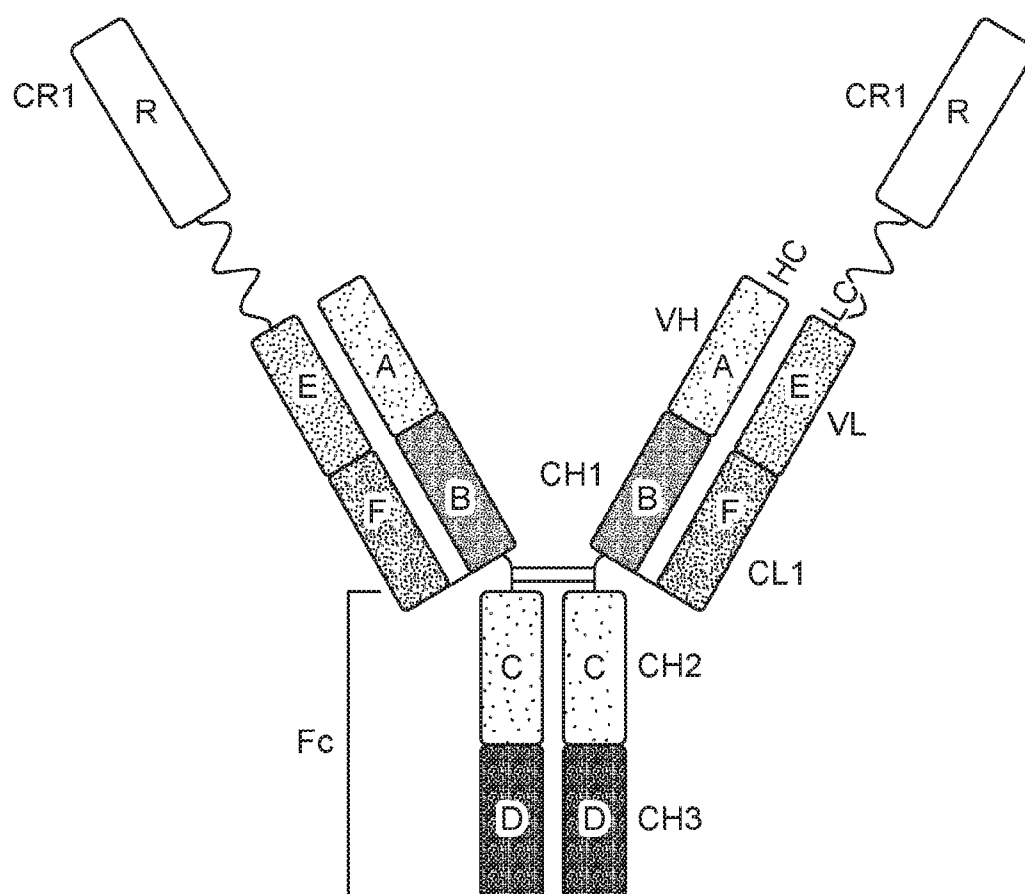


FIG. 10

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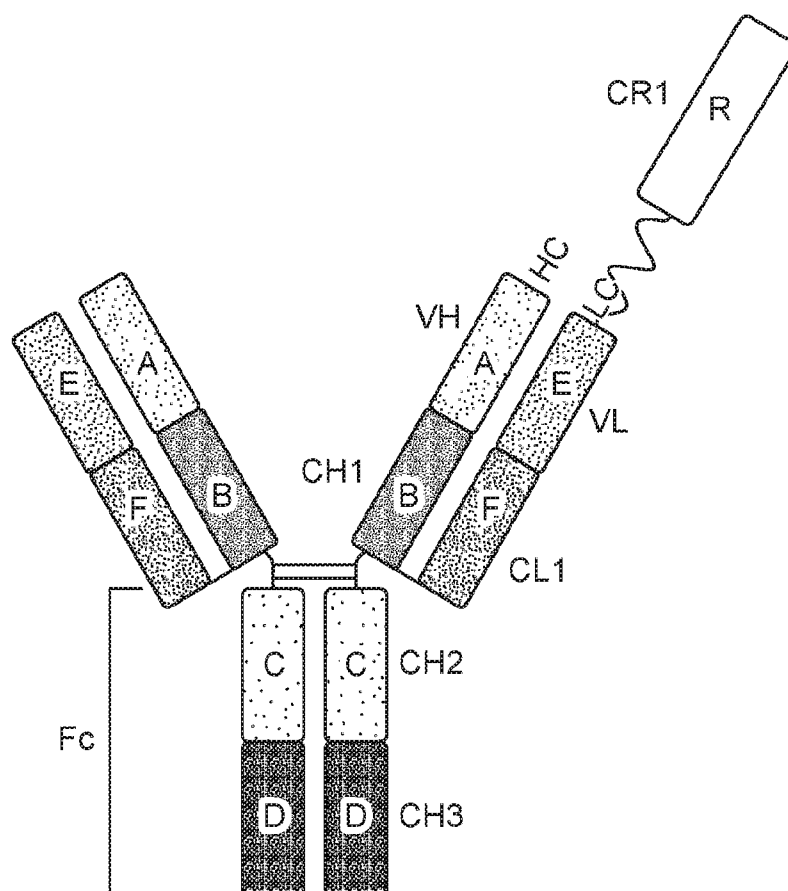


FIG. 11

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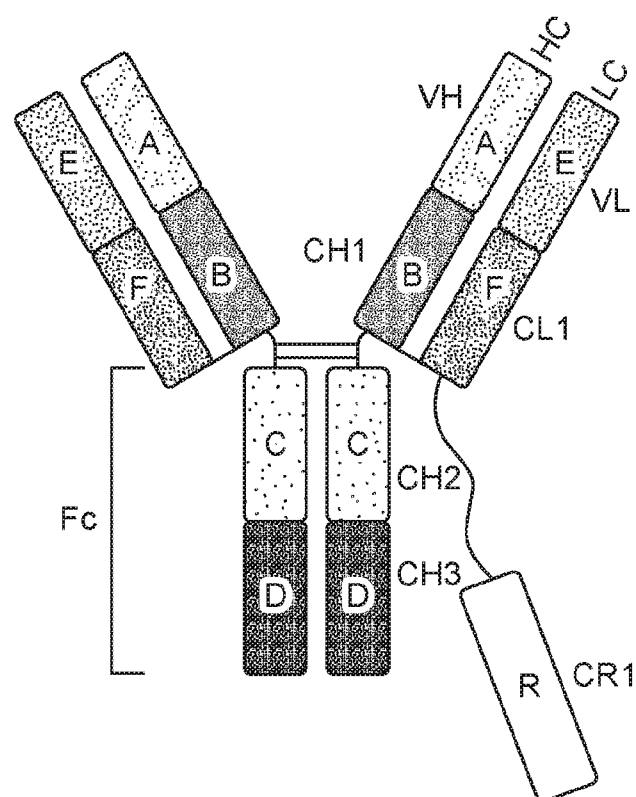


FIG. 12

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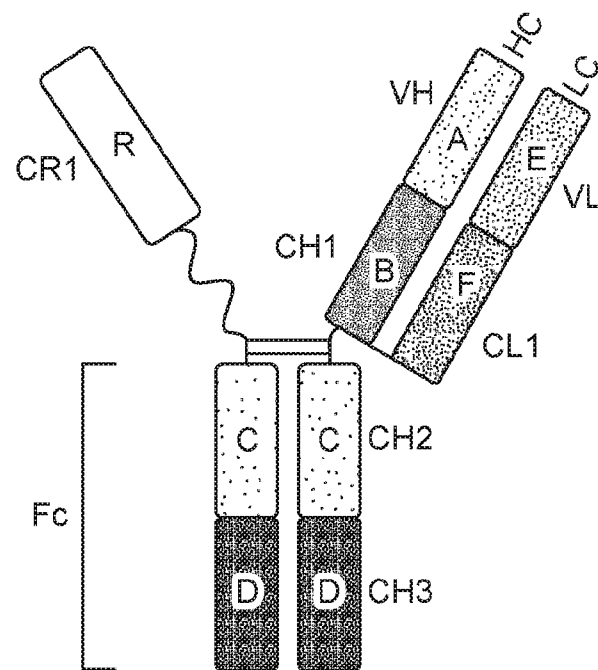


FIG. 13

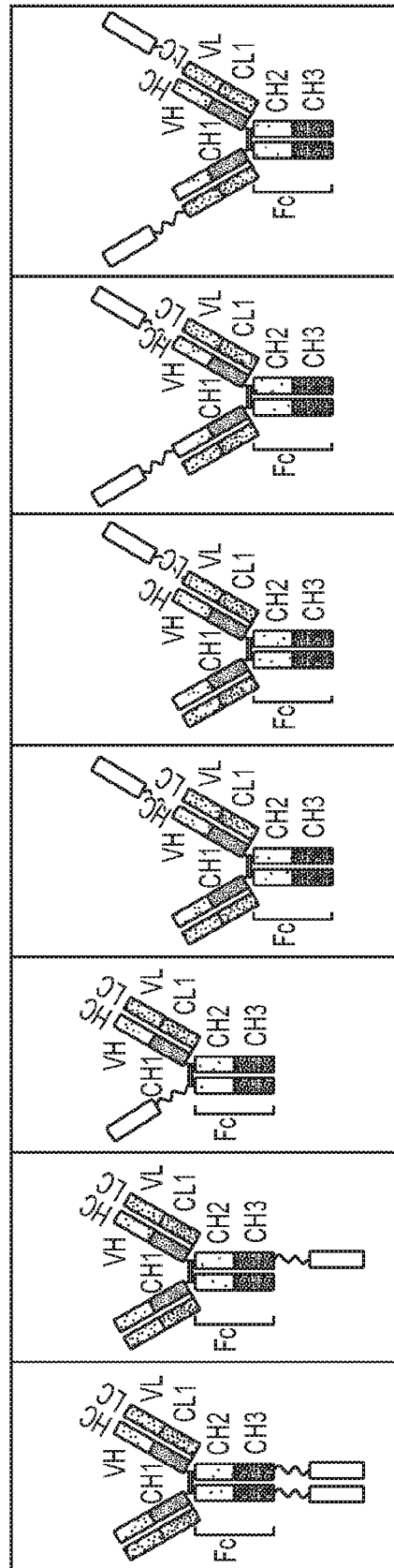
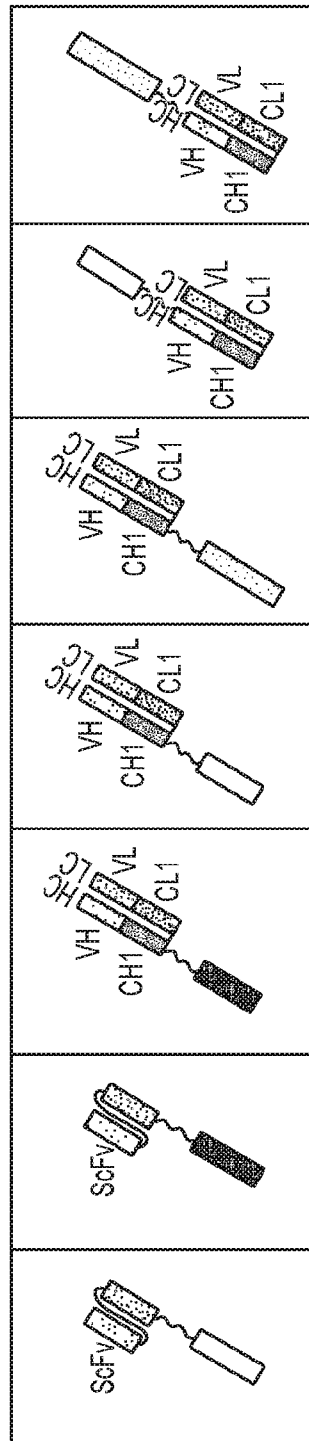


FIG. 14

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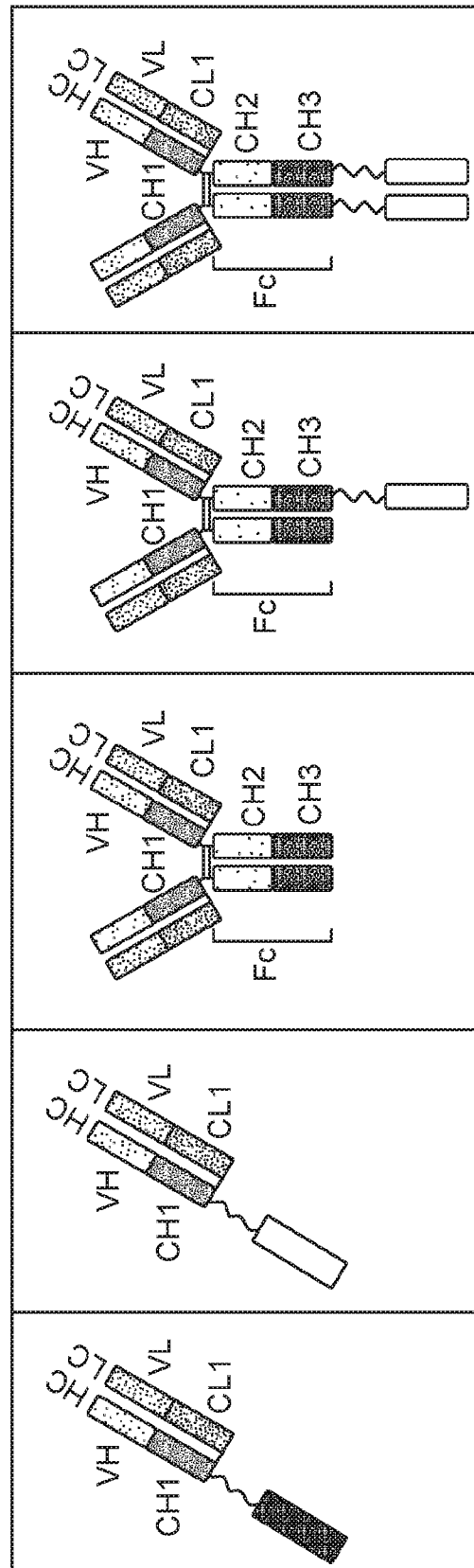


FIG. 15

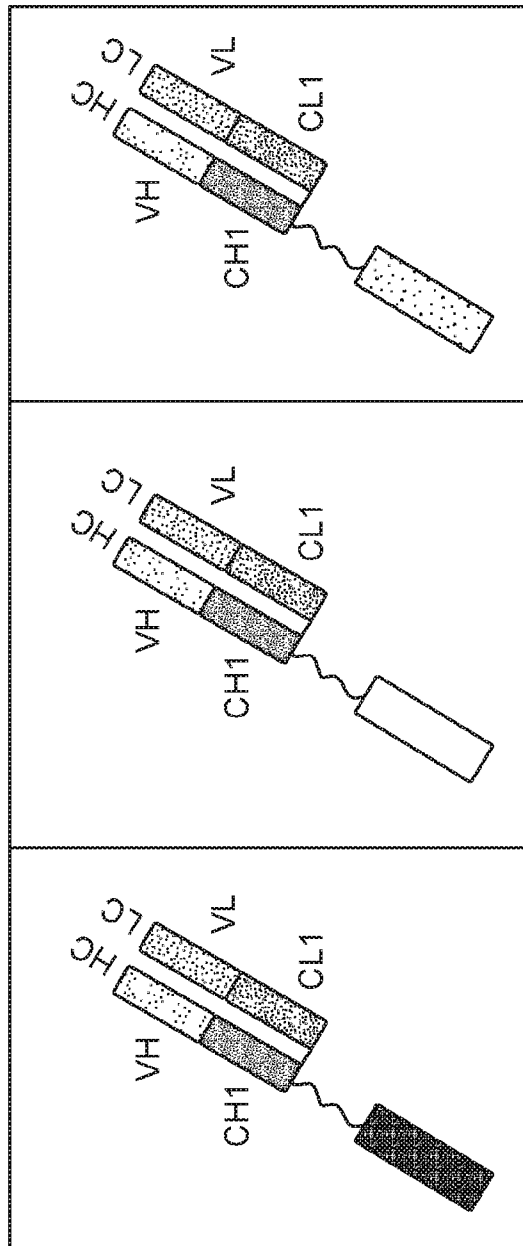


FIG. 16

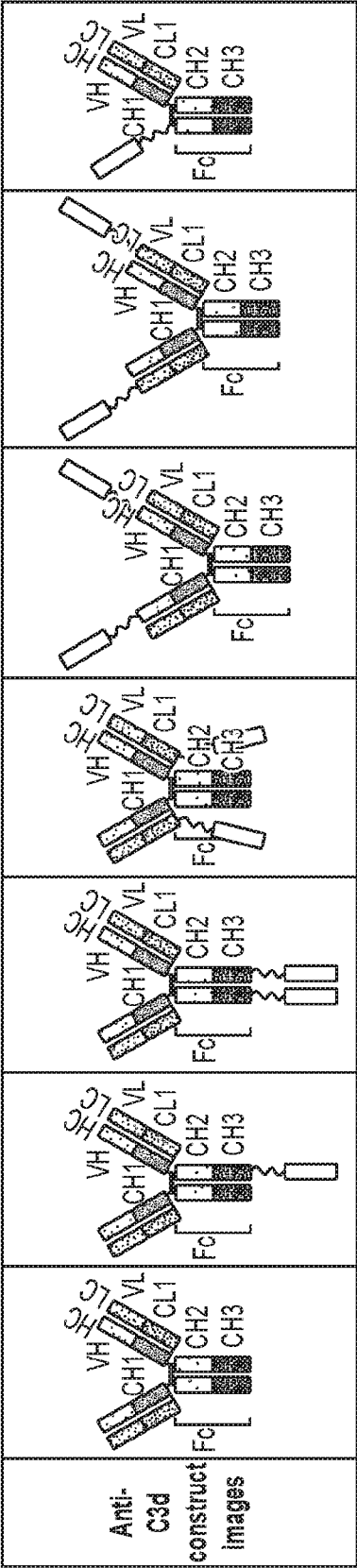


FIG. 17

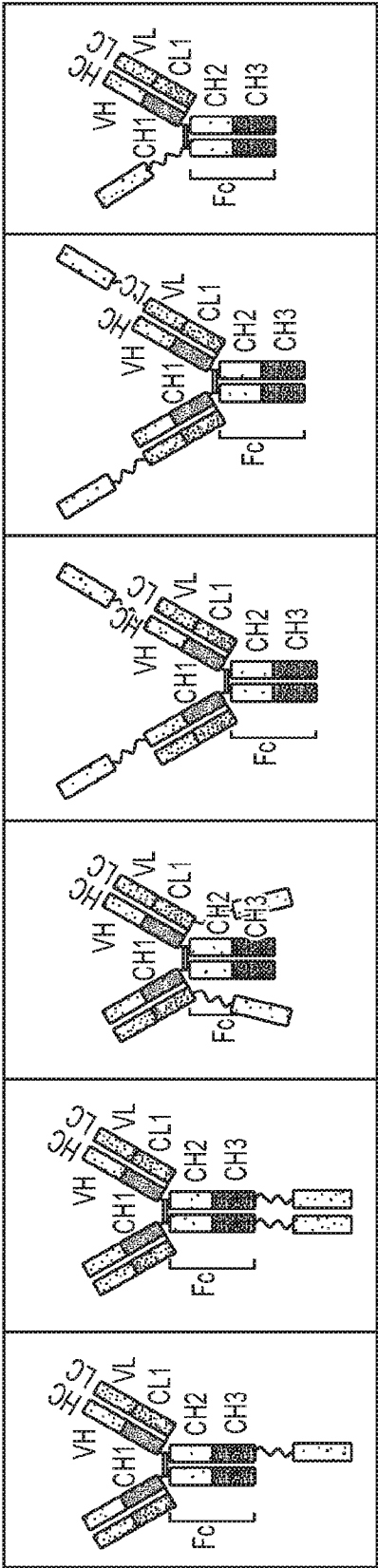


FIG. 18

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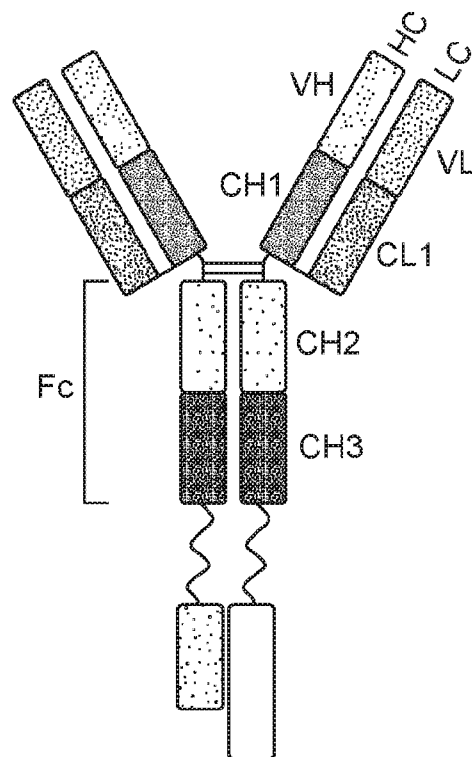


FIG. 19

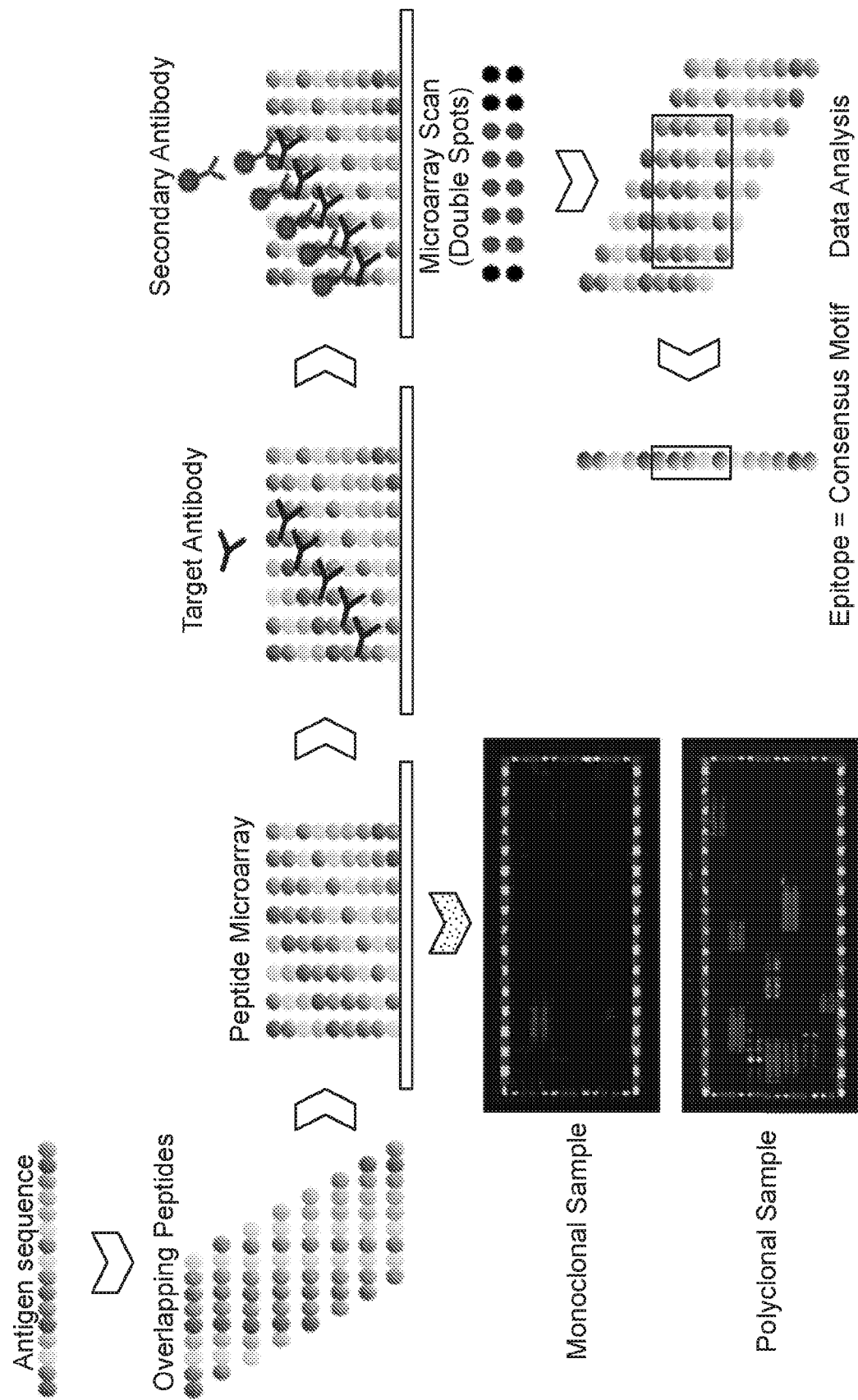


FIG. 20

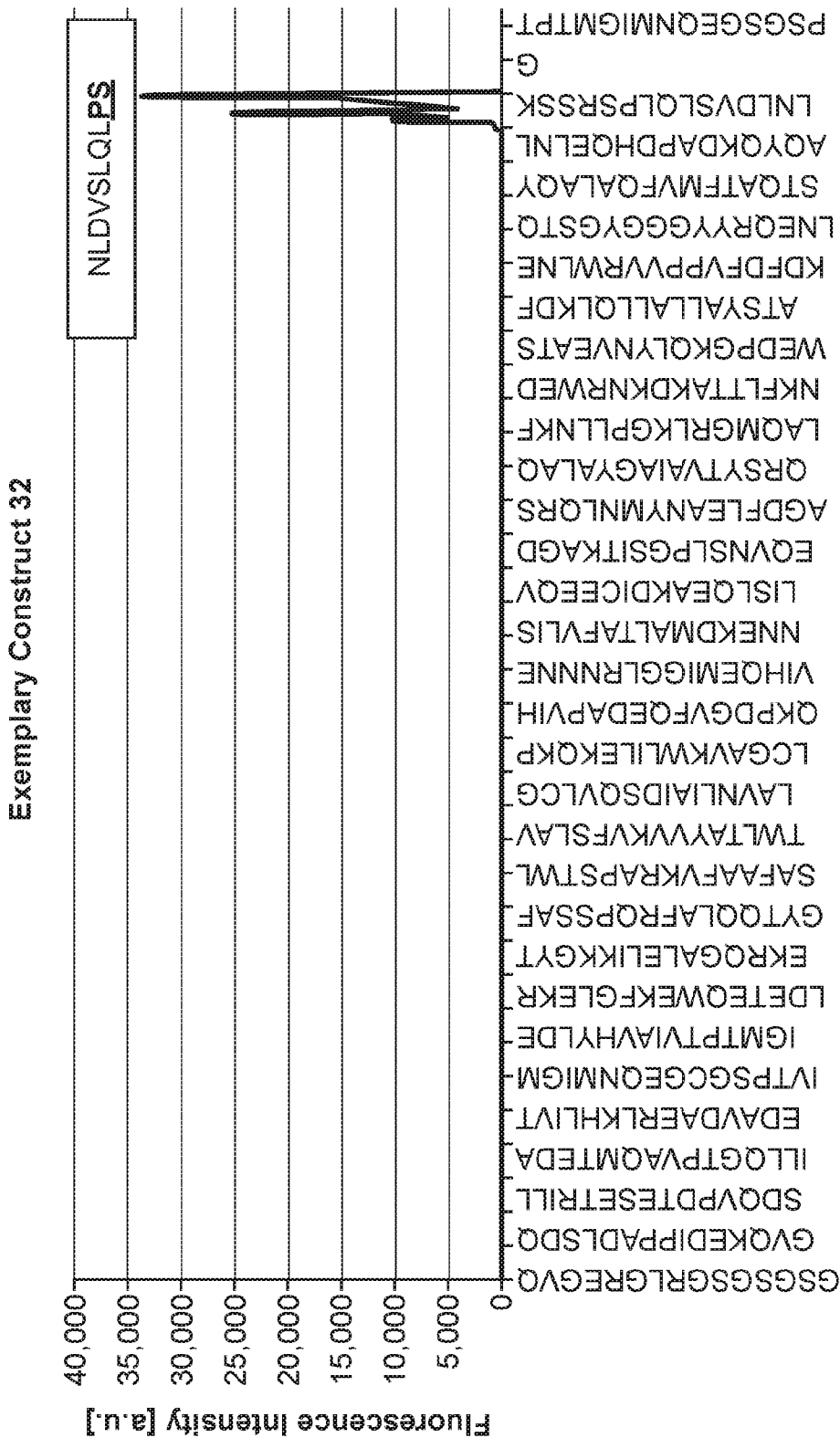


FIG. 21

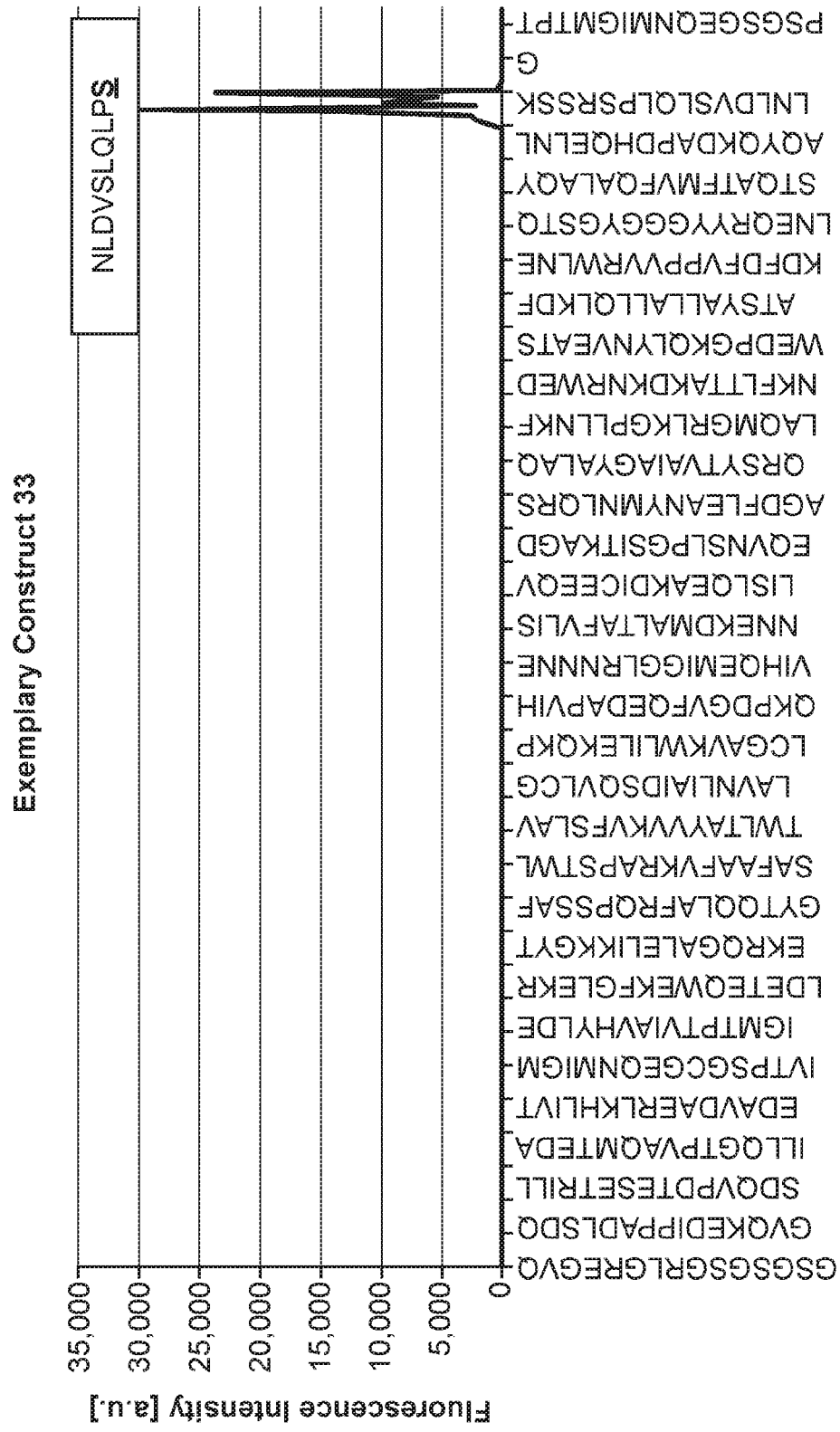


FIG. 22

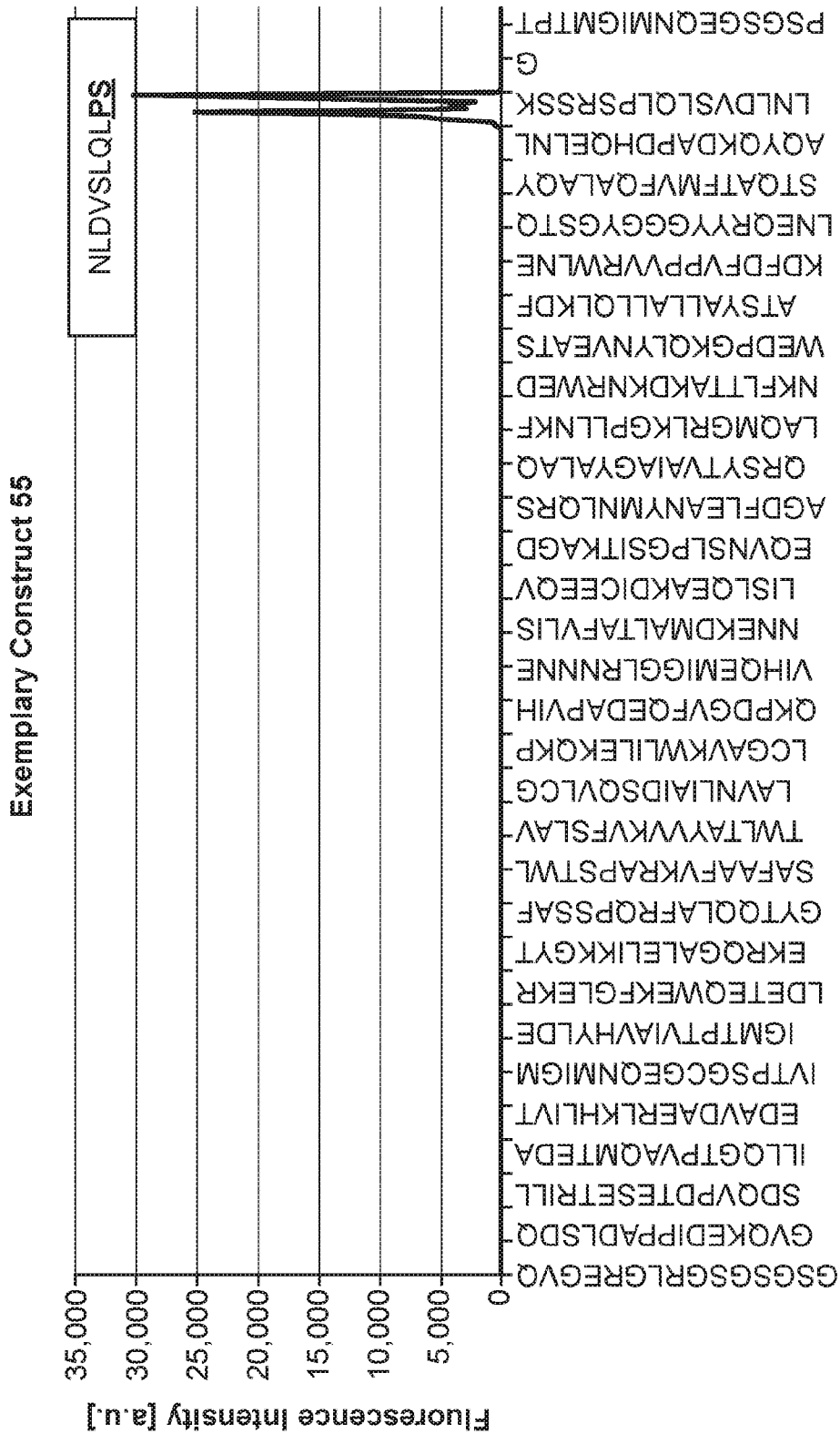


FIG. 23

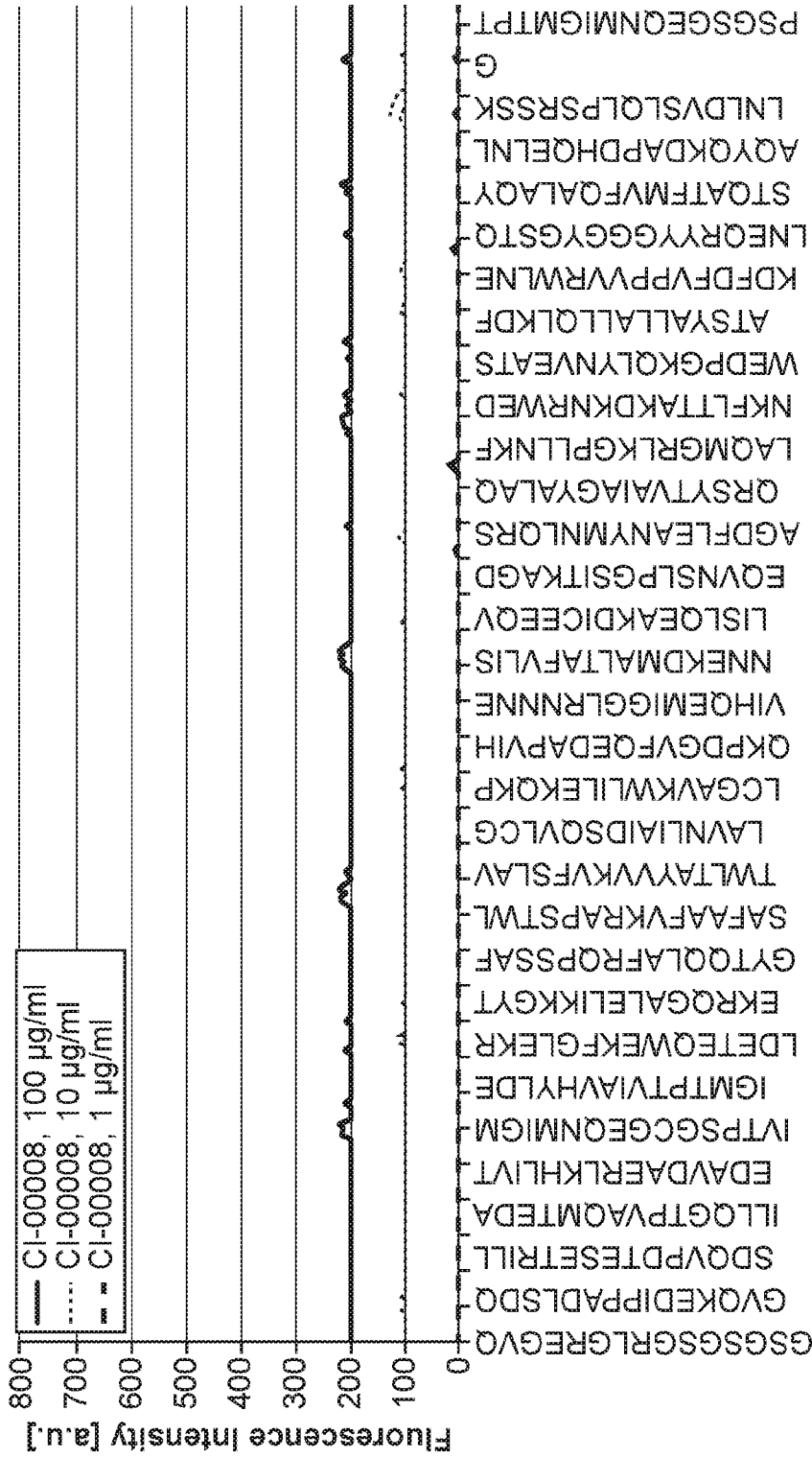


FIG. 24

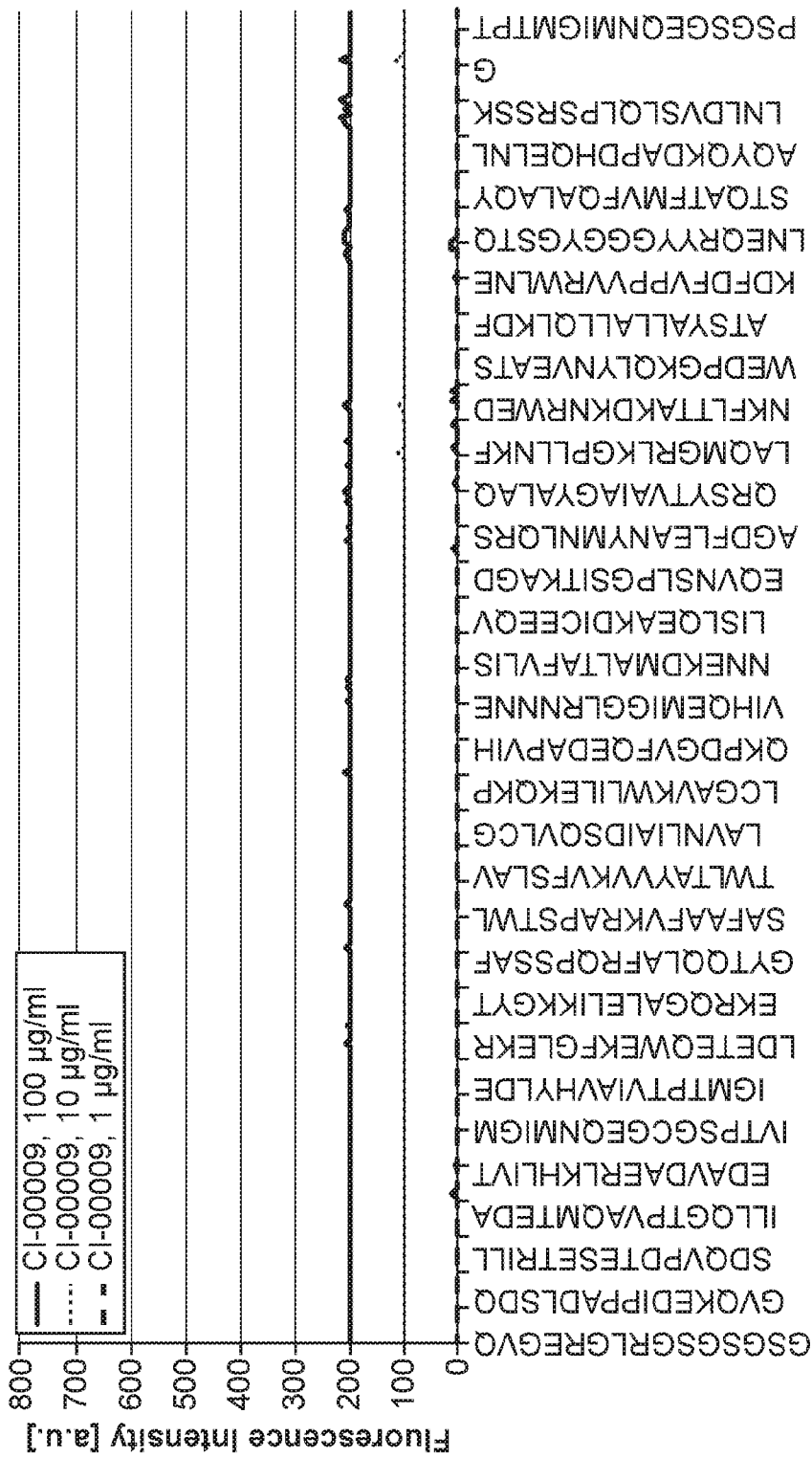


FIG. 25

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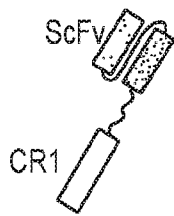


FIG. 26A

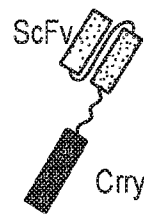


FIG. 26B

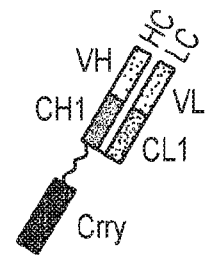


FIG. 26C

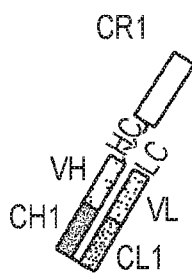


FIG. 26D

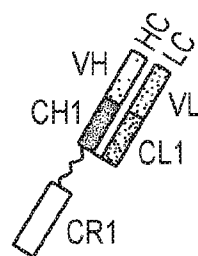


FIG. 26E

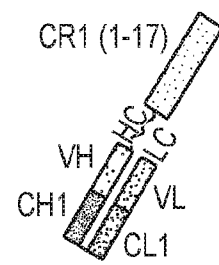


FIG. 26F

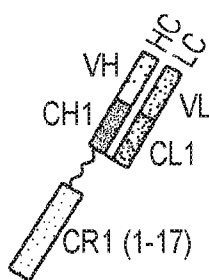


FIG. 26G

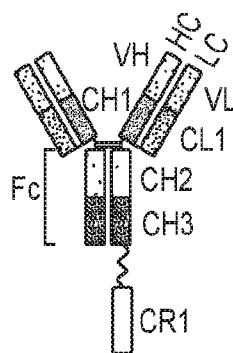


FIG. 26H

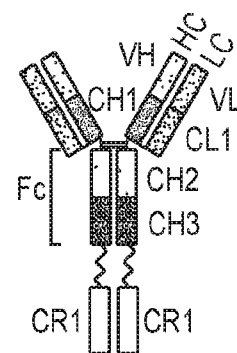


FIG. 26I

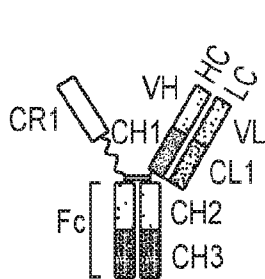


FIG. 26J

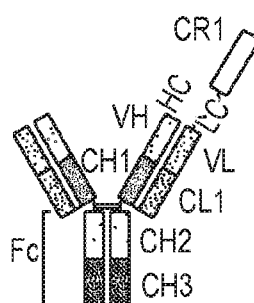


FIG. 26K

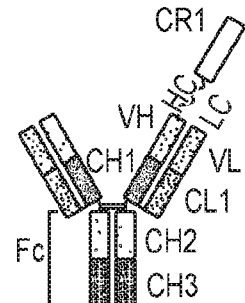


FIG. 26L

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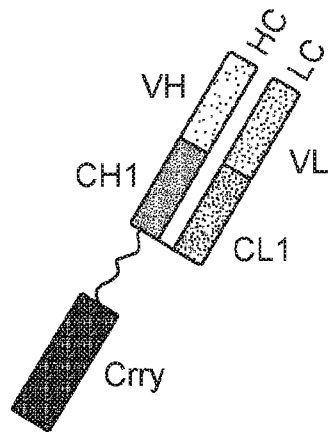


FIG. 27A

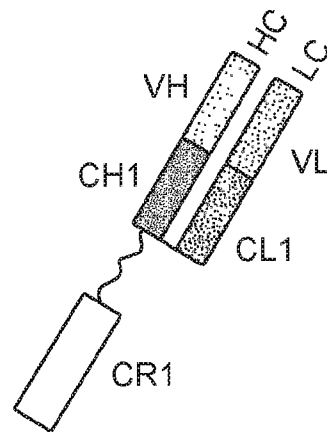


FIG. 27B

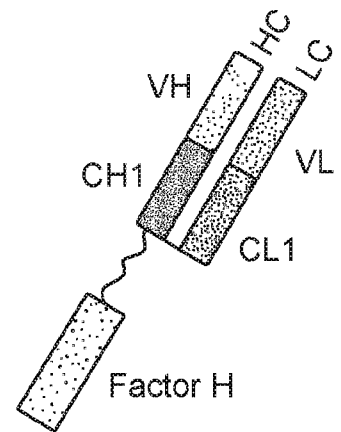


FIG. 27C

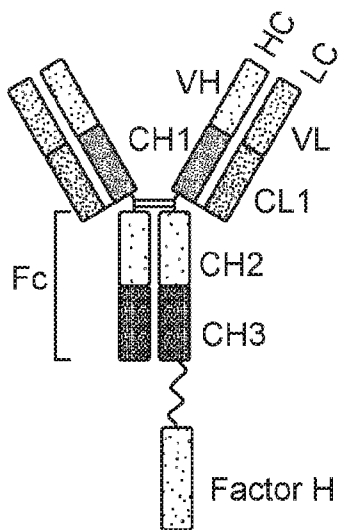


FIG. 27D

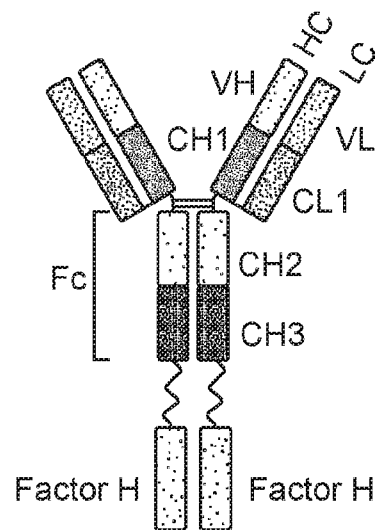


FIG. 27E

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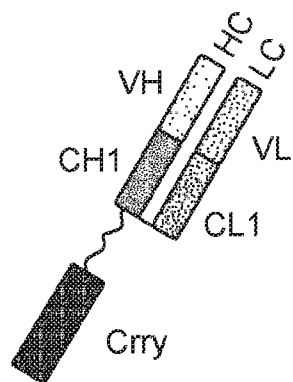


FIG. 28A

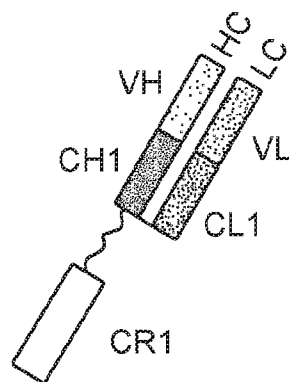


FIG. 28B

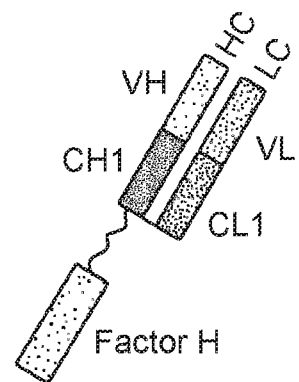


FIG. 28C

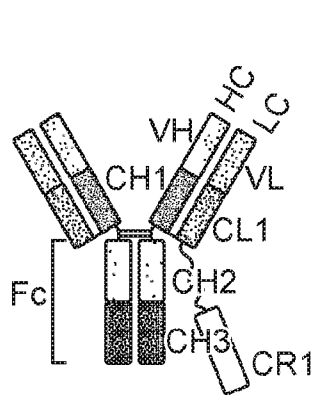


FIG. 28D

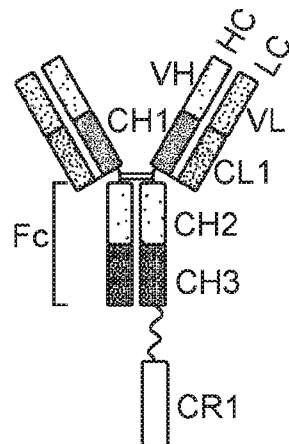


FIG. 28E

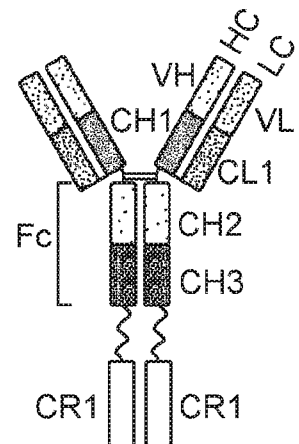


FIG. 28F

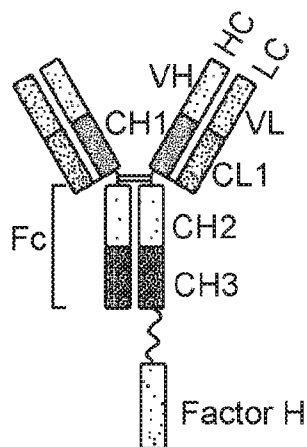


FIG. 28G

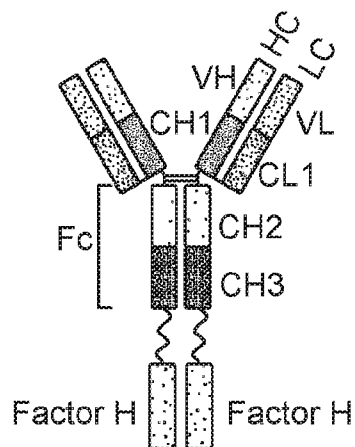


FIG. 28H

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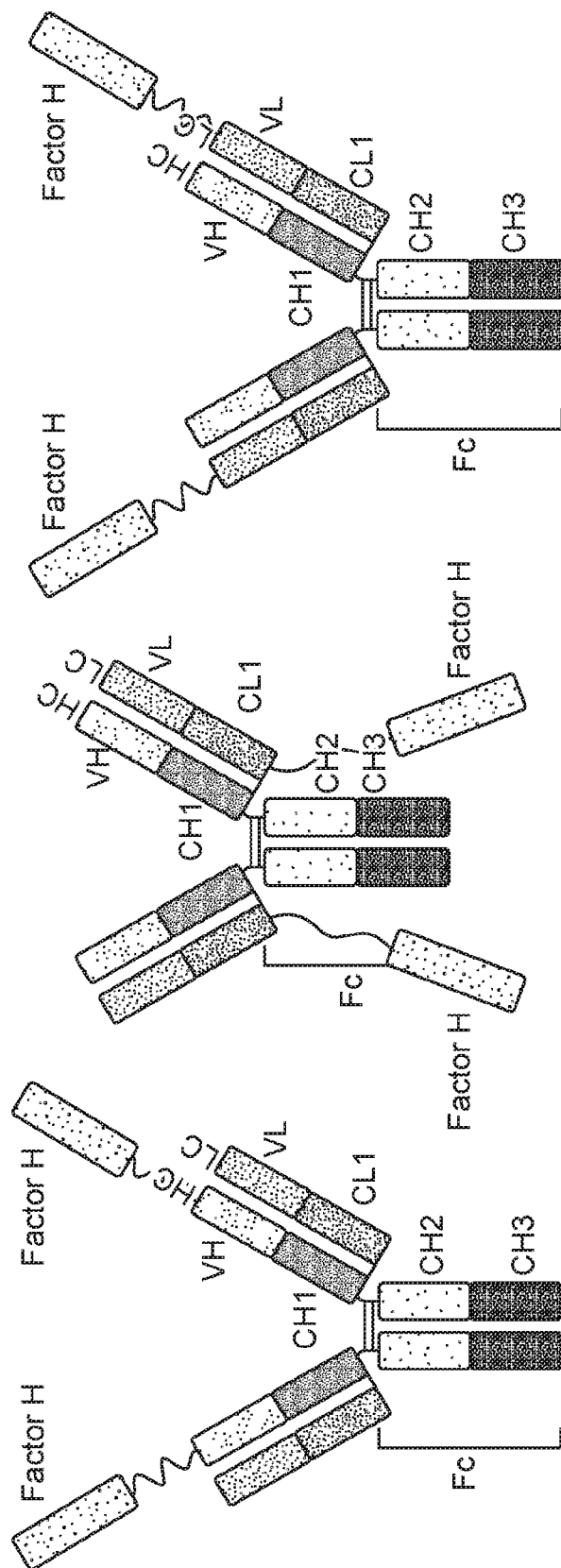


FIG. 29C

FIG. 29B

FIG. 29A

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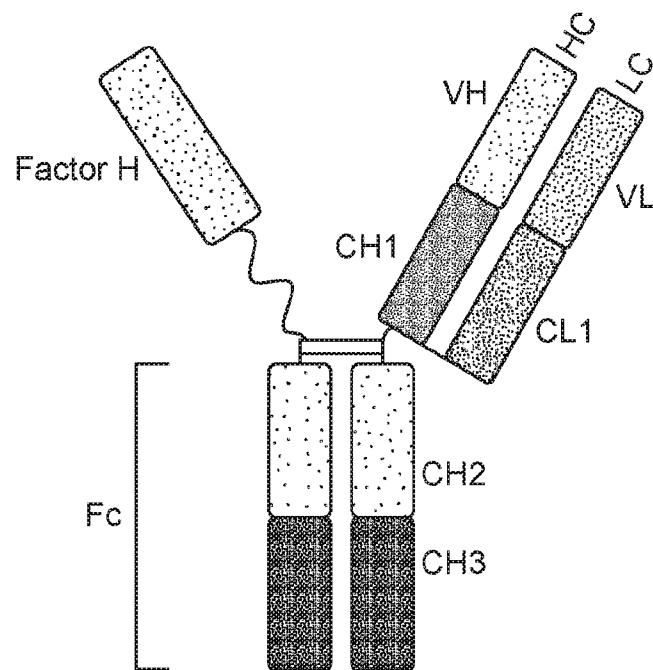


FIG. 30

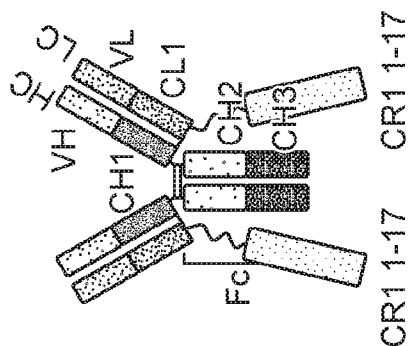


FIG. 31A

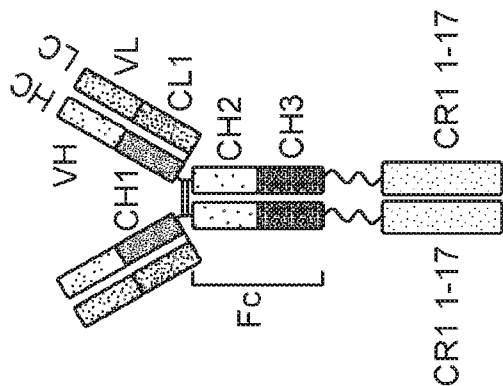


FIG. 31B

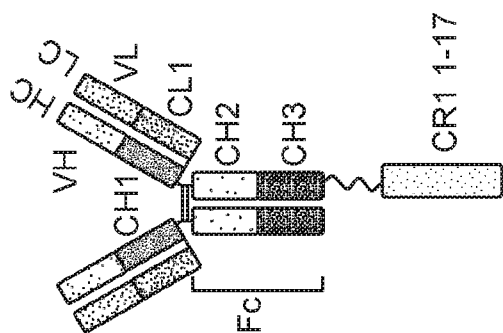


FIG. 31C

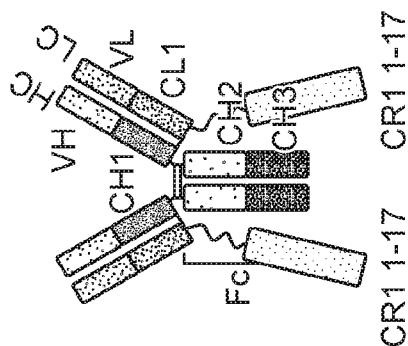


FIG. 31D

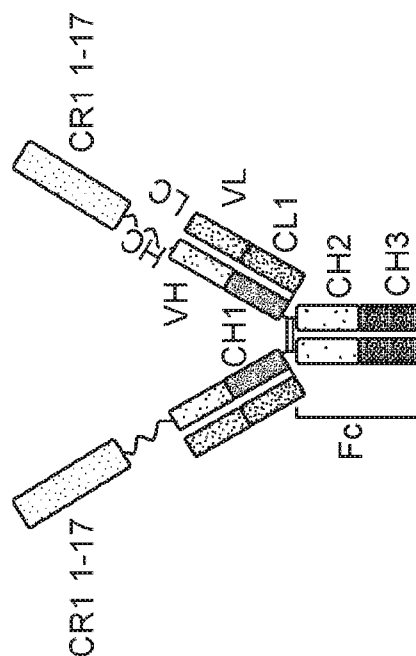


FIG. 31E

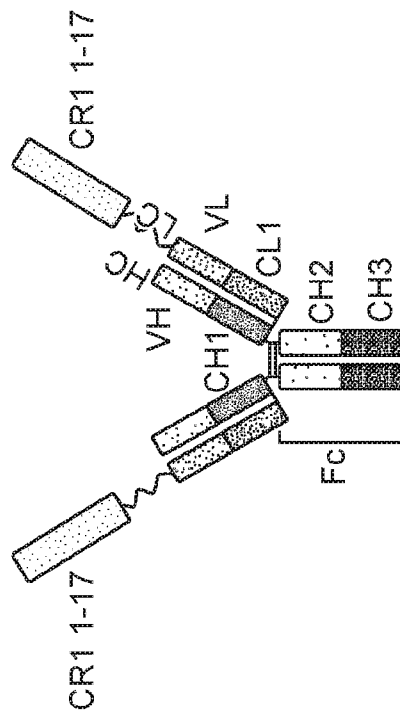


FIG. 31F

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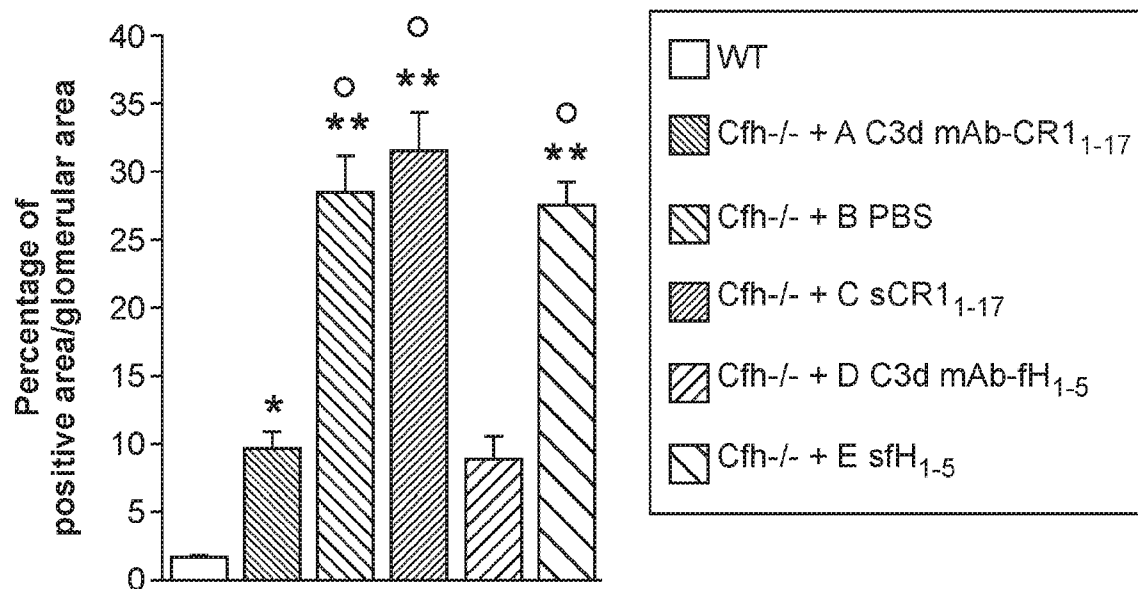


FIG. 32A

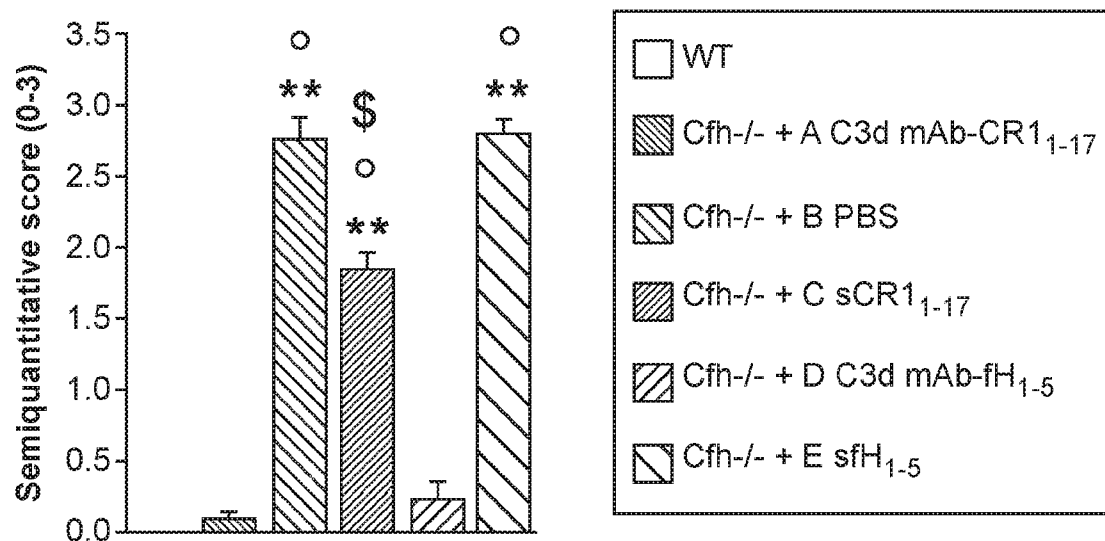


FIG. 32B

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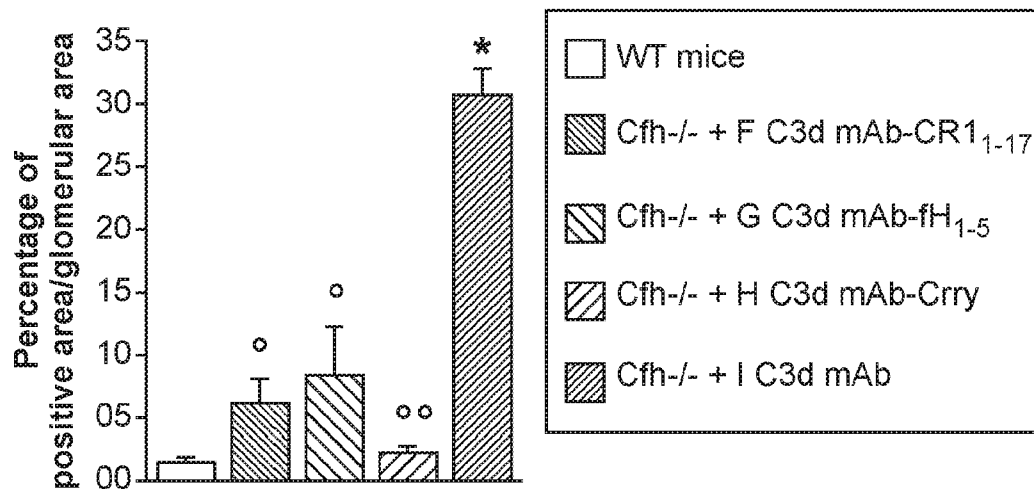


FIG. 33A

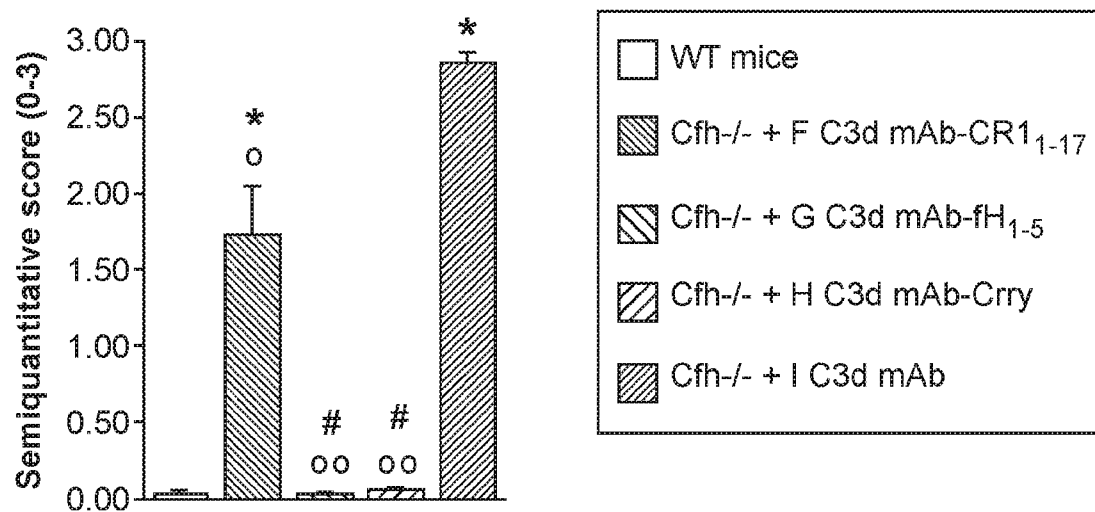


FIG. 33B

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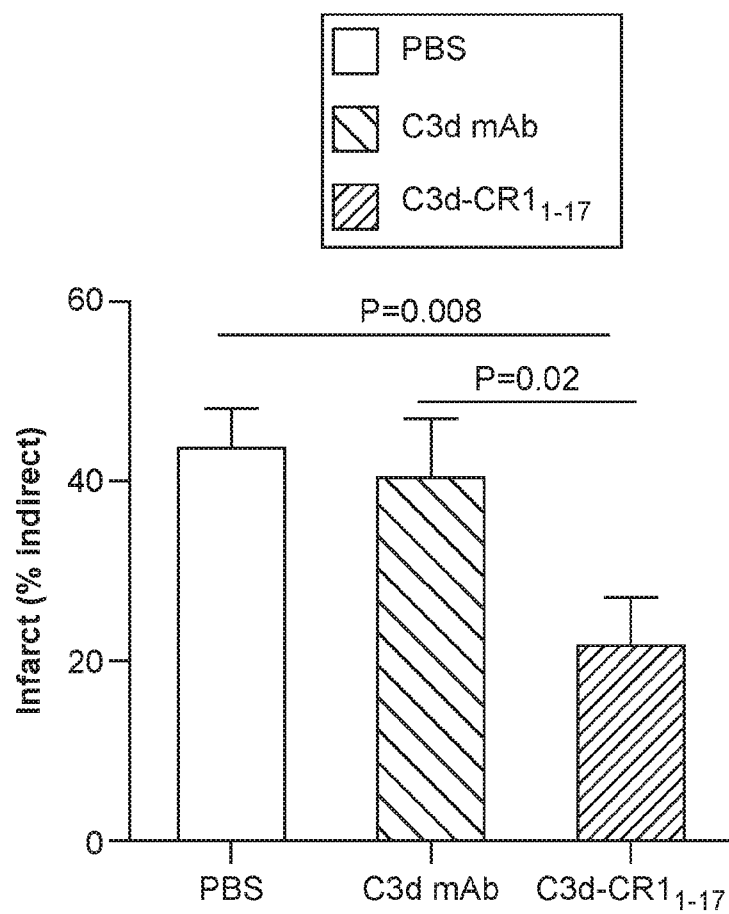


FIG. 34

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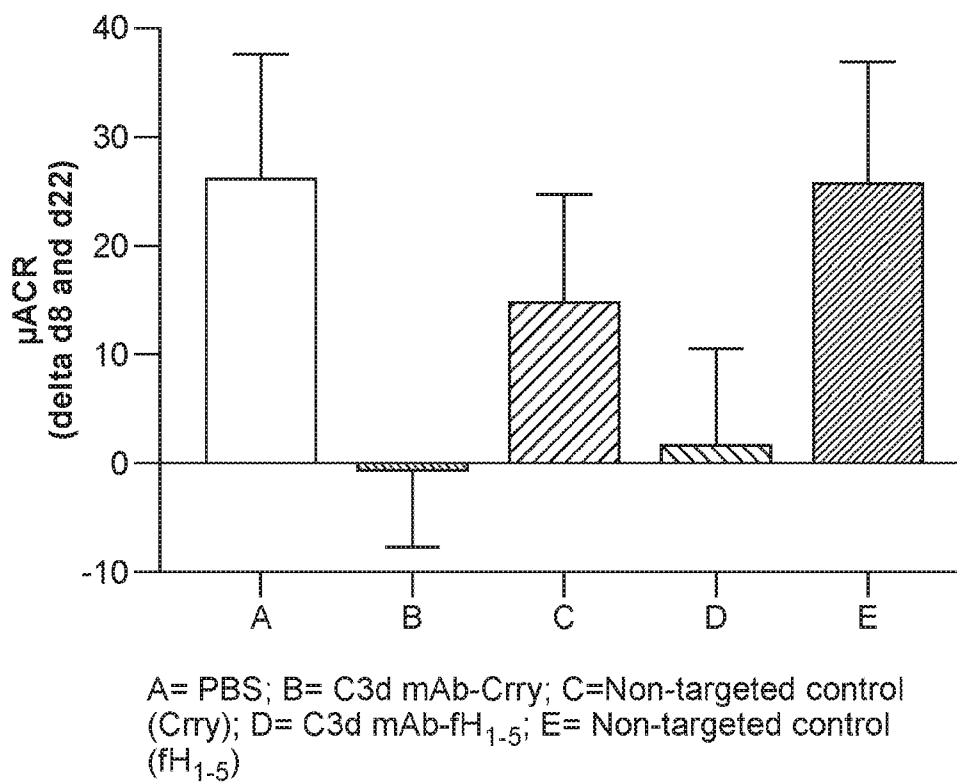


FIG. 35

SEQUENCE LISTING

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Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
245 250 255

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

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Leu Pro
275 280 285

Pro Ser Ser Thr Lys Pro Pro Ala Leu Ser His Ser Val Ser Thr Ser
290 295 300

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

Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu Glu
325 330 335

Gly Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val Ile
340 345 350

Ala Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg Tyr
355 360 365

Leu Gln Arg Arg Lys Lys Lys Gly Thr Tyr Leu Thr Asp Glu Thr His
370 375 380

Arg Glu Val Lys Phe Thr Ser Leu
385 390

<210> 2
<211> 381
<212> PRT
<213> Homo sapiens

<400> 2

Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
1 5 10 15

Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
20 25 30

Trp Gly Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala
35 40 45

Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys
50 55 60

Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile
65 70 75 80

Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg
85 90 95

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

Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu
115 120 125

Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr
130 135 140

Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys
145 150 155 160

Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val
165 170 175

Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr
180 185 190

Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly
195 200 205

Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr
210 215 220

Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg
225 230 235 240

Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly
245 250 255

Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp
260 265 270

Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu
275 280 285

Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val
290 295 300

Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr
305 310 315 320

Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr
325 330 335

Thr Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr
340 345 350

Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr
355 360 365

Gly Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
370 375 380

<210> 3

<211> 390

<212> PRT

<213> Mus musculus

<400> 3

Met Ile Arg Gly Arg Ala Pro Arg Thr Arg Pro Ser Pro Pro Pro Pro
1 5 10 15

Leu Leu Pro Leu Leu Ser Leu Ser Leu Leu Leu Leu Ser Pro Thr Val
20 25 30

Arg Gly Asp Cys Gly Pro Pro Pro Asp Ile Pro Asn Ala Arg Pro Ile
35 40 45

Leu Gly Arg His Ser Lys Phe Ala Glu Gln Ser Lys Val Ala Tyr Ser
50 55 60

Cys Asn Asn Gly Phe Lys Gln Val Pro Asp Lys Ser Asn Ile Val Val
65 70 75 80

Cys Leu Glu Asn Gly Gln Trp Ser Ser His Glu Thr Phe Cys Glu Lys
85 90 95

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

Tyr Leu Asn Met Asn Phe Phe Pro Val Gly Thr Ile Val Glu Tyr Glu
115 120 125

Cys Arg Pro Gly Phe Arg Lys Gln Pro Pro Leu Pro Gly Lys Ala Thr
130 135 140

Cys Leu Glu Asp Leu Val Trp Ser Pro Val Ala Gln Phe Cys Lys Lys
145 150 155 160

Lys Ser Cys Pro Asn Pro Lys Asp Leu Asp Asn Gly His Ile Asn Ile
165 170 175

Pro Thr Gly Ile Leu Phe Gly Ser Glu Ile Asn Phe Ser Cys Asn Pro
180 185 190

Gly Tyr Arg Leu Val Gly Val Ser Ser Thr Phe Cys Ser Val Thr Gly
195 200 205

Asn Thr Val Asp Trp Asp Asp Glu Phe Pro Val Cys Thr Glu Ile His
210 215 220

Cys Pro Glu Pro Pro Lys Ile Asn Asn Gly Ile Met Arg Gly Glu Ser
225 230 235 240

Asp Ser Tyr Thr Tyr Ser Gln Val Val Thr Tyr Ser Cys Asp Lys Gly
245 250 255

Phe Ile Leu Val Gly Asn Ala Ser Ile Tyr Cys Thr Val Ser Lys Ser
260 265 270

Asp Val Gly Gln Trp Ser Ser Pro Pro Pro Arg Cys Ile Glu Lys Ser
275 280 285

Lys Val Pro Thr Lys Lys Pro Thr Ile Asn Val Pro Ser Thr Gly Thr
290 295 300

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

Asp Gln Pro Thr Pro Gln Lys Pro Ser Thr Val Lys Val Ser Ala Thr
325 330 335

Gln His Val Pro Val Thr Lys Thr Thr Val Arg His Pro Ile Arg Thr
340 345 350

Ser Thr Asp Lys Gly Glu Pro Asn Thr Gly Gly Asp Arg Tyr Ile Tyr
355 360 365

Gly His Thr Cys Leu Ile Thr Leu Thr Val Leu His Val Met Leu Ser
370 375 380

Leu Ile Gly Tyr Leu Thr
385 390

<210> 4
<211> 128
<212> PRT
<213> Homo sapiens

<400> 4
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
1 5 10 15

Ala Val Phe Cys His Ser Gly His Ser Leu Gln Cys Tyr Asn Cys Pro
20 25 30

Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe
35 40 45

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

Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg
65 70 75 80

Glu Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe
85 90 95

Asn Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val
100 105 110

Leu Leu Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro
115 120 125

<210> 5
<211> 123
<212> PRT
<213> Mus musculus

<400> 5
Met Arg Ala Gln Arg Gly Leu Ile Leu Leu Leu Leu Leu Ala Val
1 5 10 15

Phe Cys Ser Thr Ala Val Ser Leu Thr Cys Tyr His Cys Phe Gln Pro
20 25 30

Val Val Ser Ser Cys Asn Met Asn Ser Thr Cys Ser Pro Asp Gln Asp
35 40 45

Ser Cys Leu Tyr Ala Val Ala Gly Met Gln Val Tyr Gln Arg Cys Trp

50

55

60

Lys Gln Ser Asp Cys His Gly Glu Ile Ile Met Asp Gln Leu Glu Glu
65 70 75 80

Thr Lys Leu Lys Phe Arg Cys Cys Gln Phe Asn Leu Cys Asn Lys Ser
85 90 95

Asp Gly Ser Leu Gly Lys Thr Pro Leu Leu Gly Thr Ser Val Leu Val
100 105 110

Ala Ile Leu Asn Leu Cys Phe Leu Ser His Leu
115 120

<210> 6

<211> 129

<212> PRT

<213> Mus musculus

<400> 6

Met Arg Ala Gln Arg Gly Leu Ile Leu Leu Leu Leu Leu Ala Val
1 5 10 15

Phe Cys Ser Thr Ala Val Ser Leu Lys Cys Tyr Asn Cys Leu Asp Pro
20 25 30

Val Ser Ser Cys Lys Ile Asn Thr Thr Cys Ser Pro Asn Leu Asp Ser
35 40 45

Cys Leu Tyr Ala Val Ala Gly Arg Gln Val Tyr Gln Gln Cys Trp Lys
50 55 60

Leu Ser Asp Cys Asn Ser Asn Tyr Ile Met Ser Arg Leu Asp Val Ala
65 70 75 80

Gly Ile Gln Ser Lys Cys Cys Gln Trp Asp Leu Cys Asn Lys Asn Leu
85 90 95

Asp Gly Leu Glu Glu Pro Asn Asn Ala Glu Thr Ser Ser Leu Arg Lys
100 105 110

Thr Ala Leu Leu Gly Thr Ser Val Leu Val Ala Ile Leu Lys Phe Cys
115 120 125

Phe

<210> 7

<211> 483

<212> PRT

<213> Mus musculus

<400> 7

Met	Glu	Val	Ser	Ser	Arg	Ser	Ser	Glu	Pro	Leu	Asp	Pro	Val	Trp	Leu
1			5					10					15		
Leu	Val	Ala	Phe	Gly	Arg	Gly	Gly	Val	Lys	Leu	Glu	Val	Leu	Leu	Leu
		20					25					30			
Phe	Leu	Leu	Pro	Phe	Thr	Leu	Gly	Glu	Leu	Arg	Gly	Gly	Leu	Gly	Lys
	35						40				45				
His	Gly	His	Thr	Val	His	Arg	Glu	Pro	Ala	Val	Asn	Arg	Leu	Cys	Ala
	50				55						60				
Asp	Ser	Lys	Arg	Trp	Ser	Gly	Leu	Pro	Val	Ser	Ala	Gln	Arg	Pro	Phe
65					70					75					80
Pro	Met	Gly	His	Cys	Pro	Ala	Pro	Ser	Gln	Leu	Pro	Ser	Ala	Lys	Pro
				85					90					95	
Ile	Asn	Leu	Thr	Asp	Glu	Ser	Met	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Leu
			100					105					110		
Tyr	Glu	Cys	Leu	Pro	Gly	Tyr	Ile	Lys	Arg	Gln	Phe	Ser	Ile	Thr	Cys
		115					120					125			
Lys	Gln	Asp	Ser	Thr	Trp	Thr	Ser	Ala	Glu	Asp	Lys	Cys	Ile	Arg	Lys
	130					135					140				
Gln	Cys	Lys	Thr	Pro	Ser	Asp	Pro	Glu	Asn	Gly	Leu	Val	His	Val	His
145					150					155					160
Thr	Gly	Ile	Gln	Phe	Gly	Ser	Arg	Ile	Asn	Tyr	Thr	Cys	Asn	Gln	Gly
			165						170					175	
Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ser	Ala	Val	Cys	Val	Ile	Thr	Asp	Gln
		180						185					190		
Ser	Val	Asp	Trp	Asp	Thr	Glu	Ala	Pro	Ile	Cys	Glu	Trp	Ile	Pro	Cys
		195					200					205			
Glu	Ile	Pro	Pro	Gly	Ile	Pro	Asn	Gly	Asp	Phe	Phe	Ser	Ser	Thr	Arg
	210					215					220				
Glu	Asp	Phe	His	Tyr	Gly	Met	Val	Val	Thr	Tyr	Arg	Cys	Asn	Thr	Asp
225					230					235					240
Ala	Arg	Gly	Lys	Ala	Leu	Phe	Asn	Leu	Val	Gly	Glu	Pro	Ser	Leu	Tyr
				245					250					255	

Cys Thr Ser Asn Asp Gly Glu Ile Gly Val Trp Ser Gly Pro Pro Pro
 260 265 270

Gln Cys Ile Glu Leu Asn Lys Cys Thr Pro Pro Pro Tyr Val Glu Asn
 275 280 285

Ala Val Met Leu Ser Glu Asn Arg Ser Leu Phe Ser Leu Arg Asp Ile
 290 295 300

Val Glu Phe Arg Cys His Pro Gly Phe Ile Met Lys Gly Ala Ser Ser
 305 310 315 320

Val His Cys Gln Ser Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
 325 330 335

Phe Lys Gly Val Ile Cys Arg Leu Pro Gln Glu Met Ser Gly Phe Gln
 340 345 350

Lys Gly Leu Gly Met Lys Lys Glu Tyr Tyr Tyr Gly Glu Asn Val Thr
 355 360 365

Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly Ser Ser Gln Ser Gln
 370 375 380

Cys Gln Ser Asp Gly Ser Trp Asn Pro Leu Leu Ala Lys Cys Val Ser
 385 390 395 400

Arg Ser Ile Ser Gly Leu Ile Val Gly Ile Phe Ile Gly Ile Ile Val
 405 410 415

Phe Ile Leu Val Ile Ile Val Phe Ile Trp Met Ile Leu Lys Tyr Lys
 420 425 430

Lys Arg Asn Thr Thr Asp Glu Lys Tyr Lys Glu Val Gly Ile His Leu
 435 440 445

Asn Tyr Lys Glu Asp Ser Cys Val Arg Leu Gln Ser Leu Leu Thr Ser
 450 455 460

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

Glu Val Ser

<210> 8
 <211> 2039
 <212> PRT
 <213> Homo sapiens

<400> 8

Met	Gly	Ala	Ser	Ser	Pro	Arg	Ser	Pro	Glu	Pro	Val	Gly	Pro	Pro	Ala
1			5						10					15	
Pro	Gly	Leu	Pro	Phe	Cys	Cys	Gly	Gly	Ser	Leu	Leu	Ala	Val	Val	Val
			20					25					30		
Leu	Leu	Ala	Leu	Pro	Val	Ala	Trp	Gly	Gln	Cys	Asn	Ala	Pro	Glu	Trp
		35					40					45			
Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro
	50					55					60				
Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg
65					70					75					80
Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys
				85					90					95	
Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn
			100					105					110		
Gly	Met	Val	His	Val	Ile	Lys	Gly	Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys
		115					120					125			
Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr
	130					135					140				
Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile
145					150					155					160
Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp
				165					170					175	
Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr
			180					185					190		
Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val
		195					200					205			
Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile
	210					215					220				
Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro
225					230					235					240
Pro	Asn	Val	Glu	Asn	Gly	Ile	Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe
				245					250					255	

Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met
260 265 270

Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro
275 280 285

Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu
290 295 300

His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln
305 310 315 320

Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala
325 330 335

Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr
340 345 350

Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly
355 360 365

Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe
370 375 380

Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys
385 390 395 400

Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys
405 410 415

Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His
420 425 430

Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr
435 440 445

Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly
450 455 460

Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp
465 470 475 480

Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro
485 490 495

Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp
500 505 510

Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr
515 520 525

Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser
530 535 540

Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro
545 550 555 560

Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg
565 570 575

Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser
580 585 590

Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro
595 600 605

Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn
610 615 620

Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val
625 630 635 640

Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu
645 650 655

Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
660 665 670

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys
675 680 685

Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser
690 695 700

Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe
705 710 715 720

Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp
725 730 735

Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp
740 745 750

Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro
755 760 765

Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly

770

775

780

Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala
785 790 795 800

Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu
805 810 815

Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val
820 825 830

Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser
835 840 845

Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro
850 855 860

Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly
865 870 875 880

Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Ala Val
885 890 895

Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu
900 905 910

Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly
915 920 925

Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln
930 935 940

Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala
945 950 955 960

Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu
965 970 975

Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp
980 985 990

Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro
995 1000 1005

Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val
1010 1015 1020

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile
1025 1030 1035

Gly	His	Ser	Ser	Ala	Glu	Cys	Ile	Leu	Ser	Gly	Asn	Thr	Ala	His
1040						1045					1050			
Trp	Ser	Thr	Lys	Pro	Pro	Ile	Cys	Gln	Arg	Ile	Pro	Cys	Gly	Leu
1055						1060					1065			
Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu
1070						1075					1080			
Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Leu	Gly
1085						1090					1095			
Ser	Arg	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile
1100						1105					1110			
Tyr	Cys	Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro
1115						1120					1125			
Ala	Pro	Gln	Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val
1130						1135					1140			
Glu	Asn	Gly	Ile	Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu
1145						1150					1155			
Asn	Glu	Val	Val	Glu	Phe	Arg	Cys	Gln	Pro	Gly	Phe	Val	Met	Lys
1160						1165					1170			
Gly	Pro	Arg	Arg	Val	Lys	Cys	Gln	Ala	Leu	Asn	Lys	Trp	Glu	Pro
1175						1180					1185			
Glu	Leu	Pro	Ser	Cys	Ser	Arg	Val	Cys	Gln	Pro	Pro	Pro	Glu	Ile
1190						1195					1200			
Leu	His	Gly	Glu	His	Thr	Pro	Ser	His	Gln	Asp	Asn	Phe	Ser	Pro
1205						1210					1215			
Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	Pro	Gly	Tyr	Asp	Leu	Arg
1220						1225					1230			
Gly	Ala	Ala	Ser	Leu	His	Cys	Thr	Pro	Gln	Gly	Asp	Trp	Ser	Pro
1235						1240					1245			
Glu	Ala	Pro	Arg	Cys	Ala	Val	Lys	Ser	Cys	Asp	Asp	Phe	Leu	Gly
1250						1255					1260			
Gln	Leu	Pro	His	Gly	Arg	Val	Leu	Phe	Pro	Leu	Asn	Leu	Gln	Leu
1265						1270					1275			

Gly	Ala	Lys	Val	Ser	Phe	Val	Cys	Asp	Glu	Gly	Phe	Arg	Leu	Lys
1280						1285					1290			
Gly	Ser	Ser	Val	Ser	His	Cys	Val	Leu	Val	Gly	Met	Arg	Ser	Leu
1295						1300					1305			
Trp	Asn	Asn	Ser	Val	Pro	Val	Cys	Glu	His	Ile	Phe	Cys	Pro	Asn
1310						1315					1320			
Pro	Pro	Ala	Ile	Leu	Asn	Gly	Arg	His	Thr	Gly	Thr	Pro	Ser	Gly
1325						1330					1335			
Asp	Ile	Pro	Tyr	Gly	Lys	Glu	Ile	Ser	Tyr	Thr	Cys	Asp	Pro	His
1340						1345					1350			
Pro	Asp	Arg	Gly	Met	Thr	Phe	Asn	Leu	Ile	Gly	Glu	Ser	Thr	Ile
1355						1360					1365			
Arg	Cys	Thr	Ser	Asp	Pro	His	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro
1370						1375					1380			
Ala	Pro	Arg	Cys	Glu	Leu	Ser	Val	Arg	Ala	Gly	His	Cys	Lys	Thr
1385						1390					1395			
Pro	Glu	Gln	Phe	Pro	Phe	Ala	Ser	Pro	Thr	Ile	Pro	Ile	Asn	Asp
1400						1405					1410			
Phe	Glu	Phe	Pro	Val	Gly	Thr	Ser	Leu	Asn	Tyr	Glu	Cys	Arg	Pro
1415						1420					1425			
Gly	Tyr	Phe	Gly	Lys	Met	Phe	Ser	Ile	Ser	Cys	Leu	Glu	Asn	Leu
1430						1435					1440			
Val	Trp	Ser	Ser	Val	Glu	Asp	Asn	Cys	Arg	Arg	Lys	Ser	Cys	Gly
1445						1450					1455			
Pro	Pro	Pro	Glu	Pro	Phe	Asn	Gly	Met	Val	His	Ile	Asn	Thr	Asp
1460						1465					1470			
Thr	Gln	Phe	Gly	Ser	Thr	Val	Asn	Tyr	Ser	Cys	Asn	Glu	Gly	Phe
1475						1480					1485			
Arg	Leu	Ile	Gly	Ser	Pro	Ser	Thr	Thr	Cys	Leu	Val	Ser	Gly	Asn
1490						1495					1500			
Asn	Val	Thr	Trp	Asp	Lys	Lys	Ala	Pro	Ile	Cys	Glu	Ile	Ile	Ser
1505						1510					1515			

Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp Phe Tyr Ser Asn
1520 1525 1530

Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr Tyr Gln Cys
1535 1540 1545

His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val Gly Glu
1550 1555 1560

Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val Trp
1565 1570 1575

Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala
1580 1585 1590

Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe
1595 1600 1605

Phe Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe
1610 1615 1620

Val Met Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg
1625 1630 1635

Trp Gly Pro Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro
1640 1645 1650

Pro Glu Ile Leu His Gly Glu His Thr Leu Ser His Gln Asp Asn
1655 1660 1665

Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr
1670 1675 1680

Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr Pro Gln Gly Asp
1685 1690 1695

Trp Ser Pro Glu Ala Pro Arg Cys Thr Val Lys Ser Cys Asp Asp
1700 1705 1710

Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Leu Pro Leu Asn
1715 1720 1725

Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly Phe
1730 1735 1740

Arg Leu Lys Gly Arg Ser Ala Ser His Cys Val Leu Ala Gly Met
1745 1750 1755

Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe

1760					1765					1770				
Cys	Pro	Asn	Pro	Pro	Ala	Ile	Leu	Asn	Gly	Arg	His	Thr	Gly	Thr
	1775					1780					1785			
Pro	Phe	Gly	Asp	Ile	Pro	Tyr	Gly	Lys	Glu	Ile	Ser	Tyr	Ala	Cys
	1790					1795					1800			
Asp	Thr	His	Pro	Asp	Arg	Gly	Met	Thr	Phe	Asn	Leu	Ile	Gly	Glu
	1805					1810					1815			
Ser	Ser	Ile	Arg	Cys	Thr	Ser	Asp	Pro	Gln	Gly	Asn	Gly	Val	Trp
	1820					1825					1830			
Ser	Ser	Pro	Ala	Pro	Arg	Cys	Glu	Leu	Ser	Val	Pro	Ala	Ala	Cys
	1835					1840					1845			
Pro	His	Pro	Pro	Lys	Ile	Gln	Asn	Gly	His	Tyr	Ile	Gly	Gly	His
	1850					1855					1860			
Val	Ser	Leu	Tyr	Leu	Pro	Gly	Met	Thr	Ile	Ser	Tyr	Ile	Cys	Asp
	1865					1870					1875			
Pro	Gly	Tyr	Leu	Leu	Val	Gly	Lys	Gly	Phe	Ile	Phe	Cys	Thr	Asp
	1880					1885					1890			
Gln	Gly	Ile	Trp	Ser	Gln	Leu	Asp	His	Tyr	Cys	Lys	Glu	Val	Asn
	1895					1900					1905			
Cys	Ser	Phe	Pro	Leu	Phe	Met	Asn	Gly	Ile	Ser	Lys	Glu	Leu	Glu
	1910					1915					1920			
Met	Lys	Lys	Val	Tyr	His	Tyr	Gly	Asp	Tyr	Val	Thr	Leu	Lys	Cys
	1925					1930					1935			
Glu	Asp	Gly	Tyr	Thr	Leu	Glu	Gly	Ser	Pro	Trp	Ser	Gln	Cys	Gln
	1940					1945					1950			
Ala	Asp	Asp	Arg	Trp	Asp	Pro	Pro	Leu	Ala	Lys	Cys	Thr	Ser	Arg
	1955					1960					1965			
Thr	His	Asp	Ala	Leu	Ile	Val	Gly	Thr	Leu	Ser	Gly	Thr	Ile	Phe
	1970					1975					1980			
Phe	Ile	Leu	Leu	Ile	Ile	Phe	Leu	Ser	Trp	Ile	Ile	Leu	Lys	His
	1985					1990					1995			
Arg	Lys	Gly	Asn	Asn	Ala	His	Glu	Asn	Pro	Lys	Glu	Val	Ala	Ile
	2000					2005					2010			

His Leu His Ser Gln Gly Gly Ser Ser Val His Pro Arg Thr Leu
2015 2020 2025

Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro
2030 2035

<210> 9
<211> 1231
<212> PRT
<213> Homo sapiens

<400> 9
Met Arg Leu Leu Ala Lys Ile Ile Cys Leu Met Leu Trp Ala Ile Cys
1 5 10 15

Val Ala Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile
20 25 30

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

Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met
50 55 60

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

Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe
85 90 95

Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr
100 105 110

Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu
115 120 125

Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val
130 135 140

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

Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe
165 170 175

Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys
180 185 190

Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile

195

200

205

Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys
 210 215 220

Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly
 225 230 235 240

Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp
 245 250 255

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

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

Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly
 290 295 300

Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys
 305 310 315 320

Thr Leu Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr
 325 330 335

His Glu Asn Met Arg Arg Pro Tyr Phe Pro Val Ala Val Gly Lys Tyr
 340 345 350

Tyr Ser Tyr Tyr Cys Asp Glu His Phe Glu Thr Pro Ser Gly Ser Tyr
 355 360 365

Trp Asp His Ile His Cys Thr Gln Asp Gly Trp Ser Pro Ala Val Pro
 370 375 380

Cys Leu Arg Lys Cys Tyr Phe Pro Tyr Leu Glu Asn Gly Tyr Asn Gln
 385 390 395 400

Asn Tyr Gly Arg Lys Phe Val Gln Gly Lys Ser Ile Asp Val Ala Cys
 405 410 415

His Pro Gly Tyr Ala Leu Pro Lys Ala Gln Thr Thr Val Thr Cys Met
 420 425 430

Glu Asn Gly Trp Ser Pro Thr Pro Arg Cys Ile Arg Val Lys Thr Cys
 435 440 445

Ser Lys Ser Ser Ile Asp Ile Glu Asn Gly Phe Ile Ser Glu Ser Gln
 450 455 460

Tyr	Thr	Tyr	Ala	Leu	Lys	Glu	Lys	Ala	Lys	Tyr	Gln	Cys	Lys	Leu	Gly	465	470	475	480
Tyr	Val	Thr	Ala	Asp	Gly	Glu	Thr	Ser	Gly	Ser	Ile	Thr	Cys	Gly	Lys		485	490	495
Asp	Gly	Trp	Ser	Ala	Gln	Pro	Thr	Cys	Ile	Lys	Ser	Cys	Asp	Ile	Pro	500		505	510
Val	Phe	Met	Asn	Ala	Arg	Thr	Lys	Asn	Asp	Phe	Thr	Trp	Phe	Lys	Leu	515		520	525
Asn	Asp	Thr	Leu	Asp	Tyr	Glu	Cys	His	Asp	Gly	Tyr	Glu	Ser	Asn	Thr	530	535	540	
Gly	Ser	Thr	Thr	Gly	Ser	Ile	Val	Cys	Gly	Tyr	Asn	Gly	Trp	Ser	Asp	545	550	555	560
Leu	Pro	Ile	Cys	Tyr	Glu	Arg	Glu	Cys	Glu	Leu	Pro	Lys	Ile	Asp	Val	565		570	575
His	Leu	Val	Pro	Asp	Arg	Lys	Lys	Asp	Gln	Tyr	Lys	Val	Gly	Glu	Val	580		585	590
Leu	Lys	Phe	Ser	Cys	Lys	Pro	Gly	Phe	Thr	Ile	Val	Gly	Pro	Asn	Ser	595		600	605
Val	Gln	Cys	Tyr	His	Phe	Gly	Leu	Ser	Pro	Asp	Leu	Pro	Ile	Cys	Lys	610	615	620	
Glu	Gln	Val	Gln	Ser	Cys	Gly	Pro	Pro	Pro	Glu	Leu	Leu	Asn	Gly	Asn	625	630	635	640
Val	Lys	Glu	Lys	Thr	Lys	Glu	Glu	Tyr	Gly	His	Ser	Glu	Val	Val	Glu	645		650	655
Tyr	Tyr	Cys	Asn	Pro	Arg	Phe	Leu	Met	Lys	Gly	Pro	Asn	Lys	Ile	Gln	660		665	670
Cys	Val	Asp	Gly	Glu	Trp	Thr	Thr	Leu	Pro	Val	Cys	Ile	Val	Glu	Glu	675		680	685
Ser	Thr	Cys	Gly	Asp	Ile	Pro	Glu	Leu	Glu	His	Gly	Trp	Ala	Gln	Leu	690	695	700	
Ser	Ser	Pro	Pro	Tyr	Tyr	Tyr	Gly	Asp	Ser	Val	Glu	Phe	Asn	Cys	Ser	705	710	715	720

Glu Ser Phe Thr Met Ile Gly His Arg Ser Ile Thr Cys Ile His Gly
725 730 735

Val Trp Thr Gln Leu Pro Gln Cys Val Ala Ile Asp Lys Leu Lys Lys
740 745 750

Cys Lys Ser Ser Asn Leu Ile Ile Leu Glu Glu His Leu Lys Asn Lys
755 760 765

Lys Glu Phe Asp His Asn Ser Asn Ile Arg Tyr Arg Cys Arg Gly Lys
770 775 780

Glu Gly Trp Ile His Thr Val Cys Ile Asn Gly Arg Trp Asp Pro Glu
785 790 795 800

Val Asn Cys Ser Met Ala Gln Ile Gln Leu Cys Pro Pro Pro Pro Gln
805 810 815

Ile Pro Asn Ser His Asn Met Thr Thr Thr Leu Asn Tyr Arg Asp Gly
820 825 830

Glu Lys Val Ser Val Leu Cys Gln Glu Asn Tyr Leu Ile Gln Glu Gly
835 840 845

Glu Glu Ile Thr Cys Lys Asp Gly Arg Trp Gln Ser Ile Pro Leu Cys
850 855 860

Val Glu Lys Ile Pro Cys Ser Gln Pro Pro Gln Ile Glu His Gly Thr
865 870 875 880

Ile Asn Ser Ser Arg Ser Ser Gln Glu Ser Tyr Ala His Gly Thr Lys
885 890 895

Leu Ser Tyr Thr Cys Glu Gly Gly Phe Arg Ile Ser Glu Glu Asn Glu
900 905 910

Thr Thr Cys Tyr Met Gly Lys Trp Ser Ser Pro Pro Gln Cys Glu Gly
915 920 925

Leu Pro Cys Lys Ser Pro Pro Glu Ile Ser His Gly Val Val Ala His
930 935 940

Met Ser Asp Ser Tyr Gln Tyr Gly Glu Glu Val Thr Tyr Lys Cys Phe
945 950 955 960

Glu Gly Phe Gly Ile Asp Gly Pro Ala Ile Ala Lys Cys Leu Gly Glu
965 970 975

Lys Trp Ser His Pro Pro Ser Cys Ile Lys Thr Asp Cys Leu Ser Leu
980 985 990

Pro Ser Phe Glu Asn Ala Ile Pro Met Gly Glu Lys Lys Asp Val Tyr
995 1000 1005

Lys Ala Gly Glu Gln Val Thr Tyr Thr Cys Ala Thr Tyr Tyr Lys
1010 1015 1020

Met Asp Gly Ala Ser Asn Val Thr Cys Ile Asn Ser Arg Trp Thr
1025 1030 1035

Gly Arg Pro Thr Cys Arg Asp Thr Ser Cys Val Asn Pro Pro Thr
1040 1045 1050

Val Gln Asn Ala Tyr Ile Val Ser Arg Gln Met Ser Lys Tyr Pro
1055 1060 1065

Ser Gly Glu Arg Val Arg Tyr Gln Cys Arg Ser Pro Tyr Glu Met
1070 1075 1080

Phe Gly Asp Glu Glu Val Met Cys Leu Asn Gly Asn Trp Thr Glu
1085 1090 1095

Pro Pro Gln Cys Lys Asp Ser Thr Gly Lys Cys Gly Pro Pro Pro
1100 1105 1110

Pro Ile Asp Asn Gly Asp Ile Thr Ser Phe Pro Leu Ser Val Tyr
1115 1120 1125

Ala Pro Ala Ser Ser Val Glu Tyr Gln Cys Gln Asn Leu Tyr Gln
1130 1135 1140

Leu Glu Gly Asn Lys Arg Ile Thr Cys Arg Asn Gly Gln Trp Ser
1145 1150 1155

Glu Pro Pro Lys Cys Leu His Pro Cys Val Ile Ser Arg Glu Ile
1160 1165 1170

Met Glu Asn Tyr Asn Ile Ala Leu Arg Trp Thr Ala Lys Gln Lys
1175 1180 1185

Leu Tyr Ser Arg Thr Gly Glu Ser Val Glu Phe Val Cys Lys Arg
1190 1195 1200

Gly Tyr Arg Leu Ser Ser Arg Ser His Thr Leu Arg Thr Thr Cys
1205 1210 1215

Trp Asp Gly Lys Leu Glu Tyr Pro Thr Cys Ala Lys Arg

1220

1225

1230

<210> 10

<211> 1234

<212> PRT

<213> Mus musculus

<400> 10

Met Arg Leu Ser Ala Arg Ile Ile Trp Leu Ile Leu Trp Thr Val Cys
 1 5 10 15

Ala Ala Glu Asp Cys Lys Gly Pro Pro Arg Glu Asn Ser Glu Ile
 20 25 30

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

Thr Tyr Lys Cys Arg Pro Gly Tyr Arg Thr Leu Gly Thr Ile Val Lys
 50 55 60

Val Cys Lys Asn Gly Lys Trp Val Ala Ser Asn Pro Ser Arg Ile Cys
 65 70 75 80

Arg Lys Lys Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Ser Phe
 85 90 95

Arg Leu Ala Val Gly Ser Gln Phe Glu Phe Gly Ala Lys Val Val Tyr
 100 105 110

Thr Cys Asp Asp Gly Tyr Gln Leu Leu Gly Glu Ile Asp Tyr Arg Glu
 115 120 125

Cys Gly Ala Asp Gly Trp Ile Asn Asp Ile Pro Leu Cys Glu Val Val
 130 135 140

Lys Cys Leu Pro Val Thr Glu Leu Glu Asn Gly Arg Ile Val Ser Gly
 145 150 155 160

Ala Ala Glu Thr Asp Gln Glu Tyr Tyr Phe Gly Gln Val Val Arg Phe
 165 170 175

Glu Cys Asn Ser Gly Phe Lys Ile Glu Gly His Lys Glu Ile His Cys
 180 185 190

Ser Glu Asn Gly Leu Trp Ser Asn Glu Lys Pro Arg Cys Val Glu Ile
 195 200 205

Leu Cys Thr Pro Pro Arg Val Glu Asn Gly Asp Gly Ile Asn Val Lys
 210 215 220

Pro Val Tyr Lys Glu Asn Glu Arg Tyr His Tyr Lys Cys Lys His Gly
225 230 235 240

Tyr Val Pro Lys Glu Arg Gly Asp Ala Val Cys Thr Gly Ser Gly Trp
245 250 255

Ser Ser Gln Pro Phe Cys Glu Glu Lys Arg Cys Ser Pro Pro Tyr Ile
260 265 270

Leu Asn Gly Ile Tyr Thr Pro His Arg Ile Ile His Arg Ser Asp Asp
275 280 285

Glu Ile Arg Tyr Glu Cys Asn Tyr Gly Phe Tyr Pro Val Thr Gly Ser
290 295 300

Thr Val Ser Lys Cys Thr Pro Thr Gly Trp Ile Pro Val Pro Arg Cys
305 310 315 320

Thr Leu Lys Pro Cys Glu Phe Pro Gln Phe Lys Tyr Gly Arg Leu Tyr
325 330 335

Tyr Glu Glu Ser Leu Arg Pro Asn Phe Pro Val Ser Ile Gly Asn Lys
340 345 350

Tyr Ser Tyr Lys Cys Asp Asn Gly Phe Ser Pro Pro Ser Gly Tyr Ser
355 360 365

Trp Asp Tyr Leu Arg Cys Thr Ala Gln Gly Trp Glu Pro Glu Val Pro
370 375 380

Cys Val Arg Lys Cys Val Phe His Tyr Val Glu Asn Gly Asp Ser Ala
385 390 395 400

Tyr Trp Glu Lys Val Tyr Val Gln Gly Gln Ser Leu Lys Val Gln Cys
405 410 415

Tyr Asn Gly Tyr Ser Leu Gln Asn Gly Gln Asp Thr Met Thr Cys Thr
420 425 430

Glu Asn Gly Trp Ser Pro Pro Pro Lys Cys Ile Arg Ile Lys Thr Cys
435 440 445

Ser Ala Ser Asp Ile His Ile Asp Asn Gly Phe Leu Ser Glu Ser Ser
450 455 460

Ser Ile Tyr Ala Leu Asn Arg Glu Thr Ser Tyr Arg Cys Lys Gln Gly
465 470 475 480

Tyr Val Thr Asn Thr Gly Glu Ile Ser Gly Ser Ile Thr Cys Leu Gln

485

490

495

Asn Gly Trp Ser Pro Gln Pro Ser Cys Ile Lys Ser Cys Asp Met Pro
 500 505 510

Val Phe Glu Asn Ser Ile Thr Lys Asn Thr Arg Thr Trp Phe Lys Leu
 515 520 525

Asn Asp Lys Leu Asp Tyr Glu Cys Leu Val Gly Phe Glu Asn Glu Tyr
 530 535 540

Lys His Thr Lys Gly Ser Ile Thr Cys Thr Tyr Tyr Gly Trp Ser Asp
 545 550 555 560

Thr Pro Ser Cys Tyr Glu Arg Glu Cys Ser Val Pro Thr Leu Asp Arg
 565 570 575

Lys Leu Val Val Ser Pro Arg Lys Glu Lys Tyr Arg Val Gly Asp Leu
 580 585 590

Leu Glu Phe Ser Cys His Ser Gly His Arg Val Gly Pro Asp Ser Val
 595 600 605

Gln Cys Tyr His Phe Gly Trp Ser Pro Gly Phe Pro Thr Cys Lys Gly
 610 615 620

Gln Val Ala Ser Cys Ala Pro Pro Leu Glu Ile Leu Asn Gly Glu Ile
 625 630 635 640

Asn Gly Ala Lys Lys Val Glu Tyr Ser His Gly Glu Val Val Lys Tyr
 645 650 655

Asp Cys Lys Pro Arg Phe Leu Leu Lys Gly Pro Asn Lys Ile Gln Cys
 660 665 670

Val Asp Gly Asn Trp Thr Thr Leu Pro Val Cys Ile Glu Glu Glu Arg
 675 680 685

Thr Cys Gly Asp Ile Pro Glu Leu Glu His Gly Ser Ala Lys Cys Ser
 690 695 700

Val Pro Pro Tyr His His Gly Asp Ser Val Glu Phe Ile Cys Glu Glu
 705 710 715 720

Asn Phe Thr Met Ile Gly His Gly Ser Val Ser Cys Ile Ser Gly Lys
 725 730 735

Trp Thr Gln Leu Pro Lys Cys Val Ala Thr Asp Gln Leu Glu Lys Cys
 740 745 750

Arg Val Leu Lys Ser Thr Gly Ile Glu Ala Ile Lys Pro Lys Leu Thr
755 760 765

Glu Phe Thr His Asn Ser Thr Met Asp Tyr Lys Cys Arg Asp Lys Gln
770 775 780

Glu Tyr Glu Arg Ser Ile Cys Ile Asn Gly Lys Trp Asp Pro Glu Pro
785 790 795 800

Asn Cys Thr Ser Lys Thr Ser Cys Pro Pro Pro Gln Ile Pro Asn
805 810 815

Thr Gln Val Ile Glu Thr Thr Val Lys Tyr Leu Asp Gly Glu Lys Leu
820 825 830

Ser Val Leu Cys Gln Asp Asn Tyr Leu Thr Gln Asp Ser Glu Glu Met
835 840 845

Val Cys Lys Asp Gly Arg Trp Gln Ser Leu Pro Arg Cys Ile Glu Lys
850 855 860

Ile Pro Cys Ser Gln Pro Pro Thr Ile Glu His Gly Ser Ile Asn Leu
865 870 875 880

Pro Arg Ser Ser Glu Glu Arg Arg Asp Ser Ile Glu Ser Ser Ser His
885 890 895

Glu His Gly Thr Thr Phe Ser Tyr Val Cys Asp Asp Gly Phe Arg Ile
900 905 910

Pro Glu Glu Asn Arg Ile Thr Cys Tyr Met Gly Lys Trp Ser Thr Pro
915 920 925

Pro Arg Cys Val Gly Leu Pro Cys Gly Pro Pro Pro Ser Ile Pro Leu
930 935 940

Gly Thr Val Ser Leu Glu Leu Glu Ser Tyr Gln His Gly Glu Glu Val
945 950 955 960

Thr Tyr His Cys Ser Thr Gly Phe Gly Ile Asp Gly Pro Ala Phe Ile
965 970 975

Ile Cys Glu Gly Gly Lys Trp Ser Asp Pro Pro Lys Cys Ile Lys Thr
980 985 990

Asp Cys Asp Val Leu Pro Thr Val Lys Asn Ala Ile Ile Arg Gly Lys
995 1000 1005

Ser	Lys	Lys	Ser	Tyr	Arg	Thr	Gly	Glu	Gln	Val	Thr	Phe	Arg	Cys
1010						1015					1020			
Gln	Ser	Pro	Tyr	Gln	Met	Asn	Gly	Ser	Asp	Thr	Val	Thr	Cys	Val
1025						1030					1035			
Asn	Ser	Arg	Trp	Ile	Gly	Gln	Pro	Val	Cys	Lys	Asp	Asn	Ser	Cys
1040						1045					1050			
Val	Asp	Pro	Pro	His	Val	Pro	Asn	Ala	Thr	Ile	Val	Thr	Arg	Thr
1055						1060					1065			
Lys	Asn	Lys	Tyr	Leu	His	Gly	Asp	Arg	Val	Arg	Tyr	Glu	Cys	Asn
1070						1075					1080			
Lys	Pro	Leu	Glu	Leu	Phe	Gly	Gln	Val	Glu	Val	Met	Cys	Glu	Asn
1085						1090					1095			
Gly	Ile	Trp	Thr	Glu	Lys	Pro	Lys	Cys	Arg	Asp	Ser	Thr	Gly	Lys
1100						1105					1110			
Cys	Gly	Pro	Pro	Pro	Pro	Ile	Asp	Asn	Gly	Asp	Ile	Thr	Ser	Leu
1115						1120					1125			
Ser	Leu	Pro	Val	Tyr	Glu	Pro	Leu	Ser	Ser	Val	Glu	Tyr	Gln	Cys
1130						1135					1140			
Gln	Lys	Tyr	Tyr	Leu	Leu	Lys	Gly	Lys	Lys	Thr	Ile	Thr	Cys	Arg
1145						1150					1155			
Asn	Gly	Lys	Trp	Ser	Glu	Pro	Pro	Thr	Cys	Leu	His	Ala	Cys	Val
1160						1165					1170			
Ile	Pro	Glu	Asn	Ile	Met	Glu	Ser	His	Asn	Ile	Ile	Leu	Lys	Trp
1175						1180					1185			
Arg	His	Thr	Glu	Lys	Ile	Tyr	Ser	His	Ser	Gly	Glu	Asp	Ile	Glu
1190						1195					1200			
Phe	Gly	Cys	Lys	Tyr	Gly	Tyr	Tyr	Lys	Ala	Arg	Asp	Ser	Pro	Pro
1205						1210					1215			
Phe	Arg	Thr	Lys	Cys	Ile	Asn	Gly	Thr	Ile	Asn	Tyr	Pro	Thr	Cys
1220						1225					1230			

Val

<210> 11
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic peptide

 <400> 11
 Gly Tyr Thr Phe Thr Asp Tyr Tyr
 1 5

 <210> 12
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic peptide

 <400> 12
 Ile Asn Pro Asn Asn Gly Gly Thr
 1 5

 <210> 13
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
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 <400> 13
 Ala Arg Tyr Asp Tyr Ala Trp Tyr Phe Asp Val
 1 5 10

 <210> 14
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
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 <400> 14
 Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr
 1 5 10

 <210> 15
 <211> 3
 <212> PRT
 <213> Artificial Sequence

 <220>
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<400> 15
Lys Val Ser
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<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 16
Phe Gln Gly Ser His Val Pro Tyr Thr
1 5

<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 17
Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 18
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 18
Ile Asn Pro Ser Asn Gly Gly Thr
1 5

<210> 19
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 19
Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr
1 5 10

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 20
Gln Asp Val Gly Thr Ala
1 5

<210> 21
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 21
Trp Ala Ser
1

<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 22
Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 23
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 23
Gly Tyr Thr Phe Thr Ala Tyr Tyr
1 5

<210> 24
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 24
Ile Asn Pro Tyr Asn Gly Gly Thr
1 5

<210> 25
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 25
Ser Ser Pro Tyr
1

<210> 26
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 26
Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
1 5 10

<210> 27
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 27
Leu Val Ser
1

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 28
Trp Gln Gly Thr His Phe Pro Arg Thr
1 5

<210> 29
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 29

Gly Tyr Thr Phe Thr Asn Tyr Tyr

1 5

<210> 30

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 30

Ile Asn Pro Tyr Asn Gly Gly Thr

1 5

<210> 31

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 31

Ser Ser Pro Tyr

1

<210> 32

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 32

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr

1 5 10

<210> 33

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 33

Leu Val Ser

1

<210> 34

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 34

Trp Gln Gly Thr His Phe Pro Arg Thr
1 5

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 35

Gly Tyr Thr Phe Thr Asp Tyr Tyr
1 5

<210> 36

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 36

Ile Asn Pro Tyr Asn Gly Gly Thr
1 5

<210> 37

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 37

Ser Arg Gly Gly Pro Tyr
1 5

<210> 38

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 38

Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
1 5 10

<210> 39
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 39
Leu Val Ser
1

<210> 40
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 40
Trp Gln Gly Thr His Phe Pro Arg Thr
1 5

<210> 41
<211> 646
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 41
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile

100

105

110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys
645

<210> 42
<211> 1096
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
645 650 655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
945 950 955 960

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val

965

970

975

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 995 1000 1005

Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile
 1010 1015 1020

Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
 1025 1030 1035

Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
 1040 1045 1050

Cys Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly
 1055 1060 1065

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile
 1070 1075 1080

Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
 1085 1090 1095

<210> 43

<211> 897

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 43

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser His Lys Phe
130 135 140

Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
210 215 220

Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro
245 250 255

Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu
260 265 270

Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser
275 280 285

Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr Gly
290 295 300

Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro
305 310 315 320

Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser Gln
325 330 335

Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser

340

345

350

Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu Thr
 355 360 365

Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn
 370 375 380

Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val
 385 390 395 400

Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu
 405 410 415

Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
 420 425 430

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys
 435 440 445

Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser
 450 455 460

Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe
 465 470 475 480

Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp
 485 490 495

Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp
 500 505 510

Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro
 515 520 525

Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly
 530 535 540

Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala
 545 550 555 560

Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu
 565 570 575

Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val
 580 585 590

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

Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro
 610 615 620

Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly
 625 630 635 640

Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr Val
 645 650 655

Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu
 660 665 670

Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly
 675 680 685

Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln
 690 695 700

Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala
 705 710 715 720

Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu
 725 730 735

Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp
 740 745 750

Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro
 755 760 765

Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly
 770 775 780

Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His
 785 790 795 800

Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser Thr
 805 810 815

Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile
 820 825 830

Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly
 835 840 845

Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val
 850 855 860

Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp
865 870 875 880

Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn
885 890 895

Lys

<210> 44
<211> 570
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 44
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser His Lys Phe
130 135 140

Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
 180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
 210 215 220

Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
 225 230 235 240

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys Pro Ala Pro Ser
 245 250 255

Gln Leu Pro Ser Ala Lys Pro Ile Asn Leu Thr Asp Glu Ser Met Phe
 260 265 270

Pro Ile Gly Thr Tyr Leu Leu Tyr Glu Cys Leu Pro Gly Tyr Ile Lys
 275 280 285

Arg Gln Phe Ser Ile Thr Cys Lys Gln Asp Ser Thr Trp Thr Ser Ala
 290 295 300

Glu Asp Lys Cys Ile Arg Lys Gln Cys Lys Thr Pro Ser Asp Pro Glu
 305 310 315 320

Asn Gly Leu Val His Val His Thr Gly Ile Gln Phe Gly Ser Arg Ile
 325 330 335

Asn Tyr Thr Cys Asn Gln Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala
 340 345 350

Val Cys Val Ile Thr Asp Gln Ser Val Asp Trp Asp Thr Glu Ala Pro
 355 360 365

Ile Cys Glu Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly
 370 375 380

Asp Phe Phe Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val
 385 390 395 400

Thr Tyr Arg Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu
 405 410 415

Val Gly Glu Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly
 420 425 430

Val Trp Ser Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr
435 440 445

Pro Pro Pro Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser
450 455 460

Leu Phe Ser Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe
465 470 475 480

Ile Met Lys Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp
485 490 495

Glu Pro Glu Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro
500 505 510

Gln Glu Met Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr
515 520 525

Tyr Tyr Gly Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu
530 535 540

Glu Gly Ser Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro
545 550 555 560

Leu Leu Ala Lys Cys Val Ser Arg Ser Ile
565 570

<210> 45
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 45
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
100 105 110

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

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130 135 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145 150 155 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> 46
<211> 551
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 46
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65					70						75					80
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Arg	Arg	Gly	Ile	Arg	Leu	Arg	His	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	
			100					105					110			
Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Pro	Pro	Ser	Val	Tyr	
		115					120					125				
Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	Thr	Asn	Ser	Met	Val	Thr	Leu	
	130					135					140					
Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	
145					150					155					160	
Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
			165						170					175		
Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Pro	Ser	Ser	
			180					185					190			
Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	
		195					200					205				
Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	Cys	Gly	Gly	Gly	
	210					215					220					
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Cys	Pro	Ala	Pro	Ser	Gln	Leu	Pro	
225					230					235					240	
Ser	Ala	Lys	Pro	Ile	Asn	Leu	Thr	Asp	Glu	Ser	Met	Phe	Pro	Ile	Gly	
			245						250					255		
Thr	Tyr	Leu	Leu	Tyr	Glu	Cys	Leu	Pro	Gly	Tyr	Ile	Lys	Arg	Gln	Phe	
		260						265					270			
Ser	Ile	Thr	Cys	Lys	Gln	Asp	Ser	Thr	Trp	Thr	Ser	Ala	Glu	Asp	Lys	
		275					280					285				
Cys	Ile	Arg	Lys	Gln	Cys	Lys	Thr	Pro	Ser	Asp	Pro	Glu	Asn	Gly	Leu	
	290					295					300					
Val	His	Val	His	Thr	Gly	Ile	Gln	Phe	Gly	Ser	Arg	Ile	Asn	Tyr	Thr	
305					310					315					320	
Cys	Asn	Gln	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ser	Ala	Val	Cys	Val	
				325					330					335		

Ile Thr Asp Gln Ser Val Asp Trp Asp Thr Glu Ala Pro Ile Cys Glu
340 345 350

Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly Asp Phe Phe
355 360 365

Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val Thr Tyr Arg
370 375 380

Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu Val Gly Glu
385 390 395 400

Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly Val Trp Ser
405 410 415

Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr Pro Pro Pro
420 425 430

Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser Leu Phe Ser
435 440 445

Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe Ile Met Lys
450 455 460

Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp Glu Pro Glu
465 470 475 480

Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro Gln Glu Met
485 490 495

Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr Tyr Tyr Gly
500 505 510

Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly Ser
515 520 525

Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro Leu Leu Ala
530 535 540

Lys Cys Val Ser Arg Ser Ile
545 550

<210> 47

<211> 878

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 47

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu
225 230 235 240

Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile
245 250 255

Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro
 260 265 270

Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp
 275 280 285

Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly
 290 295 300

Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr
 305 310 315 320

Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys
 325 330 335

Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys
 340 345 350

Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe
 355 360 365

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr
 370 375 380

Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly
 385 390 395 400

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp
 405 410 415

Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro
 420 425 430

Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser
 435 440 445

Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys
 450 455 460

Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu
 465 470 475 480

Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His
 485 490 495

Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu
 500 505 510

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

Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys
 530 535 540

Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg
 545 550 555 560

Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val
 565 570 575

Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val
 580 585 590

Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu
 595 600 605

Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr
 610 615 620

Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr
 625 630 635 640

Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu
 645 650 655

Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser
 660 665 670

Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp
 675 680 685

His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe
 690 695 700

Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly
 705 710 715 720

Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro
 725 730 735

Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val
 740 745 750

Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile
 755 760 765

Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala
770 775 780

Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro
785 790 795 800

Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly
805 810 815

Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val
820 825 830

Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
835 840 845

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly
850 855 860

Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
865 870 875

<210> 48
<211> 1328
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 48
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Gly Gly
 210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu
 225 230 235 240

Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile
 245 250 255

Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro
 260 265 270

Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp
 275 280 285

Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly
 290 295 300

Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr
 305 310 315 320

Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys
 325 330 335

Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys
 340 345 350

Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe
 355 360 365

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr
370 375 380

Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly
385 390 395 400

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp
405 410 415

Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro
420 425 430

Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser
435 440 445

Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys
450 455 460

Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu
465 470 475 480

Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His
485 490 495

Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu
500 505 510

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

Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys
530 535 540

Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg
545 550 555 560

Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val
565 570 575

Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val
580 585 590

Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu
595 600 605

Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr
610 615 620

Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr

625		630		635		640
Cys Asp Pro His	Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu	645		650		655
Ser Thr Ile Arg Cys Thr Ser Asp	Pro Gln Gly Asn Gly Val Trp Ser	660		665		670
Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp		675		680		685
His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe		690		695		700
Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly		705		710		720
Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro		725		730		735
Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val		740		745		750
Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile		755		760		765
Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala		770		775		780
Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro		785		790		800
Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly		805		810		815
Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val		820		825		830
Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu		835		840		845
Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly		850		855		860
Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr		865		870		875
Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu		885		890		895

Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val
 900 905 910

Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu
 915 920 925

Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val
 930 935 940

Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly
 945 950 955 960

Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala
 965 970 975

Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro
 980 985 990

Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn
 995 1000 1005

Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val
 1010 1015 1020

Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
 1025 1030 1035

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser
 1040 1045 1050

Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
 1055 1060 1065

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe
 1070 1075 1080

Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 1085 1090 1095

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser
 1100 1105 1110

Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 1115 1120 1125

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala
 1130 1135 1140

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
660 665 670

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
675 680 685

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
690 695 700

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
705 710 715 720

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
725 730 735

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
740 745 750

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
755 760 765

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
770 775 780

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu

785 790 795 800

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
805 810 815

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
820 825 830

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
835 840 845

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
850 855 860

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
865 870 875

<210> 50
<211> 1328
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 50
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro

385					390						395					400
Phe	Gly	Lys	Thr	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	Arg	Gly	
				405					410					415		
Thr	Ser	Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	Ser	Asp	
			420					425					430			
Pro	Gln	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	Gly	Ile	
		435					440					445				
Leu	Gly	His	Cys	Gln	Ala	Pro	Asp	His	Phe	Leu	Phe	Ala	Lys	Leu	Lys	
	450					455					460					
Thr	Gln	Thr	Asn	Ala	Ser	Asp	Phe	Pro	Ile	Gly	Thr	Ser	Leu	Lys	Tyr	
465					470					475					480	
Glu	Cys	Arg	Pro	Glu	Tyr	Tyr	Gly	Arg	Pro	Phe	Ser	Ile	Thr	Cys	Leu	
				485					490					495		
Asp	Asn	Leu	Val	Trp	Ser	Ser	Pro	Lys	Asp	Val	Cys	Lys	Arg	Lys	Ser	
			500					505					510			
Cys	Lys	Thr	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Thr	
		515					520					525				
Asp	Ile	Gln	Val	Gly	Ser	Arg	Ile	Asn	Tyr	Ser	Cys	Thr	Thr	Gly	His	
	530					535					540					
Arg	Leu	Ile	Gly	His	Ser	Ser	Ala	Glu	Cys	Ile	Leu	Ser	Gly	Asn	Ala	
545					550					555					560	
Ala	His	Trp	Ser	Thr	Lys	Pro	Pro	Ile	Cys	Gln	Arg	Ile	Pro	Cys	Gly	
				565					570					575		
Leu	Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	
			580					585					590			
Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	
		595					600					605				
Gly	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	
	610					615					620					
Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	
625					630					635					640	
Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	
				645					650					655		

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
 660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
945 950 955 960

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
965 970 975

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
980 985 990

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
995 1000 1005

Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile
1010 1015 1020

Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
1025 1030 1035

Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
1040 1045 1050

Cys Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly
1055 1060 1065

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile
1070 1075 1080

Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Gly Gly
1085 1090 1095

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Pro
1100 1105 1110

Gly Thr Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys
1115 1120 1125

Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met His Trp Val
1130 1135 1140

Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Asn Ile Asn
1145 1150 1155

Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys Ser Lys
1160 1165 1170

Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
1175 1180 1185

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
1190 1195 1200

Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
1205 1210 1215

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
1220 1225 1230

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
1235 1240 1245

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
1250 1255 1260

Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
1265 1270 1275

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val
1280 1285 1290

Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
1295 1300 1305

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
1310 1315 1320

Pro Arg Asp Cys Gly
1325

<210> 51
<211> 442
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 51
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
 210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
 225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
 245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
 260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly
435 440

<210> 52

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 52

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys 65	Ser	Lys	Ala	Thr	Leu 70	Thr	Val	Asp	Lys	Ser 75	Ser	Ser	Thr	Ala	Tyr 80
Met	Gln	Leu	Ser	Ser 85	Leu	Thr	Ser	Glu	Asp 90	Ser	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Arg	Gly 100	Ile	Arg	Leu	Arg	His 105	Phe	Asp	Tyr	Trp	Gly 110	Gln	Gly
Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala 120	Lys	Thr	Thr	Pro	Pro 125	Ser	Val	Tyr
Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala 135	Gln	Thr	Asn	Ser	Met	Val	Thr	Leu
Gly 145	Cys	Leu	Val	Lys	Gly 150	Tyr	Phe	Pro	Glu	Pro 155	Val	Thr	Val	Thr	Trp 160
Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His 170	Thr	Phe	Pro	Ala	Val 175	Leu
Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser 185	Ser	Val	Thr	Val	Pro	Ser 190	Ser
Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His 205	Pro	Ala	Ser
Ser	Thr 210	Lys	Val	Asp	Lys	Lys 215	Ile	Val	Pro	Arg	Asp 220	Cys	Gly	Cys	Lys
Pro 225	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	Ser	Ser 235	Val	Phe	Ile	Phe	Pro 240
Pro	Lys	Pro	Lys	Asp 245	Val	Leu	Thr	Ile	Thr 250	Leu	Thr	Pro	Lys	Val 255	Thr
Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp 265	Asp	Pro	Glu	Val	Gln 270	Phe	Ser
Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His 280	Thr	Ala	Gln	Thr	Gln 285	Pro	Arg
Glu 290	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser 300	Glu	Leu	Pro	Ile
Met 305	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe 315	Lys	Cys	Arg	Val	Asn 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser Gly
435 440 445

Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg
450 455 460

Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu
465 470 475 480

Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile
485 490 495

Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg
500 505 510

Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
515 520 525

Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
530 535 540

Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly
545 550 555 560

Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro
565 570 575

Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn

580

585

590

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
595 600 605

Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
610 615 620

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
625 630 635 640

Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
645 650 655

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
660 665 670

Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
675 680 685

Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
690 695 700

Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr
705 710 715 720

Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
725 730 735

Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr
740 745 750

Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser
755 760 765

Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro
770 775 780

Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly
785 790 795 800

Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
805 810 815

Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys
820 825 830

Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu
835 840 845

Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His
 850 855 860

Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg
 865 870 875 880

Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 885 890 895

Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe
 900 905 910

Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr
 915 920 925

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
 930 935 940

Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
 945 950 955 960

Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
 965 970 975

His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
 980 985 990

Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
 995 1000 1005

Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
 1010 1015 1020

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
 1025 1030 1035

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr
 1040 1045 1050

Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
 1055 1060 1065

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
 1070 1075 1080

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
 1085 1090 1095

<210> 53
<211> 1098
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
 225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
 245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
 260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
 290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
 305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
 325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Ser Cys Ala Ile Thr Asp Phe
 355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
 370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
 385 390 395 400

Phe Val Val Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
 405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
 420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser Gly
 435 440 445

Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg
 450 455 460

Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu
 465 470 475 480

Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile
485 490 495

Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg
500 505 510

Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
515 520 525

Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
530 535 540

Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly
545 550 555 560

Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro
565 570 575

Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn
580 585 590

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
595 600 605

Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
610 615 620

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
625 630 635 640

Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
645 650 655

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
660 665 670

Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
675 680 685

Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
690 695 700

Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr
705 710 715 720

Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
725 730 735

Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr
 740 745 750

Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser
 755 760 765

Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro
 770 775 780

Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly
 785 790 795 800

Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
 805 810 815

Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys
 820 825 830

Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu
 835 840 845

Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His
 850 855 860

Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg
 865 870 875 880

Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 885 890 895

Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe
 900 905 910

Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr
 915 920 925

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
 930 935 940

Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
 945 950 955 960

Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
 965 970 975

His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
 980 985 990

Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu

995

1000

1005

Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
 1010 1015 1020

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
 1025 1030 1035

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr
 1040 1045 1050

Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
 1055 1060 1065

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
 1070 1075 1080

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
 1085 1090 1095

<210> 54

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 54

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Trp Cys Met Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala

370

375

380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
 385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
 405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
 420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 435 440

<210> 55

<211> 877

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 55

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly

405

410

415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 645 650 655

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
 660 665 670

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
675 680 685

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
690 695 700

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
705 710 715 720

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
725 730 735

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
740 745 750

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
755 760 765

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
770 775 780

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Ser Cys Ala Ile
785 790 795 800

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
805 810 815

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
820 825 830

Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
835 840 845

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
850 855 860

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
865 870 875

<210> 56

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu

1	5	10	15																
Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys				
		20						25					30						
Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	Asn				
		35					40					45							
Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	Arg				
	50					55					60								
Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	Ile				
65					70					75					80				
Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	Leu				
				85					90					95					
Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	Ile				
			100					105					110						
Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	Pro				
		115					120					125							
Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe				
	130					135					140								
His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	Gly				
145					150					155					160				
Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser				
				165					170					175					
Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile				
			180					185					190						
Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	Leu	Val				
		195					200					205							
Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	Phe	Arg				
	210					215					220								
Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys	Cys	Gln				
225					230					235					240				
Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg	Val	Cys				
				245					250					255					
Gln	Pro	Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg	Asp	Lys				
			260					265					270						

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
660 665 670

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
675 680 685

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
690 695 700

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
705 710 715 720

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
725 730 735

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
740 745 750

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
755 760 765

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
770 775 780

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
785 790 795 800

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
805 810 815

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
820 825 830

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
835 840 845

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
850 855 860

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
865 870 875 880

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
885 890 895

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
900 905 910

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
915 920 925

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
930 935 940

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
945 950 955 960

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
965 970 975

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
980 985 990

Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu
995 1000 1005

Gln Met Ala Lys Asp Lys Val Ser Leu Ser Cys Ala Ile Thr Asp
1010 1015 1020

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
1025 1030 1035

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp

1040

1045

1050

Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val Gln Lys Ser Asn
 1055 1060 1065

Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly
 1070 1075 1080

Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 1085 1090 1095

<210> 57

<211> 870

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 57

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp

420

425

430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Ser
 645 650 655

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
 660 665 670

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
 675 680 685

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
690 695 700

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
705 710 715 720

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
725 730 735

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
740 745 750

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala
755 760 765

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
770 775 780

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
785 790 795 800

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
805 810 815

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
820 825 830

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
835 840 845

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
850 855 860

Phe Asn Arg Asn Glu Cys
865 870

<210> 58

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 58

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

20

25

30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
 65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
 145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
 165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
 180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
 195 200 205

Lys Ile Val Pro Arg Asp Cys Gly
 210 215

<210> 59

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 59

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Glu Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 60

<211> 545

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 60

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 100 105 110
 Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser
 115 120 125
 Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
 130 135 140
 Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
 145 150 155 160
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
 165 170 175
 Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
 180 185 190
 Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
 195 200 205
 Lys Ile Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly
 210 215 220
 Gly Ser Cys Pro Ala Pro Ser Gln Leu Pro Ser Ala Lys Pro Ile Asn
 225 230 235 240
 Leu Thr Asp Glu Ser Met Phe Pro Ile Gly Thr Tyr Leu Leu Tyr Glu
 245 250 255
 Cys Leu Pro Gly Tyr Ile Lys Arg Gln Phe Ser Ile Thr Cys Lys Gln
 260 265 270

Asp Ser Thr Trp Thr Ser Ala Glu Asp Lys Cys Ile Arg Lys Gln Cys
275 280 285

Lys Thr Pro Ser Asp Pro Glu Asn Gly Leu Val His Val His Thr Gly
290 295 300

Ile Gln Phe Gly Ser Arg Ile Asn Tyr Thr Cys Asn Gln Gly Tyr Arg
305 310 315 320

Leu Ile Gly Ser Ser Ser Ala Val Cys Val Ile Thr Asp Gln Ser Val
325 330 335

Asp Trp Asp Thr Glu Ala Pro Ile Cys Glu Trp Ile Pro Cys Glu Ile
340 345 350

Pro Pro Gly Ile Pro Asn Gly Asp Phe Phe Ser Ser Thr Arg Glu Asp
355 360 365

Phe His Tyr Gly Met Val Val Thr Tyr Arg Cys Asn Thr Asp Ala Arg
370 375 380

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

Ser Asn Asp Gly Glu Ile Gly Val Trp Ser Gly Pro Pro Pro Gln Cys
405 410 415

Ile Glu Leu Asn Lys Cys Thr Pro Pro Pro Tyr Val Glu Asn Ala Val
420 425 430

Met Leu Ser Glu Asn Arg Ser Leu Phe Ser Leu Arg Asp Ile Val Glu
435 440 445

Phe Arg Cys His Pro Gly Phe Ile Met Lys Gly Ala Ser Ser Val His
450 455 460

Cys Gln Ser Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Phe Lys
465 470 475 480

Gly Val Ile Cys Arg Leu Pro Gln Glu Met Ser Gly Phe Gln Lys Gly
485 490 495

Leu Gly Met Lys Lys Glu Tyr Tyr Tyr Gly Glu Asn Val Thr Leu Glu
500 505 510

Cys Glu Asp Gly Tyr Thr Leu Glu Gly Ser Ser Gln Ser Gln Cys Gln
515 520 525

Ser Asp Gly Ser Trp Asn Pro Leu Leu Ala Lys Cys Val Ser Arg Ser

530

535

540

Ile
545

<210> 61

<211> 872

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 61

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly
210 215 220

Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr
225 230 235 240

Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr
245 250 255

Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu
260 265 270

Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser
275 280 285

Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys
290 295 300

Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr
305 310 315 320

Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr
325 330 335

Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly
340 345 350

Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
355 360 365

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
370 375 380

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
385 390 395 400

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
405 410 415

Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
420 425 430

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
435 440 445

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys

450

455

460

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 465 470 475 480

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 485 490 495

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 500 505 510

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 515 520 525

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 530 535 540

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 545 550 555 560

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

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 580 585 590

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 595 600 605

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 610 615 620

Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 625 630 635 640

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 645 650 655

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 660 665 670

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 675 680 685

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 690 695 700

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 705 710 715 720

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
725 730 735

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
740 745 750

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
755 760 765

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
770 775 780

Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
785 790 795 800

Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
805 810 815

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
820 825 830

Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
835 840 845

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
850 855 860

Pro Gln Cys Ile Ile Pro Asn Lys
865 870

<210> 62
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 62
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
340 345 350

Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly
435

<210> 63

<211> 1092

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 63

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85

90

95

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
 145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
 165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
 180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
 195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
 210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
 225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
 245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
 260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
 275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
 290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
 305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
 325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
 340 345 350

Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys
435 440 445

Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp
450 455 460

Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro
465 470 475 480

Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val
485 490 495

Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro
500 505 510

Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe
515 520 525

Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly
530 535 540

Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp
545 550 555 560

Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr
565 570 575

Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr
580 585 590

Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys
595 600 605

Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp
610 615 620

Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro
625 630 635 640

Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp
645 650 655

Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln
660 665 670

Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu
675 680 685

Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro
690 695 700

Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn
705 710 715 720

Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp
725 730 735

Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser
740 745 750

Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly
755 760 765

Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly
770 775 780

Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
785 790 795 800

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser
805 810 815

Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
820 825 830

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly
835 840 845

Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser
850 855 860

Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln
865 870 875 880

Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly
885 890 895

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
900 905 910

Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
915 920 925

Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
930 935 940

Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys
945 950 955 960

Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile
965 970 975

Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu
980 985 990

Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His
995 1000 1005

Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu
1010 1015 1020

Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
1025 1030 1035

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly
1040 1045 1050

Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
1055 1060 1065

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
1070 1075 1080

Ala Pro Gln Cys Ile Ile Pro Asn Lys
1085 1090

<210> 64

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 64

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
340 345 350

Val Ser Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly
435

<210> 65
<211> 1092
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 65
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 100 105 110
 Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser
 115 120 125
 Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
 130 135 140
 Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
 145 150 155 160
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
 165 170 175
 Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
 180 185 190
 Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
 195 200 205
 Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
 210 215 220
 Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
 225 230 235 240
 Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
 245 250 255
 Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
 260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
340 345 350

Val Ser Leu Trp Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys
435 440 445

Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp
450 455 460

Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro
465 470 475 480

Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val
485 490 495

Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro
500 505 510

Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe
515 520 525

Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly

530

535

540

Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp
545 550 555 560

Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr
565 570 575

Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr
580 585 590

Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys
595 600 605

Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp
610 615 620

Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro
625 630 635 640

Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp
645 650 655

Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln
660 665 670

Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu
675 680 685

Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro
690 695 700

Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn
705 710 715 720

Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp
725 730 735

Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser
740 745 750

Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly
755 760 765

Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly
770 775 780

Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
785 790 795 800

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser
805 810 815

Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
820 825 830

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly
835 840 845

Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser
850 855 860

Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln
865 870 875 880

Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly
885 890 895

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
900 905 910

Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
915 920 925

Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
930 935 940

Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys
945 950 955 960

Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile
965 970 975

Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu
980 985 990

Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His
995 1000 1005

Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu
1010 1015 1020

Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
1025 1030 1035

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly
1040 1045 1050

Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
1055 1060 1065

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
1070 1075 1080

Ala Pro Gln Cys Ile Ile Pro Asn Lys
1085 1090

<210> 66

<211> 1092

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 66

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
 180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
 195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
 210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
 225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
 245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
 260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
 275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
 290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
 305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
 325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
 340 345 350

Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
 355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
 370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
 385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
 405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
 420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys
435 440 445

Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp
450 455 460

Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro
465 470 475 480

Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val
485 490 495

Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro
500 505 510

Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe
515 520 525

Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly
530 535 540

Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp
545 550 555 560

Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr
565 570 575

Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr
580 585 590

Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys
595 600 605

Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp
610 615 620

Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro
625 630 635 640

Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp
645 650 655

Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln
660 665 670

Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu
675 680 685

Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro
690 695 700

Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn
705 710 715 720

Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp
725 730 735

Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser
740 745 750

Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly
755 760 765

Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly
770 775 780

Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
785 790 795 800

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser
805 810 815

Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
820 825 830

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly
835 840 845

Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser
850 855 860

Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln
865 870 875 880

Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly
885 890 895

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
900 905 910

Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
915 920 925

Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
930 935 940

Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys

945 950 955 960

Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile
965 970 975

Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu
980 985 990

Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His
995 1000 1005

Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu
1010 1015 1020

Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
1025 1030 1035

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly
1040 1045 1050

Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
1055 1060 1065

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
1070 1075 1080

Ala Pro Gln Cys Ile Ile Pro Asn Lys
1085 1090

<210> 67
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 67
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly
210

<210> 68

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 68

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 69

<211> 543

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 69

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 210 215 220

Cys Pro Ala Pro Ser Gln Leu Pro Ser Ala Lys Pro Ile Asn Leu Thr
 225 230 235 240

Asp Glu Ser Met Phe Pro Ile Gly Thr Tyr Leu Leu Tyr Glu Cys Leu
 245 250 255

Pro Gly Tyr Ile Lys Arg Gln Phe Ser Ile Thr Cys Lys Gln Asp Ser
 260 265 270

Thr Trp Thr Ser Ala Glu Asp Lys Cys Ile Arg Lys Gln Cys Lys Thr
 275 280 285

Pro Ser Asp Pro Glu Asn Gly Leu Val His Val His Thr Gly Ile Gln
 290 295 300

Phe Gly Ser Arg Ile Asn Tyr Thr Cys Asn Gln Gly Tyr Arg Leu Ile
 305 310 315 320

Gly Ser Ser Ser Ala Val Cys Val Ile Thr Asp Gln Ser Val Asp Trp
 325 330 335
 Asp Thr Glu Ala Pro Ile Cys Glu Trp Ile Pro Cys Glu Ile Pro Pro
 340 345 350
 Gly Ile Pro Asn Gly Asp Phe Phe Ser Ser Thr Arg Glu Asp Phe His
 355 360 365
 Tyr Gly Met Val Val Thr Tyr Arg Cys Asn Thr Asp Ala Arg Gly Lys
 370 375 380
 Ala Leu Phe Asn Leu Val Gly Glu Pro Ser Leu Tyr Cys Thr Ser Asn
 385 390 395 400
 Asp Gly Glu Ile Gly Val Trp Ser Gly Pro Pro Pro Gln Cys Ile Glu
 405 410 415
 Leu Asn Lys Cys Thr Pro Pro Pro Tyr Val Glu Asn Ala Val Met Leu
 420 425 430
 Ser Glu Asn Arg Ser Leu Phe Ser Leu Arg Asp Ile Val Glu Phe Arg
 435 440 445
 Cys His Pro Gly Phe Ile Met Lys Gly Ala Ser Ser Val His Cys Gln
 450 455 460
 Ser Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Phe Lys Gly Val
 465 470 475 480
 Ile Cys Arg Leu Pro Gln Glu Met Ser Gly Phe Gln Lys Gly Leu Gly
 485 490 495
 Met Lys Lys Glu Tyr Tyr Tyr Gly Glu Asn Val Thr Leu Glu Cys Glu
 500 505 510
 Asp Gly Tyr Thr Leu Glu Gly Ser Ser Gln Ser Gln Cys Gln Ser Asp
 515 520 525
 Gly Ser Trp Asn Pro Leu Leu Ala Lys Cys Val Ser Arg Ser Ile
 530 535 540

<210> 70

<211> 870

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 70

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Val	Leu	Val	Lys	Pro	Gly	Ala	
1			5					10						15		
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
			20					25						30		
Tyr	Ile	Asn	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	
		35					40					45				
Gly	Val	Ile	Asn	Pro	Tyr	Asn	Gly	Gly	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	
	50					55					60					
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	
65					70					75					80	
Met	Glu	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	
			85						90						95	
Ser	Ser	Pro	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala	
			100					105						110		
Lys	Thr	Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	
		115					120					125				
Gln	Thr	Asn	Ser	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	
		130					135					140				
Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	
145					150					155					160	
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	
				165					170						175	
Ser	Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	
			180					185					190			
Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	
		195					200					205				
Val	Pro	Arg	Asp	Cys	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	
	210					215					220					
Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	Leu	
225					230					235					240	
Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys	
				245					250					255		

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 260 265 270

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 275 280 285

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 290 295 300

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 305 310 315 320

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 325 330 335

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 340 345 350

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 355 360 365

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 370 375 380

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

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 405 410 415

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 420 425 430

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 435 440 445

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 450 455 460

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 465 470 475 480

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 485 490 495

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 500 505 510

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
515 520 525

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
530 535 540

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
545 550 555 560

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

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
580 585 590

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
595 600 605

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
610 615 620

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
625 630 635 640

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
645 650 655

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
660 665 670

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
675 680 685

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
690 695 700

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
705 710 715 720

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
725 730 735

Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr
740 745 750

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
755 760 765

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala

770

775

780

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 785 790 795 800

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 805 810 815

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 820 825 830

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 835 840 845

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 850 855 860

Cys Ile Ile Pro Asn Lys
 865 870

<210> 71

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 71

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
210 215 220

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
225 230 235 240

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
245 250 255

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
260 265 270

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
275 280 285

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
290 295 300

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
305 310 315 320

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
325 330 335

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
340 345 350

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

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys

370

375

380

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
 385 390 395 400

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
 405 410 415

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
 420 425 430

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
 435 440 445

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
 450 455 460

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn
 465 470 475 480

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
 485 490 495

Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr
 500 505 510

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
 515 520 525

Lys

<210> 72

<211> 305

<212> PRT

<213> Homo sapiens

<400> 72

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
 1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
 20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
 35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
 50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65 70 75 80

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

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225 230 235 240

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

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
260 265 270

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

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
290 295 300

Lys
305

<210> 73

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 73

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly

<210> 74

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 74

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Trp Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly

<210> 75

<211> 1090

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 75

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala
435 440 445

Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe
450 455 460

Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr
465 470 475 480

Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr
485 490 495

Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp
500 505 510

Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser
515 520 525

Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser
530 535 540

Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu

445				550				555				560			
Thr	Pro	Ile	Cys	Asp 565	Arg	Ile	Pro	Cys	Gly 570	Leu	Pro	Pro	Thr	Ile 575	Thr
Asn	Gly	Asp	Phe 580	Ile	Ser	Thr	Asn	Arg 585	Glu	Asn	Phe	His	Tyr 590	Gly	Ser
Val	Val	Thr 595	Tyr	Arg	Cys	Asn	Pro 600	Gly	Ser	Gly	Gly	Arg 605	Lys	Val	Phe
Glu	Leu 610	Val	Gly	Glu	Pro	Ser 615	Ile	Tyr	Cys	Thr	Ser 620	Asn	Asp	Asp	Gln
Val 625	Gly	Ile	Trp	Ser	Gly 630	Pro	Ala	Pro	Gln	Cys 635	Ile	Ile	Pro	Asn	Lys 640
Cys	Thr	Pro	Pro	Asn 645	Val	Glu	Asn	Gly	Ile 650	Leu	Val	Ser	Asp	Asn 655	Arg
Ser	Leu	Phe	Ser 660	Leu	Asn	Glu	Val	Val 665	Glu	Phe	Arg	Cys	Gln 670	Pro	Gly
Phe	Val	Met 675	Lys	Gly	Pro	Arg	Arg 680	Val	Lys	Cys	Gln	Ala 685	Leu	Asn	Lys
Trp 690	Glu	Pro	Glu	Leu	Pro	Ser 695	Cys	Ser	Arg	Val	Cys 700	Gln	Pro	Pro	Pro
Asp 705	Val	Leu	His	Ala	Glu 710	Arg	Thr	Gln	Arg	Asp 715	Lys	Asp	Asn	Phe	Ser 720
Pro	Gly	Gln	Glu	Val 725	Phe	Tyr	Ser	Cys	Glu 730	Pro	Gly	Tyr	Asp	Leu 735	Arg
Gly	Ala	Ala	Ser 740	Met	Arg	Cys	Thr	Pro 745	Gln	Gly	Asp	Trp	Ser 750	Pro	Ala
Ala	Pro	Thr 755	Cys	Glu	Val	Lys	Ser 760	Cys	Asp	Asp	Phe	Met 765	Gly	Gln	Leu
Leu	Asn 770	Gly	Arg	Val	Leu	Phe 775	Pro	Val	Asn	Leu	Gln 780	Leu	Gly	Ala	Lys
Val 785	Asp	Phe	Val	Cys	Asp 790	Glu	Gly	Phe	Gln	Leu 795	Lys	Gly	Ser	Ser	Ala 800
Ser	Tyr	Cys	Val	Leu 805	Ala	Gly	Met	Glu	Ser 810	Leu	Trp	Asn	Ser	Ser 815	Val

Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn
 820 825 830

Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr
 835 840 845

Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp
 850 855 860

Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn
 865 870 875 880

Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys
 885 890 895

Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn
 900 905 910

Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro
 915 920 925

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val
 930 935 940

Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro
 945 950 955 960

Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val
 965 970 975

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly
 980 985 990

His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser
 995 1000 1005

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
 1010 1015 1020

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 1025 1030 1035

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 1040 1045 1050

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 1055 1060 1065

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
1070 1075 1080

Gln Cys Ile Ile Pro Asn Lys
1085 1090

<210> 76
<211> 1090
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 76
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala
 435 440 445

Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe
450 455 460

Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr
465 470 475 480

Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr
485 490 495

Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp
500 505 510

Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser
515 520 525

Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser
530 535 540

Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu
545 550 555 560

Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr
565 570 575

Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser
580 585 590

Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe
595 600 605

Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln
610 615 620

Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
625 630 635 640

Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg
645 650 655

Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly
660 665 670

Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys
675 680 685

Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro
690 695 700

Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser
705 710 715 720

Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg
725 730 735

Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala
740 745 750

Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
755 760 765

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys
770 775 780

Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
785 790 795 800

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val
805 810 815

Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn
820 825 830

Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr
835 840 845

Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp
850 855 860

Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn
865 870 875 880

Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys
885 890 895

Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn
900 905 910

Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro
915 920 925

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val
930 935 940

Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro
945 950 955 960

Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val

965

970

975

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly
 980 985 990

His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser
 995 1000 1005

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
 1010 1015 1020

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 1025 1030 1035

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 1040 1045 1050

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 1055 1060 1065

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
 1070 1075 1080

Gln Cys Ile Ile Pro Asn Lys
 1085 1090

<210> 77

<211> 875

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 77

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Gly Gly Gly Gly Ser
210 215 220

Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala
225 230 235 240

Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr
245 250 255

Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile
260 265 270

Ile Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg
275 280 285

Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His
290 295 300

Val Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr
305 310 315 320

Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser
325 330 335

Gly Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile

340

345

350

Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr
 355 360 365

Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn
 370 375 380

Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser
 385 390 395 400

Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
 405 410 415

Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu
 420 425 430

Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu
 435 440 445

Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg
 450 455 460

Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser
 465 470 475 480

Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg
 485 490 495

Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr
 500 505 510

Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys
 515 520 525

Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys
 530 535 540

Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe
 545 550 555 560

Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu
 565 570 575

Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly
 580 585 590

Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe
 595 600 605

Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro
 610 615 620

Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro
 625 630 635 640

His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile
 645 650 655

Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala
 660 665 670

Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu
 675 680 685

Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly
 690 695 700

Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe
 705 710 715 720

Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val
 725 730 735

Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met
 740 745 750

Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser
 755 760 765

Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile
 770 775 780

Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
 785 790 795 800

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile
 805 810 815

Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
 820 825 830

Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu
 835 840 845

Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser
 850 855 860

Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
865 870 875

<210> 78

<211> 1090

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 78

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
660 665 670

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
675 680 685

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
690 695 700

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
705 710 715 720

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
725 730 735

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
740 745 750

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
755 760 765

Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala
770 775 780

Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe
785 790 795 800

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
805 810 815

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
820 825 830

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
835 840 845

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
850 855 860

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
865 870 875 880

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
885 890 895

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
900 905 910

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
915 920 925

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
930 935 940

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
945 950 955 960

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
965 970 975

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val

980

985

990

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 995 1000 1005

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
 1010 1015 1020

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
 1025 1030 1035

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys
 1040 1045 1050

Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr
 1055 1060 1065

Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys
 1070 1075 1080

Ser Leu Ser His Ser Pro Gly
 1085 1090

<210> 79

<211> 875

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 79

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp

355

360

365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 645 650 655

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
 660 665 670

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 675 680 685

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
 690 695 700

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
 705 710 715 720

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 725 730 735

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
 740 745 750

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
 755 760 765

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 770 775 780

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 785 790 795 800

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 805 810 815

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 820 825 830

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 835 840 845

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 850 855 860

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 865 870 875

<210> 80

<211> 877

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 80

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
660 665 670

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
675 680 685

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
690 695 700

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
705 710 715 720

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
725 730 735

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
740 745 750

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
755 760 765

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
770 775 780

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Trp Cys Met Ile
785 790 795 800

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
805 810 815

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
820 825 830

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
835 840 845

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
850 855 860

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
865 870 875

<210> 81

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 81

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly

<210> 82

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 82

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asp Cys Asn
435 440 445

Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser
450 455 460

Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro
465 470 475 480

Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys Gly Glu
485 490 495

Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly
500 505 510

His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn
515 520 525

Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr
530 535 540

Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp
545 550 555 560

Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr
565 570 575

Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg
580 585 590

Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr
595 600 605

Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp
610 615 620

Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp

625		630		635		640
Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn						
	645			650		655
Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg						
	660			665		670
Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys						
	675			680		685
Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser						
	690			695		700
Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys						
	705			710		715
Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr						
	725			730		735
Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu Lys						
	740			745		
<210> 83						
<211> 749						
<212> PRT						
<213> Artificial Sequence						
<220>						
<223> Description of Artificial Sequence: Synthetic polypeptide						
<400> 83						
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala						
1		5		10		15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr						
	20			25		30
Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile						
	35			40		45
Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe						
	50			55		60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr						
	65			70		75
Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys						
	85			90		95

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu

355

360

365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asp Cys Asn
 435 440 445

Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser
 450 455 460

Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro
 465 470 475 480

Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys Gly Glu
 485 490 495

Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly
 500 505 510

His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn
 515 520 525

Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr
 530 535 540

Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp
 545 550 555 560

Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr
 565 570 575

Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg
 580 585 590

Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr
 595 600 605

Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp
 610 615 620

Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp
625 630 635 640

Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn
645 650 655

Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg
660 665 670

Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys
675 680 685

Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser
690 695 700

Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys
705 710 715 720

Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr
725 730 735

Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu Lys
740 745

<210> 84

<211> 534

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 84

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly

85

90

95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Gly Gly Gly Ser
210 215 220

Gly Gly Gly Gly Ser Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn
225 230 235 240

Thr Glu Ile Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly
245 250 255

Thr Gln Ala Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn
260 265 270

Val Ile Met Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu
275 280 285

Arg Lys Cys Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe
290 295 300

Gly Thr Phe Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys
305 310 315 320

Ala Val Tyr Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn
325 330 335

Tyr Arg Glu Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys
340 345 350

Glu Val Val Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile
355 360 365

Val Ser Ser Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala
370 375 380

Val Arg Phe Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu
385 390 395 400

Met His Cys Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys
405 410 415

Val Glu Ile Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile
420 425 430

Ser Gln Lys Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys
435 440 445

Asn Met Gly Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu
450 455 460

Ser Gly Trp Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn
465 470 475 480

Pro Tyr Ile Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg
485 490 495

Thr Gly Asp Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala
500 505 510

Thr Arg Gly Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala
515 520 525

Pro Arg Cys Thr Leu Lys
530

<210> 85

<211> 749

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 85

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr

20

25

30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
 35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
 50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
 65 70 75 80

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

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
 100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
 115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
 130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
 145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
 165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
 180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
 195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
 210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
 225 230 235 240

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

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
 260 265 270

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

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
 290 295 300

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln
 305 310 315 320

Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser
 325 330 335

Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Tyr Ile Asn Trp Val
 340 345 350

Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Val Ile Asn Pro
 355 360 365

Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr
 370 375 380

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

Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ser Ser Pro Tyr Trp
 405 410 415

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro
 420 425 430

Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met
 435 440 445

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr
 450 455 460

Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
 465 470 475 480

Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val
 485 490 495

Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His
 500 505 510

Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys
 515 520 525

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
 530 535 540

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
545 550 555 560

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
565 570 575

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
580 585 590

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
595 600 605

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
610 615 620

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
625 630 635 640

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
645 650 655

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile
660 665 670

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
675 680 685

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
690 695 700

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
705 710 715 720

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
725 730 735

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
740 745

<210> 86
<211> 534
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 86
Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
 20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
 35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
 50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
 65 70 75 80

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

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
 100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
 115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
 130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
 145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
 165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
 180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
 195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
 210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
 225 230 235 240

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

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
 260 265 270

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

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
 290 295 300

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
 305 310 315 320

Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile
 325 330 335

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
 340 345 350

Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile
 355 360 365

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly
 370 375 380

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 385 390 395 400

Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Arg
 405 410 415

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala
 420 425 430

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
 435 440 445

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 450 455 460

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 465 470 475 480

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 485 490 495

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
 500 505 510

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
 515 520 525

Phe Asn Arg Asn Glu Cys
530

<210> 87

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 87

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65 70 75 80

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

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225 230 235 240

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

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
260 265 270

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

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
290 295 300

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Cys Lys Pro Cys
305 310 315 320

Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys
325 330 335

Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val
340 345 350

Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe
355 360 365

Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu
370 375 380

Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His
385 390 395 400

Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala
405 410 415

Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg
420 425 430

Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met
435 440 445

Ala Lys Asp Lys Val Ser Leu Trp Cys Met Ile Thr Asp Phe Phe Pro
450 455 460

Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn
465 470 475 480

Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val
485 490 495

Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr
500 505 510

Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu
515 520 525

Lys Ser Leu Ser His Ser Pro Gly
530 535

<210> 88

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 88

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly

<210> 89

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 89

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly

<210> 90

<211> 877

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 90

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
660 665 670

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
675 680 685

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
690 695 700

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
705 710 715 720

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu

725

730

735

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
 740 745 750

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
 755 760 765

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
 770 775 780

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Trp Cys Met Ile
 785 790 795 800

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
 805 810 815

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
 820 825 830

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
 835 840 845

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
 850 855 860

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 865 870 875

<210> 91

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 91

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln

325

330

335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe Gln Gly His His His
645 650 655

His His His

<210> 92

<211> 1109

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 92

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe

130

135

140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
 625 630 635 640

Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
 645 650 655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
945 950 955 960

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
965 970 975

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
980 985 990

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
995 1000 1005

Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile
1010 1015 1020

Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
1025 1030 1035

Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
1040 1045 1050

Cys Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly
1055 1060 1065

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile
1070 1075 1080

Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Glu Asn
1085 1090 1095

Leu Tyr Phe Gln Gly His His His His His His
1100 1105

<210> 93

<211> 910

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 93

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser His Lys Phe
 130 135 140

Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
 145 150 155 160

Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
 180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 195 200 205

Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
 210 215 220

Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
 225 230 235 240

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro
 245 250 255

Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu
 260 265 270

Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser
275 280 285

Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr Gly
290 295 300

Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro
305 310 315 320

Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser Gln
325 330 335

Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser
340 345 350

Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu Thr
355 360 365

Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn
370 375 380

Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val
385 390 395 400

Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu
405 410 415

Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
420 425 430

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys
435 440 445

Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser
450 455 460

Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe
465 470 475 480

Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp
485 490 495

Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp
500 505 510

Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro
515 520 525

Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly

530

535

540

Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala
 545 550 555 560

Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu
 565 570 575

Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val
 580 585 590

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

Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro
 610 615 620

Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly
 625 630 635 640

Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr Val
 645 650 655

Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu
 660 665 670

Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly
 675 680 685

Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln
 690 695 700

Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala
 705 710 715 720

Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu
 725 730 735

Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp
 740 745 750

Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro
 755 760 765

Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly
 770 775 780

Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His
 785 790 795 800

Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser Thr
805 810 815

Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile
820 825 830

Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly
835 840 845

Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val
850 855 860

Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp
865 870 875 880

Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn
885 890 895

Lys Glu Asn Leu Tyr Phe Gln Gly His His His His His His
900 905 910

<210> 94
<211> 583
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 94
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly

100

105

110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser His Lys Phe
130 135 140

Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
210 215 220

Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys Pro Ala Pro Ser
245 250 255

Gln Leu Pro Ser Ala Lys Pro Ile Asn Leu Thr Asp Glu Ser Met Phe
260 265 270

Pro Ile Gly Thr Tyr Leu Leu Tyr Glu Cys Leu Pro Gly Tyr Ile Lys
275 280 285

Arg Gln Phe Ser Ile Thr Cys Lys Gln Asp Ser Thr Trp Thr Ser Ala
290 295 300

Glu Asp Lys Cys Ile Arg Lys Gln Cys Lys Thr Pro Ser Asp Pro Glu
305 310 315 320

Asn Gly Leu Val His Val His Thr Gly Ile Gln Phe Gly Ser Arg Ile
325 330 335

Asn Tyr Thr Cys Asn Gln Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala
340 345 350

Val	Cys	Val	Ile	Thr	Asp	Gln	Ser	Val	Asp	Trp	Asp	Thr	Glu	Ala	Pro
		355					360					365			

Ile Cys Glu Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly
370 375 380

Asp Phe Phe Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val
385 390 395 400

Thr Tyr Arg Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu
405 410 415

Val Gly Glu Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly
420 425 430

Val Trp Ser Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr
435 440 445

Pro Pro Pro Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser
450 455 460

Leu Phe Ser Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe
465 470 475 480

Ile Met Lys Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp
485 490 495

Glu Pro Glu Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro
500 505 510

Gln Glu Met Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr
515 520 525

Tyr Tyr Gly Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu
530 535 540

Glu Gly Ser Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro
545 550 555 560

Leu Leu Ala Lys Cys Val Ser Arg Ser Ile Glu Asn Leu Tyr Phe Gln
565 570 575

Gly His His His His His His
580

<210> 95

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 95

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
 260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
 290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
 305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
 325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
 355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
 370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
 385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
 405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
 420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser Gly
 435 440 445

Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg
 450 455 460

Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu
 465 470 475 480

Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile
 485 490 495

Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg
 500 505 510

Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
515 520 525

Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
530 535 540

Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly
545 550 555 560

Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro
565 570 575

Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn
580 585 590

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
595 600 605

Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
610 615 620

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
625 630 635 640

Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
645 650 655

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
660 665 670

Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
675 680 685

Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
690 695 700

Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr
705 710 715 720

Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
725 730 735

Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr
740 745 750

Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser
755 760 765

Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro
770 775 780

Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly
785 790 795 800

Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
805 810 815

Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys
820 825 830

Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu
835 840 845

Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His
850 855 860

Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg
865 870 875 880

Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
885 890 895

Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe
900 905 910

Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr
915 920 925

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
930 935 940

Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
945 950 955 960

Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
965 970 975

His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
980 985 990

Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
995 1000 1005

Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
1010 1015 1020

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe

1025

1030

1035

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr
 1040 1045 1050

Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
 1055 1060 1065

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
 1070 1075 1080

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
 1085 1090 1095

<210> 96

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 96

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly

405

410

415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
 420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser Gly
 435 440 445

Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg
 450 455 460

Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu
 465 470 475 480

Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile
 485 490 495

Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg
 500 505 510

Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
 515 520 525

Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
 530 535 540

Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly
 545 550 555 560

Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro
 565 570 575

Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn
 580 585 590

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
 595 600 605

Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
 610 615 620

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
 625 630 635 640

Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
 645 650 655

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
 660 665 670

Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
 675 680 685

Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
 690 695 700

Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr
 705 710 715 720

Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
 725 730 735

Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr
 740 745 750

Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser
 755 760 765

Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro
 770 775 780

Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly
 785 790 795 800

Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
 805 810 815

Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys
 820 825 830

Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu
 835 840 845

Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His
 850 855 860

Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg
 865 870 875 880

Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 885 890 895

Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe
 900 905 910

Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr
 915 920 925

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
930 935 940

Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
945 950 955 960

Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
965 970 975

His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
980 985 990

Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
995 1000 1005

Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
1010 1015 1020

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
1025 1030 1035

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr
1040 1045 1050

Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
1055 1060 1065

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
1070 1075 1080

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
1085 1090 1095

<210> 97

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 97

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
 210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
 225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
 245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
 260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
 290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Ser Cys Ala Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
385 390 395 400

Phe Val Val Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Gly Gly Gly Gly Ser Gly
435 440 445

Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg
450 455 460

Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu
465 470 475 480

Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile
485 490 495

Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg
500 505 510

Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val
515 520 525

Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys
530 535 540

Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly
545 550 555 560

Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro
565 570 575

Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn
580 585 590

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
595 600 605

Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
610 615 620

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
625 630 635 640

Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
645 650 655

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
660 665 670

Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
675 680 685

Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
690 695 700

Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr
705 710 715 720

Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
725 730 735

Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr
740 745 750

Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser
755 760 765

Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro
770 775 780

Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly
785 790 795 800

Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
805 810 815

Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys

820

825

830

Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu
835 840 845

Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His
850 855 860

Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg
865 870 875 880

Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
885 890 895

Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe
900 905 910

Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr
915 920 925

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
930 935 940

Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
945 950 955 960

Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
965 970 975

His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
980 985 990

Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
995 1000 1005

Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
1010 1015 1020

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
1025 1030 1035

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr
1040 1045 1050

Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
1055 1060 1065

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val
1070 1075 1080

Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
1085 1090 1095

<210> 98

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 98

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser

195

200

205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
 210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
 225 230 235 240

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
 245 250 255

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
 260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
 290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
 305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
 325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe
 355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
 370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
 385 390 395 400

Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
 405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
 420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 435 440

<210> 99

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 99

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
210 215 220

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro

225		230		235		240									
Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	Val	Thr
				245					250					255	
Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	Glu	Val	Gln	Phe	Ser
			260					265					270		
Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Pro	Arg
		275					280					285			
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	Ser	Glu	Leu	Pro	Ile
	290					295					300				
Met	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn
305					310					315					320
Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys
			325						330					335	
Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu
			340					345					350		
Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Trp	Cys	Met	Ile	Thr	Asp	Phe
	355						360					365			
Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala
	370					375					380				
Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro	Ile	Met	Asp	Thr	Asp	Gly	Ser	Tyr
385					390					395					400
Phe	Val	Tyr	Ser	Lys	Leu	Asn	Val	Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly
				405					410					415	
Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	His	Glu	Gly	Leu	His	Asn	His	His
			420					425					430		
Thr	Glu	Lys	Ser	Leu	Ser	His	Ser	Pro	Gly						
		435					440								

<210> 100

<211> 551

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 100

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Cys Pro Ala Pro Ser Gln Leu Pro
225 230 235 240

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

Thr Tyr Leu Leu Tyr Glu Cys Leu Pro Gly Tyr Ile Lys Arg Gln Phe

260

265

270

Ser Ile Thr Cys Lys Gln Asp Ser Thr Trp Thr Ser Ala Glu Asp Lys
 275 280 285

Cys Ile Arg Lys Gln Cys Lys Thr Pro Ser Asp Pro Glu Asn Gly Leu
 290 295 300

Val His Val His Thr Gly Ile Gln Phe Gly Ser Arg Ile Asn Tyr Thr
 305 310 315 320

Cys Asn Gln Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Val Cys Val
 325 330 335

Ile Thr Asp Gln Ser Val Asp Trp Asp Thr Glu Ala Pro Ile Cys Glu
 340 345 350

Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly Asp Phe Phe
 355 360 365

Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val Thr Tyr Arg
 370 375 380

Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu Val Gly Glu
 385 390 395 400

Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly Val Trp Ser
 405 410 415

Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr Pro Pro Pro
 420 425 430

Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser Leu Phe Ser
 435 440 445

Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe Ile Met Lys
 450 455 460

Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp Glu Pro Glu
 465 470 475 480

Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro Gln Glu Met
 485 490 495

Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr Tyr Tyr Gly
 500 505 510

Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly Ser
 515 520 525

Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro Leu Leu Ala
530 535 540

Lys Cys Val Ser Arg Ser Ile
545 550

<210> 101
<211> 878
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 101
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser

180	185	190																	
Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser				
	195						200					205							
Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	Cys	Gly	Gly	Gly				
	210					215					220								
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu				
	225					230				235					240				
Pro	Phe	Ala	Arg	Pro	Thr	Asn	Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile				
				245					250					255					
Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro				
			260					265					270						
Phe	Ser	Ile	Ile	Cys	Leu	Lys	Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp				
		275					280					285							
Arg	Cys	Arg	Arg	Lys	Ser	Cys	Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly				
	290					295					300								
Met	Val	His	Val	Ile	Lys	Gly	Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr				
	305				310					315					320				
Ser	Cys	Thr	Lys	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys				
				325					330					335					
Ile	Ile	Ser	Gly	Asp	Thr	Val	Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys				
			340					345					350						
Asp	Arg	Ile	Pro	Cys	Gly	Leu	Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe				
		355					360					365							
Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr				
	370					375					380								
Arg	Cys	Asn	Pro	Gly	Ser	Gly	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly				
	385				390					395					400				
Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp				
			405						410				415						
Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro				
			420					425					430						
Asn	Val	Glu	Asn	Gly	Ile	Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser				
	435					440						445							

Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys
 450 455 460

Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu
 465 470 475 480

Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His
 485 490 495

Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu
 500 505 510

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

Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys
 530 535 540

Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg
 545 550 555 560

Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val
 565 570 575

Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val
 580 585 590

Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu
 595 600 605

Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr
 610 615 620

Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr
 625 630 635 640

Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu
 645 650 655

Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser
 660 665 670

Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp
 675 680 685

His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe
 690 695 700

Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly
705 710 715 720

Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro
725 730 735

Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val
740 745 750

Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile
755 760 765

Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala
770 775 780

Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro
785 790 795 800

Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly
805 810 815

Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val
820 825 830

Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
835 840 845

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly
850 855 860

Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
865 870 875

<210> 102

<211> 1328

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 102

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140

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

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

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Gly Gly
 210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu
 225 230 235 240

Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile
 245 250 255

Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro
 260 265 270

Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp
 275 280 285

Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly
 290 295 300

Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr
305 310 315 320

Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys
325 330 335

Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys
340 345 350

Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe
355 360 365

Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr
370 375 380

Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly
385 390 395 400

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp
405 410 415

Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro
420 425 430

Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser
435 440 445

Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys
450 455 460

Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu
465 470 475 480

Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Asp Val Leu His
485 490 495

Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu
500 505 510

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

Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys
530 535 540

Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg
545 550 555 560

Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val
565 570 575

Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val
580 585 590

Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu
595 600 605

Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr
610 615 620

Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr
625 630 635 640

Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu
645 650 655

Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser
660 665 670

Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp
675 680 685

His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe
690 695 700

Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly
705 710 715 720

Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro
725 730 735

Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val
740 745 750

Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile
755 760 765

Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala
770 775 780

Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro
785 790 795 800

Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly
805 810 815

Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val

820

825

830

Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu
835 840 845

Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly
850 855 860

Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr
865 870 875 880

Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu
885 890 895

Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val
900 905 910

Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu
915 920 925

Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val
930 935 940

Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly
945 950 955 960

Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala
965 970 975

Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro
980 985 990

Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn
995 1000 1005

Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val
1010 1015 1020

Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
1025 1030 1035

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser
1040 1045 1050

Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
1055 1060 1065

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe
1070 1075 1080

Gly	Lys	Ala	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	Arg	Gly
1085						1090					1095			
Thr	Ser	Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	Ser
1100						1105					1110			
Asp	Pro	Gln	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys
1115						1120					1125			
Gly	Ile	Leu	Gly	His	Cys	Gln	Ala	Pro	Asp	His	Phe	Leu	Phe	Ala
1130						1135					1140			
Lys	Leu	Lys	Thr	Gln	Thr	Asn	Ala	Ser	Asp	Phe	Pro	Ile	Gly	Thr
1145						1150					1155			
Ser	Leu	Lys	Tyr	Glu	Cys	Arg	Pro	Glu	Tyr	Tyr	Gly	Arg	Pro	Phe
1160						1165					1170			
Ser	Ile	Thr	Cys	Leu	Asp	Asn	Leu	Val	Trp	Ser	Ser	Pro	Lys	Asp
1175						1180					1185			
Val	Cys	Lys	Arg	Lys	Ser	Cys	Lys	Thr	Pro	Pro	Asp	Pro	Val	Asn
1190						1195					1200			
Gly	Met	Val	His	Val	Ile	Thr	Asp	Ile	Gln	Val	Gly	Ser	Arg	Ile
1205						1210					1215			
Asn	Tyr	Ser	Cys	Thr	Thr	Gly	His	Arg	Leu	Ile	Gly	His	Ser	Ser
1220						1225					1230			
Ala	Glu	Cys	Ile	Leu	Ser	Gly	Asn	Thr	Ala	His	Trp	Ser	Thr	Lys
1235						1240					1245			
Pro	Pro	Ile	Cys	Gln	Arg	Ile	Pro	Cys	Gly	Leu	Pro	Pro	Thr	Ile
1250						1255					1260			
Ala	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe	His	Tyr
1265						1270					1275			
Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Leu	Gly	Ser	Arg	Gly	Arg
1280						1285					1290			
Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser
1295						1300					1305			
Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys
1310						1315					1320			

Ile Ile Pro Asn Lys
1325

<210> 103
<211> 877
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 103
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
660 665 670

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
675 680 685

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
690 695 700

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
705 710 715 720

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
725 730 735

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
740 745 750

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
755 760 765

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro
770 775 780

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Ser Cys Ala Ile
785 790 795 800

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
805 810 815

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
820 825 830

Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
835 840 845

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
850 855 860

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
865 870 875

<210> 104

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 104

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu

580

585

590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Ser Gly Gly Gly Ser
645 650 655

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
660 665 670

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
675 680 685

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
690 695 700

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
705 710 715 720

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
725 730 735

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
740 745 750

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
755 760 765

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
770 775 780

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
785 790 795 800

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
805 810 815

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
820 825 830

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
835 840 845

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
850 855 860

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
865 870 875 880

Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
885 890 895

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
900 905 910

Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
915 920 925

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
930 935 940

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
945 950 955 960

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
965 970 975

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
980 985 990

Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu
995 1000 1005

Gln Met Ala Lys Asp Lys Val Ser Leu Ser Cys Ala Ile Thr Asp
1010 1015 1020

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
1025 1030 1035

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
1040 1045 1050

Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val Gln Lys Ser Asn
1055 1060 1065

Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly
1070 1075 1080

Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
1085 1090 1095

<210> 105

<211> 878

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 105

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
660 665 670

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
675 680 685

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
690 695 700

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
705 710 715 720

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
725 730 735

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
740 745 750

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
755 760 765

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
770 775 780

Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
785 790 795 800

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
805 810 815

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
820 825 830

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
835 840 845

Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
850 855 860

Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
865 870 875

<210> 106
<211> 1328
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 106
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser

595

600

605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
645 650 655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 945 950 955 960

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 965 970 975

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 995 1000 1005

Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile
 1010 1015 1020

Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
 1025 1030 1035

Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
 1040 1045 1050

Cys Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly
 1055 1060 1065

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile
 1070 1075 1080

Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Gly Gly
 1085 1090 1095

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Pro
 1100 1105 1110

Gly	Thr	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys
1115						1120					1125			
Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	His	Trp	Val
1130						1135					1140			
Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Asn	Ile	Asn
1145						1150					1155			
Pro	Ser	Asn	Gly	Gly	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys	Ser	Lys
1160						1165					1170			
Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln
1175						1180					1185			
Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala
1190						1195					1200			
Arg	Arg	Gly	Ile	Arg	Leu	Arg	His	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
1205						1210					1215			
Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Pro	Pro	Ser	Val
1220						1225					1230			
Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	Thr	Asn	Ser	Met	Val
1235						1240					1245			
Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr
1250						1255					1260			
Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe
1265						1270					1275			
Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val
1280						1285					1290			
Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn
1295						1300					1305			
Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val
1310						1315					1320			
Pro	Arg	Asp	Cys	Gly										
1325														

<210> 107
 <211> 870
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 107

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
660 665 670

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
675 680 685

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
690 695 700

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
705 710 715 720

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
725 730 735

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
740 745 750

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala

755

760

765

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
 770 775 780

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 785 790 795 800

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 805 810 815

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 820 825 830

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
 835 840 845

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
 850 855 860

Phe Asn Arg Asn Glu Cys
 865 870

<210> 108

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 108

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
 1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
 20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
 35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
 50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
 65 70 75 80

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

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225 230 235 240

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

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
260 265 270

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

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
290 295 300

Lys Glu Asn Leu Tyr Phe Gln Gly His His His His His His
305 310 315

<210> 109

<211> 558

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 109

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly
210 215 220

Gly Ser Cys Pro Ala Pro Ser Gln Leu Pro Ser Ala Lys Pro Ile Asn
225 230 235 240

Leu Thr Asp Glu Ser Met Phe Pro Ile Gly Thr Tyr Leu Leu Tyr Glu
245 250 255

Cys Leu Pro Gly Tyr Ile Lys Arg Gln Phe Ser Ile Thr Cys Lys Gln
260 265 270

Asp Ser Thr Trp Thr Ser Ala Glu Asp Lys Cys Ile Arg Lys Gln Cys
275 280 285

Lys Thr Pro Ser Asp Pro Glu Asn Gly Leu Val His Val His Thr Gly
290 295 300

Ile Gln Phe Gly Ser Arg Ile Asn Tyr Thr Cys Asn Gln Gly Tyr Arg
305 310 315 320

Leu Ile Gly Ser Ser Ser Ala Val Cys Val Ile Thr Asp Gln Ser Val
325 330 335

Asp Trp Asp Thr Glu Ala Pro Ile Cys Glu Trp Ile Pro Cys Glu Ile
340 345 350

Pro Pro Gly Ile Pro Asn Gly Asp Phe Phe Ser Ser Thr Arg Glu Asp
355 360 365

Phe His Tyr Gly Met Val Val Thr Tyr Arg Cys Asn Thr Asp Ala Arg
370 375 380

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

Ser Asn Asp Gly Glu Ile Gly Val Trp Ser Gly Pro Pro Pro Gln Cys
405 410 415

Ile Glu Leu Asn Lys Cys Thr Pro Pro Pro Tyr Val Glu Asn Ala Val
420 425 430

Met Leu Ser Glu Asn Arg Ser Leu Phe Ser Leu Arg Asp Ile Val Glu
435 440 445

Phe Arg Cys His Pro Gly Phe Ile Met Lys Gly Ala Ser Ser Val His
450 455 460

Cys Gln Ser Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Phe Lys
465 470 475 480

Gly Val Ile Cys Arg Leu Pro Gln Glu Met Ser Gly Phe Gln Lys Gly
485 490 495

Leu Gly Met Lys Lys Glu Tyr Tyr Tyr Gly Glu Asn Val Thr Leu Glu
500 505 510

Cys Glu Asp Gly Tyr Thr Leu Glu Gly Ser Ser Gln Ser Gln Cys Gln

515

520

525

Ser Asp Gly Ser Trp Asn Pro Leu Leu Ala Lys Cys Val Ser Arg Ser
 530 535 540

Ile Glu Asn Leu Tyr Phe Gln Gly His His His His His His
 545 550 555

<210> 110

<211> 885

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 110

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
 65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
 145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
 165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly
210 215 220

Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr
225 230 235 240

Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr
245 250 255

Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu
260 265 270

Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser
275 280 285

Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys
290 295 300

Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr
305 310 315 320

Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr
325 330 335

Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly
340 345 350

Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
355 360 365

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
370 375 380

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
385 390 395 400

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
405 410 415

Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
420 425 430

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu

435

440

445

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 450 455 460

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 465 470 475 480

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 485 490 495

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 500 505 510

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 515 520 525

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 530 535 540

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 545 550 555 560

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

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 580 585 590

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 595 600 605

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 610 615 620

Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 625 630 635 640

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 645 650 655

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 660 665 670

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 675 680 685

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 690 695 700

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
705 710 715 720

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
725 730 735

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
740 745 750

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
755 760 765

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
770 775 780

Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
785 790 795 800

Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
805 810 815

Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
820 825 830

Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
835 840 845

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
850 855 860

Pro Gln Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe Gln Gly His
865 870 875 880

His His His His His
885

<210> 111

<211> 544

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 111

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

20

25

30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
 65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
 100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
 130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
 145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
 165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
 180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
 195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly
 210 215 220

Gly Ser Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile
 225 230 235 240

Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala
 245 250 255

Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met
 260 265 270

Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys
 275 280 285

Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe
 290 295 300

Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr
 305 310 315 320

Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu
 325 330 335

Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val
 340 345 350

Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser
 355 360 365

Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe
 370 375 380

Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys
 385 390 395 400

Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile
 405 410 415

Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys
 420 425 430

Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly
 435 440 445

Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp
 450 455 460

Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile
 465 470 475 480

Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp
 485 490 495

Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly
 500 505 510

Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys
 515 520 525

Thr Leu Lys Glu Asn Leu Tyr Phe Gln Gly His His His His His
 530 535 540

<210> 112
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 112
Glu Val Gln Leu Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
340 345 350

Val Ser Leu Trp Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly
435

<210> 113

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 113

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
 260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
 275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
 290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
 305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
 325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
 340 345 350

Val Ser Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
 355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
 370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu
 385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
 405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
 420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asp
 435 440 445

Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr Gly Ser
 450 455 460

Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr Lys Cys
 465 470 475 480

Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys
 485 490 495

Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro
 500 505 510

Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly
515 520 525

Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys Asn Glu
530 535 540

Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp Thr Asp
545 550 555 560

Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys Leu Pro
565 570 575

Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro
580 585 590

Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys Asn Ser
595 600 605

Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp Asp Gly
610 615 620

Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys Lys Ser
625 630 635 640

Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile Tyr Lys
645 650 655

Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser
660 665 670

Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro Leu Pro
675 680 685

Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn Gly Asp
690 695 700

Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr
705 710 715 720

Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr Ala Lys
725 730 735

Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu Lys Glu
740 745 750

Asn Leu Tyr Phe Gln Gly His His His His His
755 760

<210> 114
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 114
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
340 345 350

Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asp
435 440 445

Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr Gly Ser
450 455 460

Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr Lys Cys
465 470 475 480

Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys
485 490 495

Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro
500 505 510

Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly
515 520 525

Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys Asn Glu
530 535 540

Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp Thr Asp
545 550 555 560

Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys Leu Pro
565 570 575

Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro
580 585 590

Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys Asn Ser
595 600 605

Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp Asp Gly
610 615 620

Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys Lys Ser
625 630 635 640

Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile Tyr Lys
645 650 655

Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser
660 665 670

Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro Leu Pro
675 680 685

Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn Gly Asp
690 695 700

Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr
705 710 715 720

Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr Ala Lys
725 730 735

Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu Lys Glu

740

745

750

Asn Leu Tyr Phe Gln Gly His His His His His His
 755 760

<210> 115

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 115

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
210 215 220

Cys Pro Ala Pro Ser Gln Leu Pro Ser Ala Lys Pro Ile Asn Leu Thr
225 230 235 240

Asp Glu Ser Met Phe Pro Ile Gly Thr Tyr Leu Leu Tyr Glu Cys Leu
245 250 255

Pro Gly Tyr Ile Lys Arg Gln Phe Ser Ile Thr Cys Lys Gln Asp Ser
260 265 270

Thr Trp Thr Ser Ala Glu Asp Lys Cys Ile Arg Lys Gln Cys Lys Thr
275 280 285

Pro Ser Asp Pro Glu Asn Gly Leu Val His Val His Thr Gly Ile Gln
290 295 300

Phe Gly Ser Arg Ile Asn Tyr Thr Cys Asn Gln Gly Tyr Arg Leu Ile
305 310 315 320

Gly Ser Ser Ser Ala Val Cys Val Ile Thr Asp Gln Ser Val Asp Trp
325 330 335

Asp Thr Glu Ala Pro Ile Cys Glu Trp Ile Pro Cys Glu Ile Pro Pro
340 345 350

Gly Ile Pro Asn Gly Asp Phe Phe Ser Ser Thr Arg Glu Asp Phe His
355 360 365

Tyr Gly Met Val Val Thr Tyr Arg Cys Asn Thr Asp Ala Arg Gly Lys
370 375 380

Ala Leu Phe Asn Leu Val Gly Glu Pro Ser Leu Tyr Cys Thr Ser Asn
385 390 395 400

Asp Gly Glu Ile Gly Val Trp Ser Gly Pro Pro Pro Gln Cys Ile Glu
405 410 415

Leu Asn Lys Cys Thr Pro Pro Pro Tyr Val Glu Asn Ala Val Met Leu
420 425 430

Ser Glu Asn Arg Ser Leu Phe Ser Leu Arg Asp Ile Val Glu Phe Arg
435 440 445

Cys His Pro Gly Phe Ile Met Lys Gly Ala Ser Ser Val His Cys Gln

450

455

460

Ser Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Phe Lys Gly Val
 465 470 475 480

Ile Cys Arg Leu Pro Gln Glu Met Ser Gly Phe Gln Lys Gly Leu Gly
 485 490 495

Met Lys Lys Glu Tyr Tyr Tyr Gly Glu Asn Val Thr Leu Glu Cys Glu
 500 505 510

Asp Gly Tyr Thr Leu Glu Gly Ser Ser Gln Ser Gln Cys Gln Ser Asp
 515 520 525

Gly Ser Trp Asn Pro Leu Leu Ala Lys Cys Val Ser Arg Ser Ile Glu
 530 535 540

Asn Leu Tyr Phe Gln Gly His His His His His His
 545 550 555

<210> 116

<211> 883

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 116

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
210 215 220

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
225 230 235 240

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
245 250 255

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
260 265 270

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
275 280 285

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
290 295 300

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
305 310 315 320

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
325 330 335

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
340 345 350

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
355 360 365

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly

370

375

380

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

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 405 410 415

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 420 425 430

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 435 440 445

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 450 455 460

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 465 470 475 480

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 485 490 495

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 500 505 510

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 515 520 525

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 530 535 540

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 545 550 555 560

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

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 580 585 590

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 595 600 605

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 610 615 620

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 625 630 635 640

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
645 650 655

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
660 665 670

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
675 680 685

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
690 695 700

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
705 710 715 720

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
725 730 735

Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr
740 745 750

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
755 760 765

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
770 775 780

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
785 790 795 800

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
805 810 815

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
820 825 830

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
835 840 845

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
850 855 860

Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe Gln Gly His His His
865 870 875 880

His His His

<210> 117
<211> 542
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 117
Glu Val Gln Leu Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
210 215 220

Glu	Asp	Cys	Asn	Glu	Leu	Pro	Pro	Arg	Arg	Asn	Thr	Glu	Ile	Leu	Thr		225	230	235	240
Gly	Ser	Trp	Ser	Asp	Gln	Thr	Tyr	Pro	Glu	Gly	Thr	Gln	Ala	Ile	Tyr		245	250	255	
Lys	Cys	Arg	Pro	Gly	Tyr	Arg	Ser	Leu	Gly	Asn	Val	Ile	Met	Val	Cys		260	265	270	
Arg	Lys	Gly	Glu	Trp	Val	Ala	Leu	Asn	Pro	Leu	Arg	Lys	Cys	Gln	Lys		275	280	285	
Arg	Pro	Cys	Gly	His	Pro	Gly	Asp	Thr	Pro	Phe	Gly	Thr	Phe	Thr	Leu		290	295	300	
Thr	Gly	Gly	Asn	Val	Phe	Glu	Tyr	Gly	Val	Lys	Ala	Val	Tyr	Thr	Cys		305	310	315	320
Asn	Glu	Gly	Tyr	Gln	Leu	Leu	Gly	Glu	Ile	Asn	Tyr	Arg	Glu	Cys	Asp		325	330	335	
Thr	Asp	Gly	Trp	Thr	Asn	Asp	Ile	Pro	Ile	Cys	Glu	Val	Val	Lys	Cys		340	345	350	
Leu	Pro	Val	Thr	Ala	Pro	Glu	Asn	Gly	Lys	Ile	Val	Ser	Ser	Ala	Met		355	360	365	
Glu	Pro	Asp	Arg	Glu	Tyr	His	Phe	Gly	Gln	Ala	Val	Arg	Phe	Val	Cys		370	375	380	
Asn	Ser	Gly	Tyr	Lys	Ile	Glu	Gly	Asp	Glu	Glu	Met	His	Cys	Ser	Asp		385	390	395	400
Asp	Gly	Phe	Trp	Ser	Lys	Glu	Lys	Pro	Lys	Cys	Val	Glu	Ile	Ser	Cys		405	410	415	
Lys	Ser	Pro	Asp	Val	Ile	Asn	Gly	Ser	Pro	Ile	Ser	Gln	Lys	Ile	Ile		420	425	430	
Tyr	Lys	Glu	Asn	Glu	Arg	Phe	Gln	Tyr	Lys	Cys	Asn	Met	Gly	Tyr	Glu		435	440	445	
Tyr	Ser	Glu	Arg	Gly	Asp	Ala	Val	Cys	Thr	Glu	Ser	Gly	Trp	Arg	Pro		450	455	460	
Leu	Pro	Ser	Cys	Glu	Glu	Lys	Ser	Cys	Asp	Asn	Pro	Tyr	Ile	Pro	Asn		465	470	475	480

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
485 490 495

Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr
500 505 510

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
515 520 525

Lys Glu Asn Leu Tyr Phe Gln Gly His His His His His His
530 535 540

<210> 118

<211> 888

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 118

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Gly Gly Gly Gly Ser
 210 215 220

Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala
 225 230 235 240

Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr
 245 250 255

Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile
 260 265 270

Ile Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg
 275 280 285

Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His
 290 295 300

Val Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr
 305 310 315 320

Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser
 325 330 335

Gly Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile
 340 345 350

Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr
 355 360 365

Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn
 370 375 380

Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser
 385 390 395 400

Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
 405 410 415

Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu
420 425 430

Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu
435 440 445

Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg
450 455 460

Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser
465 470 475 480

Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg
485 490 495

Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr
500 505 510

Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys
515 520 525

Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys
530 535 540

Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe
545 550 555 560

Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu
565 570 575

Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly
580 585 590

Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe
595 600 605

Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro
610 615 620

Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro
625 630 635 640

His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile
645 650 655

Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala
660 665 670

Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu
675 680 685

Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly
690 695 700

Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe
705 710 715 720

Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val
725 730 735

Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met
740 745 750

Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser
755 760 765

Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile
770 775 780

Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
785 790 795 800

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile
805 810 815

Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
820 825 830

Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu
835 840 845

Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser
850 855 860

Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe
865 870 875 880

Gln Gly His His His His His
885

<210> 119

<211> 1103

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 119

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala
435 440 445

Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe
450 455 460

Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr
465 470 475 480

Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr
485 490 495

Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp
500 505 510

Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser

515

520

525

Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser
 530 535 540

Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu
 545 550 555 560

Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr
 565 570 575

Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser
 580 585 590

Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe
 595 600 605

Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln
 610 615 620

Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
 625 630 635 640

Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg
 645 650 655

Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly
 660 665 670

Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys
 675 680 685

Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro
 690 695 700

Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser
 705 710 715 720

Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg
 725 730 735

Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala
 740 745 750

Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
 755 760 765

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys
 770 775 780

Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
785 790 795 800

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val
805 810 815

Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn
820 825 830

Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr
835 840 845

Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp
850 855 860

Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn
865 870 875 880

Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys
885 890 895

Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn
900 905 910

Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro
915 920 925

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val
930 935 940

Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro
945 950 955 960

Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val
965 970 975

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly
980 985 990

His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser
995 1000 1005

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
1010 1015 1020

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
1025 1030 1035

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
1040 1045 1050

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
1055 1060 1065

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
1070 1075 1080

Gln Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe Gln Gly His
1085 1090 1095

His His His His His
1100

<210> 120
<211> 1103
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 120
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala
435 440 445

Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe
450 455 460

Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr
465 470 475 480

Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr
485 490 495

Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp
500 505 510

Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser
515 520 525

Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser
530 535 540

Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu
545 550 555 560

Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr
565 570 575

Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser
580 585 590

Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe
595 600 605

Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln
610 615 620

Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
625 630 635 640

Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg
645 650 655

Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly
660 665 670

Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys
675 680 685

Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro
690 695 700

Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser
705 710 715 720

Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg
725 730 735

Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala
740 745 750

Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
755 760 765

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys
770 775 780

Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
785 790 795 800

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val
805 810 815

Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn
820 825 830

Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr
835 840 845

Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp
850 855 860

Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn
865 870 875 880

Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys
885 890 895

Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn
900 905 910

Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro

915

920

925

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val
 930 935 940

Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro
 945 950 955 960

Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val
 965 970 975

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly
 980 985 990

His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser
 995 1000 1005

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
 1010 1015 1020

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 1025 1030 1035

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 1040 1045 1050

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 1055 1060 1065

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
 1070 1075 1080

Gln Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe Gln Gly His
 1085 1090 1095

His His His His His
 1100

<210> 121

<211> 762

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 121

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe

275

280

285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asp Cys Asn
 435 440 445

Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser
 450 455 460

Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro
 465 470 475 480

Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys Gly Glu
 485 490 495

Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly
 500 505 510

His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn
 515 520 525

Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr
 530 535 540

Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp
545 550 555 560

Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr
565 570 575

Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg
580 585 590

Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr
595 600 605

Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp
610 615 620

Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp
625 630 635 640

Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn
645 650 655

Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg
660 665 670

Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys
675 680 685

Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser
690 695 700

Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys
705 710 715 720

Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr
725 730 735

Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu Lys Glu Asn Leu
740 745 750

Tyr Phe Gln Gly His His His His His His
755 760

<210> 122

<211> 762

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 122

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asp Cys Asn
 435 440 445

Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser
 450 455 460

Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro
 465 470 475 480

Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys Gly Glu
 485 490 495

Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly
 500 505 510

His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn
515 520 525

Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr
530 535 540

Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp
545 550 555 560

Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr
565 570 575

Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg
580 585 590

Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr
595 600 605

Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp
610 615 620

Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp
625 630 635 640

Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn
645 650 655

Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg
660 665 670

Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys
675 680 685

Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser
690 695 700

Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys
705 710 715 720

Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr
725 730 735

Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu Lys Glu Asn Leu
740 745 750

Tyr Phe Gln Gly His His His His His His
755 760

<210> 123
<211> 1103
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 123
Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
660 665 670

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
675 680 685

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
690 695 700

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
705 710 715 720

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
725 730 735

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

740

745

750

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
755 760 765

Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala
770 775 780

Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe
785 790 795 800

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
805 810 815

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
820 825 830

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
835 840 845

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
850 855 860

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
865 870 875 880

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
885 890 895

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
900 905 910

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
915 920 925

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
930 935 940

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
945 950 955 960

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
965 970 975

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
980 985 990

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
995 1000 1005

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
1010 1015 1020

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
1025 1030 1035

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys
1040 1045 1050

Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr
1055 1060 1065

Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys
1070 1075 1080

Ser Leu Ser His Ser Pro Gly Glu Asn Leu Tyr Phe Gln Gly His
1085 1090 1095

His His His His His
1100

<210> 124

<211> 888

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 124

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile

100

105

110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
660 665 670

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
675 680 685

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
690 695 700

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
705 710 715 720

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
725 730 735

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
740 745 750

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
755 760 765

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
770 775 780

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
785 790 795 800

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
805 810 815

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
820 825 830

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
835 840 845

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
850 855 860

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Glu Asn Leu Tyr Phe
865 870 875 880

Gln Gly His His His His His
885

<210> 125

<211> 1092

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 125

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
340 345 350

Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys
435 440 445

Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp
450 455 460

Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro
465 470 475 480

Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val
485 490 495

Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro
500 505 510

Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe
515 520 525

Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly
530 535 540

Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp
545 550 555 560

Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr
565 570 575

Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr
580 585 590

Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys
595 600 605

Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp
610 615 620

Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro
625 630 635 640

Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp
645 650 655

Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln
660 665 670

Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu
675 680 685

Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro
690 695 700

Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn
705 710 715 720

Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp

725

730

735

Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser
740 745 750

Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly
755 760 765

Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly
770 775 780

Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
785 790 795 800

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser
805 810 815

Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
820 825 830

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly
835 840 845

Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser
850 855 860

Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln
865 870 875 880

Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly
885 890 895

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
900 905 910

Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
915 920 925

Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
930 935 940

Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys
945 950 955 960

Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile
965 970 975

Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu
980 985 990

Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His
995 1000 1005

Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu
1010 1015 1020

Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
1025 1030 1035

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly
1040 1045 1050

Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
1055 1060 1065

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
1070 1075 1080

Ala Pro Gln Cys Ile Ile Pro Asn Lys
1085 1090

<210> 126

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 126

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

100					105					110					
Ser	Ala	Lys	Thr	Thr	Pro	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Gly	Ser
		115					120					125			
Ala	Ala	Gln	Thr	Asn	Ser	Met	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly
	130					135					140				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser
145					150					155					160
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr
				165					170					175	
Leu	Ser	Ser	Ser	Val	Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Glu	Thr
			180					185					190		
Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys
		195					200					205			
Lys	Ile	Val	Pro	Arg	Asp	Cys	Gly	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val
	210					215					220				
Pro	Glu	Val	Ser	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
225					230					235					240
Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile
				245					250					255	
Ser	Lys	Asp	Asp	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val
			260					265					270		
Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser
		275					280					285			
Thr	Phe	Arg	Ser	Val	Ser	Glu	Leu	Pro	Ile	Met	His	Gln	Asp	Trp	Leu
	290					295					300				
Asn	Gly	Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala
305					310					315					320
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro
				325					330					335	
Gln	Val	Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys
			340					345					350		
Val	Ser	Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr
		355					360					365			

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
 370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
 385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
 405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
 420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys
 435 440 445

Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp
 450 455 460

Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro
 465 470 475 480

Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val
 485 490 495

Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro
 500 505 510

Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe
 515 520 525

Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly
 530 535 540

Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp
 545 550 555 560

Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr
 565 570 575

Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr
 580 585 590

Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys
 595 600 605

Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp
 610 615 620

Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro
625 630 635 640

Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp
645 650 655

Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln
660 665 670

Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu
675 680 685

Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro
690 695 700

Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn
705 710 715 720

Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp
725 730 735

Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser
740 745 750

Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly
755 760 765

Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly
770 775 780

Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
785 790 795 800

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser
805 810 815

Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
820 825 830

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly
835 840 845

Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser
850 855 860

Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln
865 870 875 880

Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly
885 890 895

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
900 905 910

Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
915 920 925

Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
930 935 940

Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys
945 950 955 960

Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile
965 970 975

Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu
980 985 990

Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His
995 1000 1005

Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu
1010 1015 1020

Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
1025 1030 1035

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly
1040 1045 1050

Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
1055 1060 1065

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
1070 1075 1080

Ala Pro Gln Cys Ile Ile Pro Asn Lys His His His His His His
1085 1090 1095

<210> 127

<211> 1098

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 127

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
340 345 350

Val Ser Leu Trp Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys
435 440 445

Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp
450 455 460

Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro
465 470 475 480

Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val
485 490 495

Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro
500 505 510

Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe

515

520

525

Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly
 530 535 540

Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp
 545 550 555 560

Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr
 565 570 575

Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr
 580 585 590

Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys
 595 600 605

Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp
 610 615 620

Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro
 625 630 635 640

Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp
 645 650 655

Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln
 660 665 670

Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu
 675 680 685

Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro
 690 695 700

Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn
 705 710 715 720

Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp
 725 730 735

Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser
 740 745 750

Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly
 755 760 765

Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly
 770 775 780

Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
 785 790 795 800

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser
 805 810 815

Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile
 820 825 830

Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly
 835 840 845

Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser
 850 855 860

Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln
 865 870 875 880

Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly
 885 890 895

His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln
 900 905 910

Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys
 915 920 925

Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn
 930 935 940

Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys
 945 950 955 960

Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile
 965 970 975

Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu
 980 985 990

Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His
 995 1000 1005

Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu
 1010 1015 1020

Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 1025 1030 1035

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly
1040 1045 1050

Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
1055 1060 1065

Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro
1070 1075 1080

Ala Pro Gln Cys Ile Ile Pro Asn Lys His His His His His His
1085 1090 1095

<210> 128

<211> 547

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 128

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Gly Gly Gly Gly Ser
 210 215 220

Gly Gly Gly Gly Ser Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn
 225 230 235 240

Thr Glu Ile Leu Thr Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly
 245 250 255

Thr Gln Ala Ile Tyr Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn
 260 265 270

Val Ile Met Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu
 275 280 285

Arg Lys Cys Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe
 290 295 300

Gly Thr Phe Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys
 305 310 315 320

Ala Val Tyr Thr Cys Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn
 325 330 335

Tyr Arg Glu Cys Asp Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys
 340 345 350

Glu Val Val Lys Cys Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile
 355 360 365

Val Ser Ser Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala
 370 375 380

Val Arg Phe Val Cys Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu
 385 390 395 400

Met His Cys Ser Asp Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys
 405 410 415

Val Glu Ile Ser Cys Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile
420 425 430

Ser Gln Lys Ile Ile Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys
435 440 445

Asn Met Gly Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu
450 455 460

Ser Gly Trp Arg Pro Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn
465 470 475 480

Pro Tyr Ile Pro Asn Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg
485 490 495

Thr Gly Asp Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala
500 505 510

Thr Arg Gly Asn Thr Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala
515 520 525

Pro Arg Cys Thr Leu Lys Glu Asn Leu Tyr Phe Gln Gly His His His
530 535 540

His His His
545

<210> 129
<211> 547
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 129
Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65 70 75 80

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

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
 100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
 115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
 130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
 145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
 165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
 180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
 195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
 210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
 225 230 235 240

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

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
 260 265 270

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

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
 290 295 300

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr
 305 310 315 320

Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile
 325 330 335

Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
340 345 350

Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile
355 360 365

Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly
370 375 380

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
385 390 395 400

Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe Pro Arg
405 410 415

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg Arg Ala Asp Ala Ala
420 425 430

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
435 440 445

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
450 455 460

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
465 470 475 480

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
485 490 495

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
500 505 510

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
515 520 525

Phe Asn Arg Asn Glu Cys Glu Asn Leu Tyr Phe Gln Gly His His His
530 535 540

His His His
545

<210> 130

<211> 877

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 130

Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	Leu
1				5					10					15	
Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys
			20					25					30		
Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	Asn
		35					40					45			
Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	Arg
	50					55					60				
Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	Ile
65					70					75					80
Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	Leu
				85					90					95	
Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	Ile
		100						105					110		
Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	Pro
		115					120					125			
Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe
		130				135					140				
His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	Gly
145					150					155					160
Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser
				165					170					175	
Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile
			180					185					190		
Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	Leu	Val
		195					200					205			
Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	Phe	Arg
	210					215					220				
Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys	Cys	Gln
225					230					235					240
Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg	Val	Cys
				245					250					255	

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 465 470 475 480

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 485 490 495

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 500 505 510

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

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
530 535 540

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
545 550 555 560

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
565 570 575

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
580 585 590

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
595 600 605

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
610 615 620

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
625 630 635 640

Cys Ile Ile Pro Asn Lys Gly Gly Gly Gly Ser Gly Gly Gly Ser
645 650 655

Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe
660 665 670

Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
675 680 685

Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val
690 695 700

Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
705 710 715 720

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
725 730 735

Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys
740 745 750

Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser
755 760 765

Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro

770

775

780

Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Trp Cys Met Ile
 785 790 795 800

Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly
 805 810 815

Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp
 820 825 830

Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp
 835 840 845

Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
 850 855 860

Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 865 870 875

<210> 131

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 131

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
 1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
 20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
 35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
 50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
 65 70 75 80

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

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
 100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225 230 235 240

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

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
260 265 270

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

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
290 295 300

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Cys Lys Pro Cys
305 310 315 320

Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys
325 330 335

Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val
340 345 350

Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe
355 360 365

Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu

370

375

380

Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His
 385 390 395 400

Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala
 405 410 415

Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg
 420 425 430

Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met
 435 440 445

Ala Lys Asp Lys Val Ser Leu Trp Cys Met Ile Thr Asp Phe Phe Pro
 450 455 460

Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn
 465 470 475 480

Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val
 485 490 495

Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr
 500 505 510

Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu
 515 520 525

Lys Ser Leu Ser His Ser Pro Gly
 530 535

<210> 132

<211> 1333

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 132

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
210 215 220

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
225 230 235 240

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
245 250 255

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
260 265 270

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
275 280 285

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
290 295 300

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu

305					310						315				320
Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	Ile
				325					330					335	
Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	Pro
			340					345					350		
Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe
		355					360					365			
His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	Gly
	370					375					380				
Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser
385					390					395					400
Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile
			405						410					415	
Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	Leu	Val
			420					425					430		
Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	Phe	Arg
		435					440					445			
Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys	Cys	Gln
	450					455					460				
Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg	Val	Cys
465					470					475					480
Gln	Pro	Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg	Asp	Lys
				485					490					495	
Asp	Asn	Phe	Ser	Pro	Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	Pro	Gly
			500					505					510		
Tyr	Asp	Leu	Arg	Gly	Ala	Ala	Ser	Met	Arg	Cys	Thr	Pro	Gln	Gly	Asp
		515					520					525			
Trp	Ser	Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp	Asp	Phe
	530					535					540				
Met	Gly	Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn	Leu	Gln
545					550					555					560
Leu	Gly	Ala	Lys	Val	Asp	Phe	Val	Cys	Asp	Glu	Gly	Phe	Gln	Leu	Lys
			565						570					575	

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 580 585 590

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 595 600 605

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 610 615 620

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 625 630 635 640

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 645 650 655

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 660 665 670

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 675 680 685

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr
 690 695 700

Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu
 705 710 715 720

Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser
 725 730 735

Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr
 740 745 750

Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
 755 760 765

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala
 770 775 780

Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly
 785 790 795 800

Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
 805 810 815

Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
 820 825 830

Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
835 840 845

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
850 855 860

Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
865 870 875 880

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
885 890 895

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
900 905 910

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
915 920 925

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
930 935 940

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
945 950 955 960

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
965 970 975

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
980 985 990

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
995 1000 1005

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe
1010 1015 1020

Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
1025 1030 1035

Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe
1040 1045 1050

Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys
1055 1060 1065

Pro Leu Glu Val Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys
1070 1075 1080

Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu
1085 1090 1095

Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp
1100 1105 1110

Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala
1115 1120 1125

Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala
1130 1135 1140

Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro
1145 1150 1155

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu
1160 1165 1170

Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys
1175 1180 1185

Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp
1190 1195 1200

Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His
1205 1210 1215

Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn
1220 1225 1230

Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
1235 1240 1245

Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr
1250 1255 1260

Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys
1265 1270 1275

Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu
1280 1285 1290

Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp
1295 1300 1305

Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Glu Asn Leu
1310 1315 1320

Tyr Phe Gln Gly His His His His His His

1325

1330

<210> 133

<211> 1553

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 133

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala
435 440 445

Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe
450 455 460

Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr

465		470		475		480
Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr						
		485		490		495
Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp						
		500		505		510
Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser						
		515		520		525
Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser						
		530		535		540
Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu						
		545		550		555
Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr						
		565		570		575
Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser						
		580		585		590
Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe						
		595		600		605
Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln						
		610		615		620
Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys						
		625		630		635
Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg						
		645		650		655
Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly						
		660		665		670
Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys						
		675		680		685
Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro						
		690		695		700
Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser						
		705		710		715
Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg						
		725		730		735

Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala
 740 745 750

Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
 755 760 765

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys
 770 775 780

Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
 785 790 795 800

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val
 805 810 815

Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn
 820 825 830

Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr
 835 840 845

Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp
 850 855 860

Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn
 865 870 875 880

Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys
 885 890 895

Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn
 900 905 910

Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro
 915 920 925

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val
 930 935 940

Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro
 945 950 955 960

Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val
 965 970 975

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly
 980 985 990

His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser
995 1000 1005

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
1010 1015 1020

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
1025 1030 1035

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
1040 1045 1050

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
1055 1060 1065

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
1070 1075 1080

Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
1085 1090 1095

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu
1100 1105 1110

Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro
1115 1120 1125

Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu
1130 1135 1140

Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His
1145 1150 1155

Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln
1160 1165 1170

Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala
1175 1180 1185

Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala
1190 1195 1200

Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
1205 1210 1215

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala
1220 1225 1230

Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
1235 1240 1245

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn
1250 1255 1260

Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
1265 1270 1275

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe
1280 1285 1290

Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
1295 1300 1305

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys
1310 1315 1320

Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
1325 1330 1335

Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu
1340 1345 1350

Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile
1355 1360 1365

Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg
1370 1375 1380

Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro
1385 1390 1395

Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro
1400 1405 1410

Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly Ser
1415 1420 1425

Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His
1430 1435 1440

Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Thr Ala His Trp Ser
1445 1450 1455

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
1460 1465 1470

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe

1475

1480

1485

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu Gly Ser Arg
 1490 1495 1500

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 1505 1510 1515

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
 1520 1525 1530

Gln Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe Gln Gly His
 1535 1540 1545

His His His His His
 1550

<210> 134

<211> 1553

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 134

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val

385				390				395				400				
Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu	
				405					410					415		
His	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys	Ser	Leu	Ser	His	Ser	
				420					425					430		
Pro	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Cys	Asn	Ala	
				435					440					445		
Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	Leu	Thr	Asp	Glu	Phe	
				450					455					460		
Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	
				465					470					475		
Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	Asn	Ser	Val	Trp	Thr	
				485					490					495		
Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	Arg	Asn	Pro	Pro	Asp	
				500					505					510		
Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	Ile	Gln	Phe	Gly	Ser	
				515					520					525		
Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	
				530					535					540		
Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	Ile	Trp	Asp	Asn	Glu	
				545					550					555		
Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	Pro	Pro	Thr	Ile	Thr	
				565					570					575		
Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe	His	Tyr	Gly	Ser	
				580					585					590		
Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	Gly	Arg	Lys	Val	Phe	
				595					600					605		
Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser	Asn	Asp	Asp	Gln	
				610					615					620		
Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile	Ile	Pro	Asn	Lys	
				625					630					635		
Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	Leu	Val	Ser	Asp	Asn	Arg	
				645					650					655		

Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly
 660 665 670

Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys
 675 680 685

Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro
 690 695 700

Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser
 705 710 715 720

Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg
 725 730 735

Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala
 740 745 750

Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
 755 760 765

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys
 770 775 780

Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
 785 790 795 800

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val
 805 810 815

Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn
 820 825 830

Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr
 835 840 845

Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp
 850 855 860

Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn
 865 870 875 880

Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys
 885 890 895

Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn
 900 905 910

Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro
915 920 925

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val
930 935 940

Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro
945 950 955 960

Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val
965 970 975

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly
980 985 990

His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser
995 1000 1005

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
1010 1015 1020

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
1025 1030 1035

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
1040 1045 1050

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
1055 1060 1065

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
1070 1075 1080

Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
1085 1090 1095

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu
1100 1105 1110

Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro
1115 1120 1125

Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu
1130 1135 1140

Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His
1145 1150 1155

Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln
1160 1165 1170

Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala
1175 1180 1185

Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala
1190 1195 1200

Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
1205 1210 1215

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala
1220 1225 1230

Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser
1235 1240 1245

Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn
1250 1255 1260

Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
1265 1270 1275

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe
1280 1285 1290

Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
1295 1300 1305

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys
1310 1315 1320

Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
1325 1330 1335

Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu
1340 1345 1350

Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile
1355 1360 1365

Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg
1370 1375 1380

Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro
1385 1390 1395

Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro

1400

1405

1410

Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val Gly Ser
 1415 1420 1425

Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly His
 1430 1435 1440

Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Thr Ala His Trp Ser
 1445 1450 1455

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
 1460 1465 1470

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 1475 1480 1485

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu Gly Ser Arg
 1490 1495 1500

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
 1505 1510 1515

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
 1520 1525 1530

Gln Cys Ile Ile Pro Asn Lys Glu Asn Leu Tyr Phe Gln Gly His
 1535 1540 1545

His His His His His
 1550

<210> 135

<211> 1338

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 135

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Gly Gly Gly Gly Ser
210 215 220

Gly Gly Gly Gly Ser Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala
225 230 235 240

Arg Pro Thr Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr
245 250 255

Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile
260 265 270

Ile Cys Leu Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg
275 280 285

Arg Lys Ser Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His
290 295 300

Val Ile Lys Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr

305		310		315		320
Lys Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser						
		325		330		335
Gly Asp Thr Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile						
		340		345		350
Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr						
		355		360		365
Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn						
		370		375		380
Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser						
		385		390		395
Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro						
		405		410		415
Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu						
		420		425		430
Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu						
		435		440		445
Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg						
		450		455		460
Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser						
		465		470		475
Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg						
		485		490		495
Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr						
		500		505		510
Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys						
		515		520		525
Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys						
		530		535		540
Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe						
		545		550		555
Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu						
		565		570		575

Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly
 580 585 590

Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe
 595 600 605

Cys Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro
 610 615 620

Leu Glu Val Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro
 625 630 635 640

His Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile
 645 650 655

Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala
 660 665 670

Pro Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu
 675 680 685

Phe Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly
 690 695 700

Thr Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe
 705 710 715 720

Ser Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val
 725 730 735

Cys Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met
 740 745 750

Val His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser
 755 760 765

Cys Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile
 770 775 780

Leu Ser Gly Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln
 785 790 795 800

Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile
 805 810 815

Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
 820 825 830

Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu
835 840 845

Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser
850 855 860

Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn
865 870 875 880

Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu
885 890 895

Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly
900 905 910

Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu
915 920 925

Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala
930 935 940

Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val
945 950 955 960

Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met
965 970 975

Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu
980 985 990

Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val
995 1000 1005

Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val
1010 1015 1020

Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys
1025 1030 1035

Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val Pro Val
1040 1045 1050

Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn Gly
1055 1060 1065

Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Ala
1070 1075 1080

Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	Arg	Gly	Thr	Ser	Phe
1085						1090					1095			
Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	Ser	Asp	Pro	Gln
1100						1105					1110			
Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	Gly	Ile	Leu
1115						1120					1125			
Gly	His	Cys	Gln	Ala	Pro	Asp	His	Phe	Leu	Phe	Ala	Lys	Leu	Lys
1130						1135					1140			
Thr	Gln	Thr	Asn	Ala	Ser	Asp	Phe	Pro	Ile	Gly	Thr	Ser	Leu	Lys
1145						1150					1155			
Tyr	Glu	Cys	Arg	Pro	Glu	Tyr	Tyr	Gly	Arg	Pro	Phe	Ser	Ile	Thr
1160						1165					1170			
Cys	Leu	Asp	Asn	Leu	Val	Trp	Ser	Ser	Pro	Lys	Asp	Val	Cys	Lys
1175						1180					1185			
Arg	Lys	Ser	Cys	Lys	Thr	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val
1190						1195					1200			
His	Val	Ile	Thr	Asp	Ile	Gln	Val	Gly	Ser	Arg	Ile	Asn	Tyr	Ser
1205						1210					1215			
Cys	Thr	Thr	Gly	His	Arg	Leu	Ile	Gly	His	Ser	Ser	Ala	Glu	Cys
1220						1225					1230			
Ile	Leu	Ser	Gly	Asn	Thr	Ala	His	Trp	Ser	Thr	Lys	Pro	Pro	Ile
1235						1240					1245			
Cys	Gln	Arg	Ile	Pro	Cys	Gly	Leu	Pro	Pro	Thr	Ile	Ala	Asn	Gly
1250						1255					1260			
Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe	His	Tyr	Gly	Ser	Val
1265						1270					1275			
Val	Thr	Tyr	Arg	Cys	Asn	Leu	Gly	Ser	Arg	Gly	Arg	Lys	Val	Phe
1280						1285					1290			
Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser	Asn	Asp	Asp
1295						1300					1305			
Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile	Ile	Pro
1310						1315					1320			
Asn	Lys	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	His	His	His	His	His	His

1325

1330

1335

<210> 136

<211> 1553

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 136

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
385 390 395 400

Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
405 410 415

Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
420 425 430

Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
435 440 445

Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
450 455 460

Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr

465		470		475		480	
Glu Cys Arg Pro	Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu	485		490		495	
Asp Asn Leu Val	Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser	500		505		510	
Cys Lys Thr Pro	Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr	515		520		525	
Asp Ile Gln Val	Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His	530		535		540	
Arg Leu Ile Gly	His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala	545		550		555	560
Ala His Trp Ser	Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly	565		570		575	
Leu Pro Pro Thr	Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu	580		585		590	
Asn Phe His Tyr	Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser	595		600		605	
Gly Gly Arg Lys	Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys	610		615		620	
Thr Ser Asn Asp	Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln	625		630		635	640
Cys Ile Ile Pro	Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile	645		650		655	
Leu Val Ser Asp	Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu	660		665		670	
Phe Arg Cys Gln	Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys	675		680		685	
Cys Gln Ala Leu	Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg	690		695		700	
Val Cys Gln Pro	Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg	705		710		715	720
Asp Lys Asp Asn	Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu	725		730		735	

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 945 950 955 960

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 965 970 975

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
995 1000 1005

Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile
1010 1015 1020

Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
1025 1030 1035

Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
1040 1045 1050

Cys Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly
1055 1060 1065

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile
1070 1075 1080

Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Gly Gly
1085 1090 1095

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser
1100 1105 1110

Gly Pro Val Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys
1115 1120 1125

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Tyr Ile Asn Trp Val
1130 1135 1140

Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Val Ile Asn
1145 1150 1155

Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys
1160 1165 1170

Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
1175 1180 1185

Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ser
1190 1195 1200

Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
1205 1210 1215

Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
1220 1225 1230

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
1235 1240 1245

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu
1250 1255 1260

Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu
1265 1270 1275

Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro
1280 1285 1290

Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr
1295 1300 1305

Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro
1310 1315 1320

Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
1325 1330 1335

Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
1340 1345 1350

Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
1355 1360 1365

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
1370 1375 1380

Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
1385 1390 1395

Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
1400 1405 1410

Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
1415 1420 1425

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
1430 1435 1440

Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
1445 1450 1455

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
1460 1465 1470

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr

1475

1480

1485

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys
 1490 1495 1500

Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr
 1505 1510 1515

Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys
 1520 1525 1530

Ser Leu Ser His Ser Pro Gly Glu Asn Leu Tyr Phe Gln Gly His
 1535 1540 1545

His His His His His
 1550

<210> 137

<211> 1338

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 137

Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15

Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30

Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45

Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60

Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80

Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95

Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110

Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125

Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
145 150 155 160

Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
165 170 175

Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
180 185 190

Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
195 200 205

Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
210 215 220

Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
225 230 235 240

Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
245 250 255

Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
260 265 270

Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
275 280 285

Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
290 295 300

Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
305 310 315 320

Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
325 330 335

Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
340 345 350

Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
355 360 365

Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
370 375 380

Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro

385		390		395		400
Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly						
	405			410		415
Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp						
	420			425		430
Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile						
	435			440		445
Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys						
	450			455		460
Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr						
	465			470		475
Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu						
	485			490		495
Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser						
	500			505		510
Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr						
	515			520		525
Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His						
	530			535		540
Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala						
	545			550		555
Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly						
	565			570		575
Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu						
	580			585		590
Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser						
	595			600		605
Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys						
	610			615		620
Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln						
	625			630		635
Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile						
	645			650		655

Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
 660 665 670

Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
 675 680 685

Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
 690 695 700

Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
 705 710 715 720

Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
 725 730 735

Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
 740 745 750

Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
 755 760 765

Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
 770 775 780

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800

Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815

Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830

Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845

Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860

Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880

Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895

Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910

Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
915 920 925

Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
930 935 940

Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
945 950 955 960

Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
965 970 975

Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
980 985 990

Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
995 1000 1005

Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile
1010 1015 1020

Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
1025 1030 1035

Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg
1040 1045 1050

Cys Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly
1055 1060 1065

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile
1070 1075 1080

Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Gly Gly
1085 1090 1095

Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr
1100 1105 1110

Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile Ser
1115 1120 1125

Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr
1130 1135 1140

Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu
1145 1150 1155

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 139

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Ser Cys Ala Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Val Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Asp Cys Asn
 435 440 445

Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr Gly Ser Trp Ser
 450 455 460

Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr Lys Cys Arg Pro
 465 470 475 480

Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys Gly Glu
 485 490 495

Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly
500 505 510

His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn
515 520 525

Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys Asn Glu Gly Tyr
530 535 540

Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp Thr Asp Gly Trp
545 550 555 560

Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys Leu Pro Val Thr
565 570 575

Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg
580 585 590

Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys Asn Ser Gly Tyr
595 600 605

Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp Asp Gly Phe Trp
610 615 620

Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys Lys Ser Pro Asp
625 630 635 640

Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile Tyr Lys Glu Asn
645 650 655

Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg
660 665 670

Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro Leu Pro Ser Cys
675 680 685

Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn Gly Asp Tyr Ser
690 695 700

Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys
705 710 715 720

Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr Ala Lys Cys Thr
725 730 735

Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu Lys
740 745

<210> 140

<211> 1090

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 140

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Trp Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Cys Asn Ala
435 440 445

Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu Thr Asp Glu Phe
450 455 460

Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys Arg Pro Gly Tyr
465 470 475 480

Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn Ser Val Trp Thr
485 490 495

Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg Asn Pro Pro Asp
500 505 510

Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile Gln Phe Gly Ser
515 520 525

Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu Ile Gly Ser Ser
530 535 540

Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile Trp Asp Asn Glu
545 550 555 560

Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr
565 570 575

Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser
580 585 590

Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe
595 600 605

Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln
610 615 620

Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
625 630 635 640

Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val Ser Asp Asn Arg
645 650 655

Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg Cys Gln Pro Gly
660 665 670

Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln Ala Leu Asn Lys
675 680 685

Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys Gln Pro Pro Pro
690 695 700

Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys Asp Asn Phe Ser
705 710 715 720

Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg
725 730 735

Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp Trp Ser Pro Ala

740

745

750

Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe Met Gly Gln Leu
755 760 765

Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln Leu Gly Ala Lys
770 775 780

Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys Gly Ser Ser Ala
785 790 795 800

Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp Asn Ser Ser Val
805 810 815

Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro Val Ile Pro Asn
820 825 830

Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro Phe Gly Lys Thr
835 840 845

Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly Thr Ser Phe Asp
850 855 860

Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn
865 870 875 880

Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile Leu Gly His Cys
885 890 895

Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys Thr Gln Thr Asn
900 905 910

Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu Lys Tyr Glu Cys Arg Pro
915 920 925

Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr Cys Leu Asp Asn Leu Val
930 935 940

Trp Ser Ser Pro Lys Asp Val Cys Lys Arg Lys Ser Cys Lys Thr Pro
945 950 955 960

Pro Asp Pro Val Asn Gly Met Val His Val Ile Thr Asp Ile Gln Val
965 970 975

Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr Gly His Arg Leu Ile Gly
980 985 990

His Ser Ser Ala Glu Cys Ile Leu Ser Gly Asn Ala Ala His Trp Ser
995 1000 1005

Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro Cys Gly Leu Pro Pro
1010 1015 1020

Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
1025 1030 1035

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
1040 1045 1050

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
1055 1060 1065

Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro
1070 1075 1080

Gln Cys Ile Ile Pro Asn Lys
1085 1090

<210> 141
<211> 695
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 141
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala

115

120

125

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Cys Gly Leu
 435 440 445

Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu Gly Arg Thr Ser
 450 455 460

Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val
 465 470 475 480

Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser Gln
 485 490 495

Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr
 500 505 510

Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr
 515 520 525

Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg
 530 535 540

Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys
 545 550 555 560

Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro
 565 570 575

Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe
 580 585 590

Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly
 595 600 605

Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser
 610 615 620

Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln
 625 630 635 640

Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg
645 650 655

Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr Met Ile Gly Glu
660 665 670

His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly Glu Trp Ser Gly
675 680 685

Pro Pro Pro Glu Cys Arg Gly
690 695

<210> 142

<211> 521

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 142

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu Gln Cys Tyr
435 440 445

Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser
450 455 460

Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr
465 470 475 480

Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr
485 490 495

Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu
500 505 510

Cys Asn Phe Asn Glu Gln Leu Glu Asn
515 520

<210> 143
<211> 805
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 143
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser His Thr Val Glu
435 440 445

Leu Asn Asn Met Phe Gly Gln Ile Gln Ser Pro Gly Tyr Pro Asp Ser
450 455 460

Tyr Pro Ser Asp Ser Glu Val Thr Trp Asn Ile Thr Val Pro Asp Gly
465 470 475 480

Phe Arg Ile Lys Leu Tyr Phe Met His Phe Asn Leu Glu Ser Ser Tyr
485 490 495

Leu Cys Glu Tyr Asp Tyr Val Lys Val Glu Thr Glu Asp Gln Val Leu
500 505 510

Ala Thr Phe Cys Gly Arg Glu Thr Thr Asp Thr Glu Gln Thr Pro Gly
515 520 525

Gln Glu Val Val Leu Ser Pro Gly Ser Phe Met Ser Ile Thr Phe Arg
530 535 540

Ser Asp Phe Ser Asn Glu Glu Arg Phe Thr Gly Phe Asp Ala His Tyr
545 550 555 560

Met Ala Val Asp Val Asp Glu Cys Lys Glu Arg Glu Asp Glu Glu Leu
565 570 575

Ser Cys Asp His Tyr Cys His Asn Tyr Ile Gly Gly Tyr Tyr Cys Ser
580 585 590

Cys Arg Phe Gly Tyr Ile Leu His Thr Asp Asn Arg Thr Cys Arg Val
595 600 605

Glu Cys Ser Asp Asn Leu Phe Thr Gln Arg Thr Gly Val Ile Thr Ser
610 615 620

Pro Asp Phe Pro Asn Pro Tyr Pro Lys Ser Ser Glu Cys Leu Tyr Thr
625 630 635 640

Ile Glu Leu Glu Glu Gly Phe Met Val Asn Leu Gln Phe Glu Asp Ile
645 650 655

Phe Asp Ile Glu Asp His Pro Glu Val Pro Cys Pro Tyr Asp Tyr Ile
660 665 670

Lys Ile Lys Val Gly Pro Lys Val Leu Gly Pro Phe Cys Gly Glu Lys
675 680 685

Ala Pro Glu Pro Ile Ser Thr Gln Ser His Ser Val Leu Ile Leu Phe
690 695 700

His Ser Asp Asn Ser Gly Glu Asn Arg Gly Trp Arg Leu Ser Tyr Arg
705 710 715 720

Ala Ala Gly Asn Glu Cys Pro Glu Leu Gln Pro Pro Val His Gly Lys
725 730 735

Ile Glu Pro Ser Gln Ala Lys Tyr Phe Phe Lys Asp Gln Val Leu Val
740 745 750

Ser Cys Asp Thr Gly Tyr Lys Val Leu Lys Asp Asn Val Glu Met Asp
755 760 765

Thr Phe Gln Ile Glu Cys Leu Lys Asp Gly Thr Trp Ser Asn Lys Ile
770 775 780

Pro Thr Cys Lys Lys Asn Glu Ile Asp Leu Glu Ser Glu Leu Lys Ser
785 790 795 800

Glu Gln Val Thr Glu
805

<210> 144

<211> 695

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 144

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
 165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
 180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
 210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
 225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
 245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val
 260 265 270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
420 425 430

Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Cys Glu Glu Pro
435 440 445

Pro Thr Phe Glu Ala Met Glu Leu Ile Gly Lys Pro Lys Pro Tyr Tyr
450 455 460

Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys Lys Lys Gly Tyr Phe Tyr
465 470 475 480

Ile Pro Pro Leu Ala Thr His Thr Ile Cys Asp Arg Asn His Thr Trp
485 490 495

Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg Glu Thr Cys Pro Tyr Ile
500 505 510

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

Phe Gly Tyr Gln Met His Phe Ile Cys Asn Glu Gly Tyr Tyr Leu Ile
530 535 540

Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys Gly Ser Val Ala Ile Trp

545 550 555 560

Ser Gly Lys Pro Pro Ile Cys Glu Lys Val Leu Cys Thr Pro Pro Pro
565 570 575

Lys Ile Lys Asn Gly Lys His Thr Phe Ser Glu Val Glu Val Phe Glu
580 585 590

Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp Pro Ala Pro Gly Pro Asp
595 600 605

Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile Tyr Cys Gly Asp Asn Ser
610 615 620

Val Trp Ser Arg Ala Ala Pro Glu Cys Lys Val Val Lys Cys Arg Phe
625 630 635 640

Pro Val Val Glu Asn Gly Lys Gln Ile Ser Gly Phe Gly Lys Lys Phe
645 650 655

Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys Asp Lys Gly Phe Tyr Leu
660 665 670

Asp Gly Ser Asp Thr Ile Val Cys Asp Ser Asn Ser Thr Trp Asp Pro
675 680 685

Pro Val Pro Lys Cys Leu Lys
690 695

```
<210> 145
<211> 113
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 145
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

Ser

<210> 146

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 146

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

<210> 147

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

peptide

<400> 147

Gly Tyr Thr Phe Thr Ser Tyr Tyr

1 5

<210> 148

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 148

Ile Tyr Pro Gly Asn Gly Asp Thr

1 5

<210> 149

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 149

Ala Lys Gly Phe Asp Tyr

1 5

<210> 150

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 150

Gln Ser Leu Val Tyr Ser Asn Gly Asn Thr Tyr

1 5 10

<210> 151

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 151

Lys Val Ser

1

<210> 152

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 152
Ser Gln Ser Thr His Val Pro Tyr Thr
1 5

<210> 153
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 153
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Lys Tyr Gly Ser Gly Tyr Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser

<210> 154
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 154
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

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

Arg

<210> 155
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 155
 Gly Tyr Thr Phe Thr Ser Tyr Tyr
 1 5

<210> 156
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 156
 Ile Tyr Pro Gly Asn Gly Asp Thr
 1 5

<210> 157
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 157

Ala Lys Tyr Gly Ser Gly Tyr

1 5

<210> 158

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 158

Gln Ser Leu Val Tyr Ser Asn Gly Asn Thr Tyr

1 5 10

<210> 159

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 159

Lys Val Ser

1

<210> 160

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 160

Ser Gln Ser Thr His Val Pro Tyr Thr

1 5

<210> 161

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(17)

<223> This sequence may encompass 0-17 residues

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 161

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Gly

<210> 162

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 162

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

Leu Asp

<210> 163

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 163

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
1 5 10

<210> 164

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<221> MISC_FEATURE

<222> (1)..(85)

<223> This sequence may encompass 0-17 'Gly Gly Gly Gly Ser'
repeating units

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 164

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser
85

<210> 165

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<221> MISC_FEATURE

<222> (1)..(85)

<223> This sequence may encompass 0-17 'Glu Ala Ala Ala Lys'
repeating units

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 165

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala
35 40 45

Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
50 55 60

Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
65 70 75 80

Glu Ala Ala Ala Lys
85

<210> 166
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MISC_FEATURE
<222> (2)..(86)
<223> This region may encompass 0-17 'Glu Ala Ala Ala Lys'
repeating units

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 166
Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
20 25 30

Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala
35 40 45

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala
50 55 60

Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
65 70 75 80

Lys Glu Ala Ala Ala Lys Ala
85

<210> 167
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 167
Gly Ser Ala Gly Ser Ala Ala Gly Ser Gly Glu Phe
1 5 10

<210> 168

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

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (21)..(21)
<223> Any amino acid

<220>

<221> MOD_RES
<222> (23)..(23)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (25)..(25)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (27)..(27)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (29)..(29)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (31)..(31)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (33)..(33)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (1)..(34)
<223> This sequence may encompass 0-17 'Xaa Pro'
repeating units

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 168
Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
1 5 10 15

Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
20 25 30

Xaa Pro

<210> 169
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 169
Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Ala Leu Glu Ala Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
35 40 45

<210> 170
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MISC_FEATURE
<222> (1)..(51)
<223> This sequence may encompass 0-17 'Pro Ala Ser'
repeating units

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 170
Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro
1 5 10 15

Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala
20 25 30

Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser Pro Ala Ser
35 40 45

Pro Ala Ser
50

<210> 171
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MISC_FEATURE
<222> (1)..(34)
<223> This sequence may encompass 0-17 'Gly Ser'
repeating units

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 171

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

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
20 25 30

Gly Ser

<210> 172

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 172

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

<210> 173

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 173

Gly Gly Ser Gly Gly His Met Gly Ser Gly Gly
1 5 10

<210> 174

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>

<221> MISC_FEATURE

<222> (1)..(51)

<223> This sequence may encompass 0-17 'Gly Gly Ser'
repeating units

<220>

<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 174

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

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
20 25 30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
35 40 45

Gly Gly Ser
50

<210> 175
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 175
Gly Gly Ser Gly Gly Gly Gly Gly
1 5

<210> 176
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 176
Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
1 5 10 15

<210> 177
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 177
Ala Ala Gly Ala Ala Thr Ala Ala
1 5

<210> 178
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 178
Gly Gly Ser Ser Gly
1 5

<210> 179
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> MISC_FEATURE
<222> (1)..(34)
<223> This sequence may encompass 0-17 'Gly Thr'
repeating units

<220>
<223> See specification as filed for detailed description of
substitutions and preferred embodiments

<400> 179
Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr
1 5 10 15

Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr Gly Thr
20 25 30

Gly Thr

<210> 180
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 180
Gly Ser Ser Ser Gly
1 5

<210> 181
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 181
Gly Ser Gly Gly Gly Thr Gly Gly Gly Ser Gly
1 5 10

<210> 182
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 182
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
1 5 10

<210> 183
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 183
Gly Ser Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly
1 5 10

<210> 184
<211> 251
<212> PRT
<213> Homo sapiens

<400> 184
Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
1 5 10 15

Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
20 25 30

Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu
35 40 45

Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys
50 55 60

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

Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg
85 90 95

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

Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys Ser
115 120 125

Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly
130 135 140

Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr
145 150 155 160

Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser
165 170 175

Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro
180 185 190

Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His
195 200 205

Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr
210 215 220

Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly
225 230 235 240

Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly
245 250

<210> 185
<211> 77
<212> PRT
<213> Homo sapiens

<400> 185
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn
65 70 75

<210> 186
<211> 361
<212> PRT
<213> Homo sapiens

<400> 186

His Thr Val Glu Leu Asn Asn Met Phe Gly Gln Ile Gln Ser Pro Gly
1 5 10 15

Tyr Pro Asp Ser Tyr Pro Ser Asp Ser Glu Val Thr Trp Asn Ile Thr
20 25 30

Val Pro Asp Gly Phe Arg Ile Lys Leu Tyr Phe Met His Phe Asn Leu
35 40 45

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

Asp Gln Val Leu Ala Thr Phe Cys Gly Arg Glu Thr Thr Asp Thr Glu
65 70 75 80

Gln Thr Pro Gly Gln Glu Val Val Leu Ser Pro Gly Ser Phe Met Ser
85 90 95

Ile Thr Phe Arg Ser Asp Phe Ser Asn Glu Glu Arg Phe Thr Gly Phe
100 105 110

Asp Ala His Tyr Met Ala Val Asp Val Asp Glu Cys Lys Glu Arg Glu
115 120 125

Asp Glu Glu Leu Ser Cys Asp His Tyr Cys His Asn Tyr Ile Gly Gly
130 135 140

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

Thr Cys Arg Val Glu Cys Ser Asp Asn Leu Phe Thr Gln Arg Thr Gly
165 170 175

Val Ile Thr Ser Pro Asp Phe Pro Asn Pro Tyr Pro Lys Ser Ser Glu
180 185 190

Cys Leu Tyr Thr Ile Glu Leu Glu Glu Gly Phe Met Val Asn Leu Gln
195 200 205

Phe Glu Asp Ile Phe Asp Ile Glu Asp His Pro Glu Val Pro Cys Pro
210 215 220

Tyr Asp Tyr Ile Lys Ile Lys Val Gly Pro Lys Val Leu Gly Pro Phe
225 230 235 240

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

Leu Ile Leu Phe His Ser Asp Asn Ser Gly Glu Asn Arg Gly Trp Arg
260 265 270

Leu Ser Tyr Arg Ala Ala Gly Asn Glu Cys Pro Glu Leu Gln Pro Pro
275 280 285

Val His Gly Lys Ile Glu Pro Ser Gln Ala Lys Tyr Phe Phe Lys Asp
290 295 300

Gln Val Leu Val Ser Cys Asp Thr Gly Tyr Lys Val Leu Lys Asp Asn
305 310 315 320

Val Glu Met Asp Thr Phe Gln Ile Glu Cys Leu Lys Asp Gly Thr Trp
325 330 335

Ser Asn Lys Ile Pro Thr Cys Lys Lys Asn Glu Ile Asp Leu Glu Ser
340 345 350

Glu Leu Lys Ser Glu Gln Val Thr Glu
355 360

<210> 187
<211> 251
<212> PRT
<213> Homo sapiens

<400> 187
Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly Lys Pro
1 5 10 15

Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys Lys Lys
20 25 30

Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys Asp Arg
35 40 45

Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg Glu Thr
50 55 60

Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro Ala Asn
65 70 75 80

Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn Glu Gly
85 90 95

Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys Gly Ser
100 105 110

Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val Leu Cys
115 120 125

Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser Glu Val
130 135 140

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

Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile Tyr Cys
165 170 175

Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys Val Val
180 185 190

Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser Gly Phe
195 200 205

Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys Asp Lys
210 215 220

Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser Asn Ser
225 230 235 240

Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys
245 250

<210> 188

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 188

Gly His Ser Phe Thr Asn Tyr Leu
1 5

<210> 189

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 189

Ile Asn Pro Gly Ser Gly Gly Thr
1 5

<210> 190

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 190

Ala Ser Tyr Tyr Ser Asn Ser Tyr Ala Met Asp Tyr
1 5 10

<210> 191

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 191

Glu Asn Ile Tyr Ser Tyr
1 5

<210> 192

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 192

Lys Ala Lys
1

<210> 193

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 193

Gln His His Tyr Gly Ile Pro Tyr Thr
1 5

<210> 194

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 194

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly His Ser Phe Thr Asn Tyr
20 25 30

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

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Val Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Ser Tyr Tyr Ser Asn Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
115

<210> 195

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 195

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

Glu Thr Val Thr Ile Ala Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
20 25 30

Leu Ala Trp Tyr Leu Gln Lys Glu Gly Lys Ser Pro Gln Leu Leu Val
35 40 45

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

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

Glu Asp Phe Gly Thr Phe Tyr Cys Gln His His Tyr Gly Ile Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 196
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 196
Gly Tyr Ala Phe Ala His Tyr Leu
1 5

<210> 197
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 197
Ile Asn Pro Gly Thr Asp Gly Thr
1 5

<210> 198
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 198
Ala Arg Glu Glu Leu Gly Phe Ala Tyr
1 5

<210> 199
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 199
Gln Asp Ile Ser Asn His
1 5

<210> 200
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<400> 200

Tyr Ile Ser

1

<210> 201

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 201

Gln Gln Gly Asp Thr Leu Pro Tyr Thr

1 5

<210> 202

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 202

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ala His Tyr

20 25 30

Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Val Ile Asn Pro Gly Thr Asp Gly Thr Asn Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Glu Glu Leu Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ala

115

<210> 203

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 203

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

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

Leu Asn Trp Tyr Gln Gln Arg Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Ile Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Thr Leu Glu Ile Arg
100 105

<210> 204

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 204

Gly Tyr Thr Phe Thr Ser Tyr
1 5

<210> 205

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 205

Ser Asp Pro Ser Asp Thr Tyr Thr
1 5

<210> 206

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 206
Ala Arg Pro Gly Arg Val Ala Tyr Tyr Phe Asp Tyr
1 5 10

<210> 207
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 207
Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 208
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 208
Lys Val Ser
1

<210> 209
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 209
Phe Gln Gly Ser His Val Pro Pro Thr
1 5

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

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 210

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Thr
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Val Ser Asp Pro Ser Asp Thr Tyr Thr Lys Asn Asn Gln Lys Phe
50 55 60

Thr Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Pro Gly Arg Val Ala Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 211

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 211

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

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

<210> 212

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 212

Gly Tyr Ala Phe Thr Asn Tyr Leu
1 5

<210> 213

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 213

Ile Asn Pro Gly Ser Gly Gly Thr
1 5

<210> 214

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 214

Ala Thr Tyr Tyr Ser Asn Ser Phe Ala Met Asp Tyr
1 5 10

<210> 215

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 215

Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr
1 5 10

<210> 216

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 216

Phe Ala Ser

1

<210> 217

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 217

Gln Gln Tyr Tyr Ser Ile Pro Phe Thr

1 5

<210> 218

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 218

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr

20 25 30

Leu Ile Glu Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr

65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Thr Tyr Tyr Ser Asn Ser Phe Ala Met Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Ser Val Thr Val Ser Ser

115

<210> 219
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 219
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Met Ser Val Gly
1 5 10 15

Gln Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Cys Pro Lys Val Leu Val Tyr Phe Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

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

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
85 90 95

Tyr Tyr Ser Ile Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 220
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 220
Gly Tyr Ala Phe Ala His Tyr Leu
1 5

<210> 221
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 221
Ile Asn Pro Gly Thr Asp Gly Thr
1 5

<210> 222
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 222
Ala Arg Glu Glu Leu Gly Phe Ala Tyr
1 5

<210> 223
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 223
Gln Asp Ile Ser Asn His
1 5

<210> 224
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 224
Tyr Ile Ser
1

<210> 225
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 225
Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> 226
<211> 116
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 226

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ala His Tyr
20 25 30

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

Gly Val Ile Asn Pro Gly Thr Asp Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Glu Leu Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ala
115

<210> 227

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 227

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

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

Leu Asn Trp Tyr Gln Gln Arg Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Ile Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Thr Leu Glu Ile Arg
100 105

<210> 228

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 228

Gly Tyr Ser Phe Thr Asp Tyr Asn
1 5

<210> 229

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 229

Ile Asn Pro Asn Tyr Gly Thr Thr
1 5

<210> 230

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 230

Ala Arg Asn Asp Tyr
1 5

<210> 231

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 231

Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr

1 5 10

<210> 232
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 232
Lys Val Ser
1

<210> 233
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 233
Phe Gln Gly Ser His Val Pro Phe Thr
1 5

<210> 234
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 234
Glu Phe Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

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

Asn Met Asn Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Asn Tyr Gly Thr Thr Phe Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

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

<210> 235

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 235

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Phe Gln Gly
85 90 95

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

<210> 236

<211> 226

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 236

Val Pro Arg Asp Ser Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
1 5 10 15

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
20 25 30

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
35 40 45

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val

50

55

60

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

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
100 105 110

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

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
130 135 140

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
145 150 155 160

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

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
180 185 190

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

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
210 215 220

Pro Gly
225

<210> 237

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 237

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Gly
225

<210> 238

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 238

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125
 Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140
 Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
 145 150 155 160
 Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190
 Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205
 Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys
 210 215 220
 Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro
 225 230 235 240
 Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
 245 250 255
 Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser
 260 265 270

Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
290 295 300

Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn
305 310 315 320

Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

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

Gln Met Ala Lys Asp Lys Val Ser Leu Ser Cys Ala Ile Thr Asp Phe
355 360 365

Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala
370 375 380

Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr
385 390 395 400

Phe Val Val Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly
405 410 415

Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
420 425 430

Thr Glu Lys Ser Leu Ser His Ser Pro Gly
435 440

<210> 239

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 239

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser His Lys Phe
130 135 140

Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
145 150 155 160

Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
210 215 220

Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys

<210> 240

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 240

Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
 115 120 125
 Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu
 130 135 140
 Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp
 145 150 155 160
 Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser
 180 185 190
 Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205
 Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
 210 215 220
 <210> 241
 <211> 15
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 peptide
 <400> 241
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10 15

<210> 242
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 242
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 243
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 243
Glu Val Gln Leu Gln Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
 165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
 180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
 195 200 205

Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val
 210 215 220

Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val
 225 230 235 240

Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile
 245 250 255

Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val
 260 265 270

Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser
 275 280 285

Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu
 290 295 300

Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala
 305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro
 325 330 335

Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys
 340 345 350

Val Ser Leu Trp Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr
 355 360 365

Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr
 370 375 380

Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu
 385 390 395 400

Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser
 405 410 415

Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser
420 425 430

His Ser Pro Gly
435

<210> 244

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 244

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65 70 75 80

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

Ser Arg Gly Gly Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
100 105 110

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

Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr
165 170 175

Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr
180 185 190

Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys
195 200 205

Lys Ile Val Pro Arg Asp Cys Gly
210 215

<210> 245

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 245

Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
1 5 10 15

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
20 25 30

Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
35 40 45

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
50 55 60

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

Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
85 90 95

Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
100 105 110

Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
115 120 125

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Trp Cys Met Ile Thr
130 135 140

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
145 150 155 160

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
165 170 175

Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu

180

185

190

Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
 195 200 205

His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 210 215 220

<210> 246

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 246

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Lys Gln Ala His Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 100 105 110

<210> 247

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 247

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

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

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 248

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 248

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 249

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 249

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 250

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 250

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr His Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 251

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 251

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Ser Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 252

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 252

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 253

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 253

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr His Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 254

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 254

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Ser Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 255

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 255

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
100 105 110

<210> 256
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 256
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 257
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 257
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 258
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 258
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 259
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 259
Ile Asn Pro Tyr His Gly Gly Thr
1 5

<210> 260

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 260
Ile Asn Pro Tyr Ser Gly Gly Thr
1 5

<210> 261
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 261
Gln Val Gln Leu Gln Gln Pro Gly Thr Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 262
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 262

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 263

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 263

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Arg Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 264
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 264
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Arg Val Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 265
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 265
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Asn Ile Asn Pro Ser Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Arg Gly Ile Arg Leu Arg His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 266

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 266

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

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

Glu Asp Phe Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 267
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 267
Asp Ile Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp 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 Phe Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 268
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 268
Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 269
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 269
Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 270
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 270
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

20

25

30

Tyr Met Asn Trp Val Lys Gln Ala His Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Tyr Asp Tyr Ala Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser
 115

<210> 271

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 271

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Tyr Met Asn Trp Val Lys Gln Ala His Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Tyr Asp Tyr Ala Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser
115

<210> 272
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 272
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Tyr Asp Tyr Ala Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 273
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 273
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Tyr Asp Tyr Ala Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser
 115

<210> 274

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 274

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Tyr Asp Tyr Ala Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr
 100 105 110

Thr Val Thr Val Ser Ser
 115

<210> 275
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 275
Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 276
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 276
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65	70	75	80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly			
85	90	95	

Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 277
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 277
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 278
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 278
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 279

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 279

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe

130

135

140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 280

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 280

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
 100 105 110

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
180 185 190

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
195 200 205

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
210 215 220

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
245 250 255

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
260 265 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
275 280 285

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
290 295 300

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
305 310 315 320

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
325 330 335

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
340 345 350

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
355 360 365

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg

385 390 395 400

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
420 425 430

Ser Leu Ser Leu Gly
435

<210> 281

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 281

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
180 185 190

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
195 200 205

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
210 215 220

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
245 250 255

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
260 265 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
275 280 285

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
290 295 300

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
305 310 315 320

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
325 330 335

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
340 345 350

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
355 360 365

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
385 390 395 400

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

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

420

425

430

Ser Leu Ser Leu Gly
435

<210> 282

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 282

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Ser Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
180 185 190

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
195 200 205

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
210 215 220

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
245 250 255

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
260 265 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
275 280 285

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
290 295 300

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
305 310 315 320

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
325 330 335

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
340 345 350

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
355 360 365

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
385 390 395 400

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

Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu
420 425 430

Ser Leu Ser Leu Gly
435

<210> 283

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 283

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Gly
225

<210> 284

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 284

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Ser Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
180 185 190

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
195 200 205

Val Glu Ser Lys Tyr Gly
210

<210> 285

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 285

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Ser Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
180 185 190

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
195 200 205

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
210 215 220

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
245 250 255

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
260 265 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
275 280 285

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
290 295 300

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
305 310 315 320

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
325 330 335

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
340 345 350

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
355 360 365

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
385 390 395 400

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

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
420 425 430

Ser Leu Ser Leu Gly
435

<210> 286
<211> 437
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 286

Gln His Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe His Asn Tyr
20 25 30

Tyr Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Tyr Ser Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Val Asp His Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
180 185 190

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
195 200 205

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
210 215 220

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

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
245 250 255

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
260 265 270

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
275 280 285

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
290 295 300

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
305 310 315 320

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
325 330 335

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
340 345 350

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
355 360 365

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

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
385 390 395 400

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

Ser Val Leu His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu
420 425 430

Ser Leu Ser Leu Gly
435

<210> 287

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 287

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly

1	5	10	15
Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser	20	25	30
Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser	35	40	45
Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Val Asp Ser Gly Val Pro	50	55	60
Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	65	70	75
Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly	85	90	95
Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	100	105	110
Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu	115	120	125
Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe	130	135	140
Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg	145	150	155
Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser	165	170	175
Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu	180	185	190
Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser	195	200	205
Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys	210	215	

<210> 288

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 288

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

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

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

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr
180 185 190

Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
195 200 205

Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu
210 215 220

Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr
225 230 235 240

Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys
245 250 255

Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val

260

265

270

His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 275 280 285

Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly
 290 295 300

Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile
 305 310 315 320

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val
 325 330 335

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser
 340 345 350

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu
 355 360 365

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro
 370 375 380

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val
 385 390 395 400

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu
 405 410 415

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser
 420 425 430

Pro Gly

<210> 289

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 289

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln
85 90 95

Tyr Leu Ser Ser Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 290

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 290

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Thr
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

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

Gly Val Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Gly Gly Gly Ser Ser Tyr Asn Arg Tyr Phe Asp Val Trp Gly
 100 105 110

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

Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
 130 135 140

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

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

Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
 180 185 190

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
 195 200 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
 210 215 220

Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
 225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
 245 250 255

Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
 260 265 270

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
 275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
290 295 300

Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
305 310 315 320

Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
355 360 365

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
370 375 380

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
385 390 395 400

Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
405 410 415

Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
420 425 430

His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
435 440

<210> 291

<211> 305

<212> PRT

<213> Mus musculus

<400> 291

Glu Asp Cys Lys Gly Pro Pro Pro Arg Glu Asn Ser Glu Ile Leu Ser
1 5 10 15

Gly Ser Trp Ser Glu Gln Leu Tyr Pro Glu Gly Thr Gln Ala Thr Tyr
20 25 30

Lys Cys Arg Pro Gly Tyr Arg Thr Leu Gly Thr Ile Val Lys Val Cys
35 40 45

Lys Asn Gly Lys Trp Val Ala Ser Asn Pro Ser Arg Ile Cys Arg Lys
50 55 60

Lys Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Ser Phe Arg Leu
65 70 75 80

Ala Val Gly Ser Gln Phe Glu Phe Gly Ala Lys Val Val Tyr Thr Cys
 85 90 95
 Asp Asp Gly Tyr Gln Leu Leu Gly Glu Ile Asp Tyr Arg Glu Cys Gly
 100 105 110
 Ala Asp Gly Trp Ile Asn Asp Ile Pro Leu Cys Glu Val Val Lys Cys
 115 120 125
 Leu Pro Val Thr Glu Leu Glu Asn Gly Arg Ile Val Ser Gly Ala Ala
 130 135 140
 Glu Thr Asp Gln Glu Tyr Tyr Phe Gly Gln Val Val Arg Phe Glu Cys
 145 150 155 160
 Asn Ser Gly Phe Lys Ile Glu Gly His Lys Glu Ile His Cys Ser Glu
 165 170 175
 Asn Gly Leu Trp Ser Asn Glu Lys Pro Arg Cys Val Glu Ile Leu Cys
 180 185 190
 Thr Pro Pro Arg Val Glu Asn Gly Asp Gly Ile Asn Val Lys Pro Val
 195 200 205
 Tyr Lys Glu Asn Glu Arg Tyr His Tyr Lys Cys Lys His Gly Tyr Val
 210 215 220
 Pro Lys Glu Arg Gly Asp Ala Val Cys Thr Gly Ser Gly Trp Ser Ser
 225 230 235 240
 Gln Pro Phe Cys Glu Glu Lys Arg Cys Ser Pro Pro Tyr Ile Leu Asn
 245 250 255
 Gly Ile Tyr Thr Pro His Arg Ile Ile His Arg Ser Asp Asp Glu Ile
 260 265 270
 Arg Tyr Glu Cys Asn Tyr Gly Phe Tyr Pro Val Thr Gly Ser Thr Val
 275 280 285
 Ser Lys Cys Thr Pro Thr Gly Trp Ile Pro Val Pro Arg Cys Thr Leu
 290 295 300
 Lys
 305

<210> 292
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(16)

<223> This sequence may encompass 0-8 'Gly Ser' repeating units

<400> 292

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

<210> 293

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(16)

<223> This sequence may encompass 1-4 'Gly Gly Gly Ser' repeating units

<400> 293

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

<210> 294

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MISC_FEATURE

<222> (1)..(16)

<223> This sequence may encompass 1-4 'Gly Ser Ser Gly' repeating units

<400> 294

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

<210> 295

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 295
Gly Gly Gly Gly Ser
1 5

<210> 296
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 6xHis tag

<400> 296
His His His His His His
1 5

<210> 297
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 297
Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 298
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 298
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
1 5 10

<210> 299
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 299
Asn Leu Asp Val Ser Leu Gln Leu Pro Ser
1 5 10

<210> 300

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

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 300
Val Pro Arg Asp Cys Gly
1 5

<210> 301
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 301
Gly Ser Gly Ser Gly Ser Gly Arg Leu Gly Arg Glu Gly Val Gln
1 5 10 15

<210> 302
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 302
Gly Arg Glu Gly Val Gln Lys Glu Asp Ile Pro Pro Ala Asp Leu
1 5 10 15

<210> 303
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 303
Ile Pro Pro Ala Asp Leu Ser Asp Gln Val Pro Asp Thr Glu Ser
1 5 10 15

<210> 304
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 304

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

<210> 305

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 305

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

<210> 306

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 306

Gln Met Thr Glu Asp Ala Val Asp Ala Glu Arg Leu Lys His Leu
1 5 10 15

<210> 307

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 307

Glu Arg Leu Lys His Leu Ile Val Thr Pro Ser Gly Cys Gly Glu
1 5 10 15

<210> 308

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 308

Pro Ser Gly Cys Gly Glu Gln Asn Met Ile Gly Met Thr Pro Thr
1 5 10 15

<210> 309

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 309

Ile	Gly	Met	Thr	Pro	Thr	Val	Ile	Ala	Val	His	Tyr	Leu	Asp	Glu
1				5					10					15

<210> 310

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 310

Val	His	Tyr	Leu	Asp	Glu	Thr	Glu	Gln	Trp	Glu	Lys	Phe	Gly	Leu
1				5					10					15

<210> 311

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 311

Trp	Glu	Lys	Phe	Gly	Leu	Glu	Lys	Arg	Gln	Gly	Ala	Leu	Glu	Leu
1				5					10					15

<210> 312

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 312

Gln	Gly	Ala	Leu	Glu	Leu	Ile	Lys	Lys	Gly	Tyr	Thr	Gln	Gln	Leu
1				5					10					15

<210> 313

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 313

Gly	Tyr	Thr	Gln	Gln	Leu	Ala	Phe	Arg	Gln	Pro	Ser	Ser	Ala	Phe
1					5				10					15

<210> 314
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 314
Gln Pro Ser Ser Ala Phe Ala Ala Phe Val Lys Arg Ala Pro Ser
1 5 10 15

<210> 315
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 315
Val Lys Arg Ala Pro Ser Thr Trp Leu Thr Ala Tyr Val Val Lys
1 5 10 15

<210> 316
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 316
Thr Ala Tyr Val Val Lys Val Phe Ser Leu Ala Val Asn Leu Ile
1 5 10 15

<210> 317
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 317
Leu Ala Val Asn Leu Ile Ala Ile Asp Ser Gln Val Leu Cys Gly
1 5 10 15

<210> 318
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 318

Ser	Gln	Val	Leu	Cys	Gly	Ala	Val	Lys	Trp	Leu	Ile	Leu	Glu	Lys
1				5					10					15

<210> 319

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 319

Trp	Leu	Ile	Leu	Glu	Lys	Gln	Lys	Pro	Asp	Gly	Val	Phe	Gln	Glu
1				5					10					15

<210> 320

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 320

Asp	Gly	Val	Phe	Gln	Glu	Asp	Ala	Pro	Val	Ile	His	Gln	Glu	Met
1				5					10					15

<210> 321

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 321

Val	Ile	His	Gln	Glu	Met	Ile	Gly	Gly	Leu	Arg	Asn	Asn	Asn	Glu
1				5					10					15

<210> 322

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 322

Leu	Arg	Asn	Asn	Asn	Glu	Lys	Asp	Met	Ala	Leu	Thr	Ala	Phe	Val
1					5				10					15

<210> 323

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 323

Ala	Leu	Thr	Ala	Phe	Val	Leu	Ile	Ser	Leu	Gln	Glu	Ala	Lys	Asp
1				5					10					15

<210> 324

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 324

Leu	Gln	Glu	Ala	Lys	Asp	Ile	Cys	Glu	Glu	Gln	Val	Asn	Ser	Leu
1				5					10					15

<210> 325

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 325

Glu	Gln	Val	Asn	Ser	Leu	Pro	Gly	Ser	Ile	Thr	Lys	Ala	Gly	Asp
1				5					10					15

<210> 326

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 326

Ile	Thr	Lys	Ala	Gly	Asp	Phe	Leu	Glu	Ala	Asn	Tyr	Met	Asn	Leu
1				5					10					15

<210> 327

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 327

Ala	Asn	Tyr	Met	Asn	Leu	Gln	Arg	Ser	Tyr	Thr	Val	Ala	Ile	Ala
1				5					10					15

<210> 328
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 328
Tyr Thr Val Ala Ile Ala Gly Tyr Ala Leu Ala Gln Met Gly Arg
1 5 10 15

<210> 329
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 329
Leu Ala Gln Met Gly Arg Leu Lys Gly Pro Leu Leu Asn Lys Phe
1 5 10 15

<210> 330
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 330
Pro Leu Leu Asn Lys Phe Leu Thr Thr Ala Lys Asp Lys Asn Arg
1 5 10 15

<210> 331
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 331
Ala Lys Asp Lys Asn Arg Trp Glu Asp Pro Gly Lys Gln Leu Tyr
1 5 10 15

<210> 332
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 332
Pro Gly Lys Gln Leu Tyr Asn Val Glu Ala Thr Ser Tyr Ala Leu
1 5 10 15

<210> 333
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 333
Ala Thr Ser Tyr Ala Leu Leu Ala Leu Leu Gln Leu Lys Asp Phe
1 5 10 15

<210> 334
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 334
Leu Gln Leu Lys Asp Phe Asp Phe Val Pro Pro Val Val Arg Trp
1 5 10 15

<210> 335
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 335
Pro Pro Val Val Arg Trp Leu Asn Glu Gln Arg Tyr Tyr Gly Gly
1 5 10 15

<210> 336
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 336
Gln Arg Tyr Tyr Gly Gly Gly Tyr Gly Ser Thr Gln Ala Thr Phe
1 5 10 15

<210> 337
<211> 15
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 337

Ser	Thr	Gln	Ala	Thr	Phe	Met	Val	Phe	Gln	Ala	Leu	Ala	Gln	Tyr
1				5					10					15

<210> 338

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 338

Gln	Ala	Leu	Ala	Gln	Tyr	Gln	Lys	Asp	Ala	Pro	Asp	His	Gln	Glu
1				5					10					15

<210> 339

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 339

Ala	Pro	Asp	His	Gln	Glu	Leu	Asn	Leu	Asp	Val	Ser	Leu	Gln	Leu
1				5					10					15

<210> 340

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 340

Asp	Val	Ser	Leu	Gln	Leu	Pro	Ser	Arg	Ser	Ser	Lys	Ile	Thr	His
1				5					10					15

<210> 341

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 341

Ile	Val	Thr	Pro	Ser	Gly	Ser	Gly	Glu	Gln	Asn	Met	Ile	Gly	Met
1				5					10					15

<210> 342
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 342
Glu Val Gln Leu Gln Ser Gly Pro Val Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Val Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Pro Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala
100 105 110

Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Cys Gly Asp
115 120 125

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

Pro Glu Ser Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Ser
145 150 155 160

Val His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Met Ser
165 170 175

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val Thr
180 185 190

Cys Ser Val Ala His Pro Ala Ser Ser Thr Thr Val Asp Lys Lys Leu
195 200 205

Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Cys Pro Pro Cys Lys

210

215

220

Glu Cys His Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly Pro Ser Val
 225 230 235 240

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

Pro Lys Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
 260 265 270

Val Arg Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
 275 280 285

Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Ile Arg Val Val Ser
 290 295 300

Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
 305 310 315 320

Cys Lys Val Asn Asn Lys Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile
 325 330 335

Ser Lys Ile Lys Gly Leu Val Arg Ala Pro Gln Val Tyr Ile Leu Pro
 340 345 350

Pro Pro Ala Glu Gln Leu Ser Arg Lys Asp Val Ser Leu Thr Cys Leu
 355 360 365

Val Val Gly Phe Asn Pro Gly Asp Ile Ser Val Glu Trp Thr Ser Asn
 370 375 380

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

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

Trp Glu Lys Thr Asp Ser Phe Ser Cys Asn Val Arg His Glu Gly Leu
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Lys Asn Tyr Tyr Leu Lys Lys Thr Ile Ser Arg Ser Pro Gly Lys
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Gly Tyr Thr Phe Thr Ser Tyr Trp

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