(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

CORRECTED VERSION

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
11 May 2018 (11.05.2018)

WIPO | PCT

(10) International Publication Number
WO 2018/085555 A8

(51) International Patent Classification:
C07K 16/28 (2006.01) *A61K 39/395* (2006.01)
C07K 19/00 (2006.01) *A61P 35/00* (2006.01)

(21) International Application Number:
PCT/US2017/059740

(22) International Filing Date:
02 November 2017 (02.11.2017)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/417,212 03 November 2016 (03.11.2016) US

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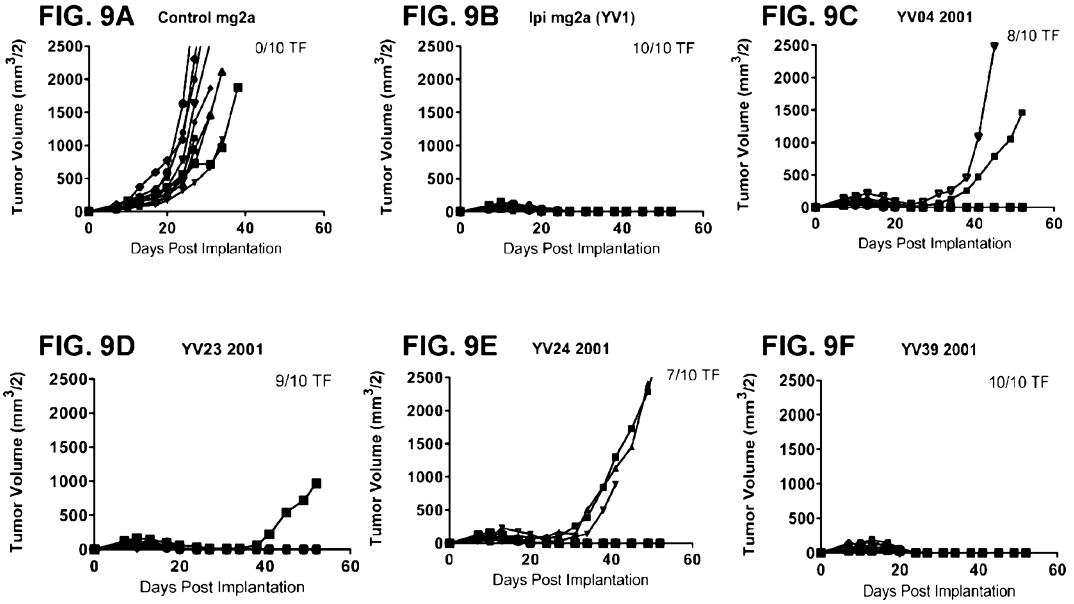
(54) Title: ACTIVATABLE ANTI-CTLA-4 ANTIBODIES AND USES THEREOF



(57) Abstract: Provided herein are activatable anti-human CTLA-4 antibodies comprising a heavy chain comprising a VH domain and a light chain comprising a masking moiety (MM), a cleavable moiety (CM), and a VL domain. Such activatable anti-human CTLA-4 antibodies have CTLA-4 binding activity in the tumor microenvironment, where the masking moiety is removed by proteolytic cleavage of the cleavable moiety by tumor-specific proteases, but exhibit greatly reduced binding to CTLA-4 outside the tumor. In this way, the activatable anti-human CTLA-4 antibodies of the present invention retain anti-tumor activity while reducing the side effects associated with anti-CTLA-4 activity outside the tumor.

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

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *of inventorship (Rule 4.17(iv))*

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

— *with sequence listing part of description (Rule 5.2(a))*

(48) Date of publication of this corrected version:
31 May 2018 (31.05.2018)

(15) Information about Correction:
see Notice of 31 May 2018 (31.05.2018)

ACTIVATABLE ANTI-CTLA-4 ANTIBODIES AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the priority benefit of U.S. Provisional Application No. 62/417,212, filed November 3, 2016, which is hereby incorporated by reference in its entirety.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY VIA EFS-WEB

[0002] The content of the electronically submitted sequence listing (Name: 3338_059PC02_SeqListing.txt; Size: 527,968 bytes; and Date of Creation: October 27, 2017) is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

[0003] The immune system is capable of controlling tumor development and mediating tumor regression. This requires the generation and activation of tumor antigen–specific T cells. Multiple T-cell co-stimulatory receptors and T-cell negative regulators, or co-inhibitory receptors, act in concert to control T-cell activation, proliferation, and gain or loss of effector function. Among the earliest and best-characterized T-cell co-stimulatory and co-inhibitory molecules are CD28 and CTLA-4. Rudd *et al.* (2009) *Immunol. Rev.* 229: 12. CD28 provides co-stimulatory signals to T-cell receptor engagement by binding to B7-1 and B7-2 ligands on antigen-presenting cells, while CTLA-4 provides a negative signal down-regulating T-cell proliferation and function. CTLA-4, which also binds the B7-1 (CD80) and B7-2 (CD86) ligands but with higher affinity than CD28, acts as a negative regulator of T-cell function through both cell autonomous (or intrinsic) and cell non-autonomous (or extrinsic) pathways. Intrinsic control of CD8 and CD4 T effector (T_{eff}) function is mediated by the inducible surface expression of CTLA-4 as a result of T-cell activation, and inhibition of T-cell proliferation and cytokine proliferation by multivalent engagement of B7 ligands on opposing cells. Peggs *et al.* (2008) *Immunol. Rev.* 224:141.

[0004] Anti-CTLA-4 antibodies, when cross-linked, suppress T cell function *in vitro*. *Krummel & Allison (1995) J. Exp. Med.* 182:459; Walunas *et al.* (1994) *Immunity* 1:405. Regulatory T cells (T_{regs}), which express CTLA-4 constitutively, control effector T cell (T_{eff}) function in a non-cell autonomous fashion. T_{regs} that are deficient for CTLA-4 have impaired suppressive ability (Wing *et al.* (2008) *Science* 322:271) and antibodies that block CTLA-4 interaction with B7 can inhibit T_{reg} function (Read *et al.* (2000) *J. Exp. Med.* 192:295; Quezada *et al.* (2006) *J. Clin. Invest.* 116:1935). More recently, T_{effs} have also been shown to control T cell function through extrinsic pathways (Corse & Allison (2012) *J. Immunol.* 189:1123; Wang *et al.* (2012) *J. Immunol.* 189:1118). Extrinsic control of T cell function by T_{regs} and T_{effs} occurs through the ability of CTLA-4-positive cells to remove B7 ligands on antigen-presenting cells, thereby limiting their co-stimulatory potential. Qureshi *et al.* (2011) *Science* 332: 600; Onishi *et al.* (2008) *Proc. Nat'l Acad. Sci. (USA)* 105:10113. Antibody blockade of CTLA-4/B7 interactions is thought to promote T_{eff} activation by interfering with negative signals transmitted by CTLA-4 engagement; this intrinsic control of T-cell activation and proliferation can promote both T_{eff} and T_{reg} proliferation (*Krummel & Allison (1995) J. Exp. Med.* 182:459; Quezada *et al.* (2006) *J. Clin. Invest.* 116:1935). In early studies with animal models, antibody blockade of CTLA-4 was shown to exacerbate autoimmunity. Perrin *et al.* (1996) *J. Immunol.* 157:1333; Hurwitz *et al.* (1997) *J. Neuroimmunol.* 73:57. By extension to tumor immunity, the ability of anti-CTLA-4 to cause regression of established tumors provided a dramatic example of the therapeutic potential of CTLA-4 blockade. Leach *et al.* (1996) *Science* 271:1734.

[0005] Human antibodies to human CTLA-4, ipilimumab and tremelimumab, were selected to inhibit CTLA-4-B7 interactions (Keler *et al.* (2003) *J. Immunol.* 171:6251; Ribas *et al.* (2007) *Oncologist* 12:873) and have been tested in a variety of clinical trials for multiple malignancies. Hoos *et al.* (2010) *Semin. Oncol.* 37:533; Ascierto *et al.* (2011) *J. Transl. Med.* 9:196. Tumor regressions and disease stabilization were frequently observed, and treatment with these antibodies has been accompanied by adverse events with inflammatory infiltrates capable of affecting a variety of organ systems. In 2011, ipilimumab, which has an IgG1 constant region, was approved in the US and EU for the treatment of unresectable or metastatic melanoma based on an improvement in overall

survival in a phase III trial of previously treated patients with advanced melanoma. Hodi *et al.* (2010) *N. Engl. J. Med.* 363:711.

[0006] Treatment with ipilimumab has, however, been hampered by dose limiting toxicities, such as colitis. Di Giacomo *et al.* (2010) *Seminars in Oncology* 37:499. Accordingly, the need exists for improved anti-CTLA-4 antibodies, such as modified forms of ipilimumab, with reduced toxicity but with comparable anti-tumor efficacy. Such improved anti-CTLA-4 antibodies may be more effective anti-tumor agents than current antibodies.

SUMMARY OF THE INVENTION

[0007] Provided herein are activatable anti-human CTLA-4 antibodies comprising a heavy chain comprising a VH domain and a light chain comprising a masking moiety (MM), a cleavable moiety (CM), and a VL domain. Such activatable anti-human CTLA-4 antibodies have CTLA-4 binding activity in the tumor microenvironment, where the masking moiety is removed by proteolytic cleavage of the cleavable moiety by tumor-specific proteases, but exhibit greatly reduced binding to CTLA-4 outside the tumor. In this way, the activatable anti-human CTLA-4 antibodies of the present invention retain anti-tumor activity while reducing the side effects associated with anti-CTLA-4 activity outside the tumor.

[0008] Provided herein are improved anti-CTLA-4 antibodies, such as an improved ipilimumab, in particular an activatable antibody that when activated binds Cytotoxic T-Lymphocyte Antigen 4 (CTLA-4). In some embodiments, the activatable anti-human CTLA-4 antibody comprises:

(i) a heavy chain comprising a heavy chain variable domain (VH) comprising complementarity determining regions (CDRs) CDRH1: SYTMH (SEQ ID NO: 557); CDRH2: FISYDGNNKYYADSVKG (SEQ ID NO: 558); and CDRH3: TGWLGPFDY (SEQ ID NO: 559); and

(ii) a light chain comprising:

(a) a light chain variable domain (VL) comprising CDRL1: RASQSVGSSYLA (SEQ ID NO: 560); CDRL2: GAFSRAT (SEQ ID NO: 561); and CDRL3: QQYGSSPWT (SEQ ID NO: 562);

(b) a cleavable moiety (CM); and

(c) a masking moiety (MM),

wherein the light chain has the structural arrangement from N-terminus to C-terminus as follows: MM-CM-VL.

[0009] In some embodiments, an activatable anti-human CTLA-4 antibody comprises:

(i) a heavy chain comprising a heavy chain variable domain (VH) comprising CDRH1: SYTMH (SEQ ID NO: 557); CDRH2: FISYDGNNKYYADSVKG (SEQ ID NO: 558); and CDRH3: TGWLGPFDY (SEQ ID NO: 559); and

(ii) a light chain comprising, from N-terminus to C-Terminus:

(a) a masking moiety (MM);

(b) a cleavable moiety (CM); and

(c) a light chain variable domain (VL) comprising CDRL1: RASQSVGSSYLA (SEQ ID NO: 560); CDRL2: GAFSRAT (SEQ ID NO: 561); and CDRL3: QQYGSSPWT (SEQ ID NO: 562).

[0010] In some embodiments, the activatable antibody comprises a heavy chain and a light chain such that the light chain has the structural arrangement, from N-terminus to C-terminus of the light chain, MM-CM-VL. As used herein, the N-terminal fragment that is joined to the VL domain is referred to as the prodomain and comprises MM and CM.

[0011] In some embodiments, the activatable antibody comprises a complete antibody, i.e., an antibody comprising two mature full-length heavy chains and two mature full-length light chains. In some embodiments, the activatable antibody comprises a Fab fragment, a $F(ab')_2$ fragment, an scFv, or a scAb. In some embodiments, the activatable antibody comprises a monoclonal antibody.

[0012] In some embodiments, the CM functions as a substrate for a protease. In some embodiments, the CM is selected from the group of CMs provided in Table 3. In some embodiments, the CM is selected from the group consisting of 2001 (SEQ ID NO: 297), 2003 (SEQ ID NO: 298), 2005 (SEQ ID NO: 299), 2006 (SEQ ID NO: 300), 2007 (SEQ ID NO: 301), 2008 (SEQ ID NO: 302), 2009 (SEQ ID NO: 303), 2011 (SEQ ID NO: 304), 2012 (SEQ ID NO: 305), 3001 (SEQ ID NO: 306), 3006 (SEQ ID NO: 307), 3007 (SEQ ID NO: 308), 3008 (SEQ ID NO: 309), 3009 (SEQ ID NO: 310), 3011 (SEQ ID NO: 311), and 3012 (SEQ ID NO: 312). In some embodiments, the CM is 2001 (SEQ ID NO: 297). In some embodiments, the CM is 2011 (SEQ ID NO: 304). In some embodiments, the CM is 2012 (SEQ ID NO: 305).

[0013] In some embodiments, the MM is selected from the group consisting of the MMs provided in Tables 4-6. In some embodiments, the MM is selected from the group consisting of YV01 (SEQ ID NO: 1), YV02 (SEQ ID NO: 2), YV03, (SEQ ID NO: 3), YV04 (SEQ ID NO: 4), YV09, (SEQ ID NO: 9), YV23 (SEQ ID NO: 23), YV24 (SEQ ID NO: 24), YV35 (SEQ ID NO: 35), YV39 (SEQ ID NO: 39), YV51 (SEQ ID NO: 51), YV61 (SEQ ID NO: 60), YV62 (SEQ IDNO: 61), YV63 (SEQ ID NO: 62), YV64 (SEQ ID NO: 63), YV65 (SEQ ID NO: 64), and YV66 (SEQ ID NO: 65); and the CM is selected from the group consisting of 2001, 2006, 2007, 2008, 2009, 2011, and 2012. In some embodiments, the MM is YV39 and the CM is 2011. In some embodiments, the MM is YV39 and the CM is 2012. In some embodiments, the MM is YV39 and the CM is 2001.

[0014] In some embodiments, the activatable antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 353 and a light chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 356 to 529.
In some embodiments, the activatable anti-CTLA-4 antibodies comprise a light chain having a prodomain and VL corresponding to the prodomain and VL of SEQ ID NOs: 356 to 529. In some embodiments, the activatable anti-CTLA-4 antibodies comprise a light chain having a prodomain and VL of SEQ ID NOs: 564, 565, or 563. In one embodiment, the activatable anti-CTLA-4 antibody comprises a light chain having a prodomain and VL of SEQ ID NO: 564.

[0015] In some embodiments, the activatable anti-CTLA-4 antibodies comprise a heavy chain variable domain amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 345. In some embodiments, the activatable anti-CTLA-4 antibodies comprise a light chain variable domain amino acid that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 564, 565, and 563.

[0016] In some embodiments, the activatable antibody comprises a combination of heavy chain sequence SEQ ID NO: 353 and light chain sequence SEQ ID NO: 449, 473, or 383. In some embodiments, the activatable antibody comprises a combination of heavy chain sequence SEQ ID NO: 349 and light chain sequence SEQ ID NO: 448, 472, or 382.

[0017] Provided herein is an activatable anti-CTLA-4 antibody that, when activated, specifically binds to human CTLA-4 and is referred to as an activated activatable anti-CTLA-4 antibody. In some embodiments, the activated activatable anti-CTLA-4 antibody binds to CTLA-4 with the same binding affinity as ipilimumab. Also provided herein is an activatable anti-CTLA-4 antibody that does not bind to CTLA-4 as effectively as ipilimumab since the activatable anti-CTLA-4 antibody comprises a heavy chain and a light chain comprising a prodomain comprising a MM and CM linked to the ipilimumab light chain such that the prodomain reduces the ability of the ipilimumab to bind to CTLA-4

[0018] In some embodiments, the activatable antibody binds to human CTLA-4 with an EC_{50} of 1 μg/mL or higher as measured by flow cytometry. In some embodiments, the activatable anti-CTLA-4 antibodies bind to CTLA-4 with an EC_{50} of 5 μg/mL or higher, 10 μg/mL or higher, 20 μg/mL or higher, or 40 μg/mL or higher.

[0019] In some embodiments, the MM is a polypeptide of no more than 40 amino acids in length. In some embodiments, the MM is a polypeptide that is no more than 50% identical to any natural binding partner of the antibody. In some embodiments, the MM does not comprise more than 25% amino acid sequence identity to CTLA-4. In some embodiments, the MM does not comprise more than 10% amino acid sequence identity to CTLA-4.

[0020] Activatable anti-CTLA-4 antibodies of the disclosure are activated when the cleavable moiety is cleaved by a protease. In some embodiments, the protease is produced by a tumor that is in proximity to T cells that express CTLA-4. In some embodiments, the protease is produced by a tumor that is co-localized with T cells that express CTLA-4. In some embodiments, the protease is selected from the group of proteases provided in Table 1 provided below. In some embodiments, the protease is selected from the group consisting of a matrix metalloprotease (MMP), a thrombin, a neutrophil elastase, a cysteine protease, a legumain, and a serine protease, such as a matriptase or a urokinase (uPA). In some embodiments, the protease is selected from the group consisting of MMP1, MMP2, MMP3, MMP8, MMP9, MMP11, MMP13, MMP14, MMP17, legumain, matriptase, and uPA, or a combination of one or more of such proteases. In some embodiments, the CM is cleaved by a matrix metalloprotease (MMP) and a serine

protease. In some embodiments, the CM is cleaved by a matrix metalloprotease (MMP), a serine protease and a legumain.

Table 1: Exemplary Proteases and/or Enzymes

ADAMS, ADAMTS, *e.g.*	Cysteine proteinases, *e.g.*,	Serine proteases, *e.g.*,
ADAM8	Cruzipain	activated protein C
ADAM9	Legumain	Cathepsin A
ADAM10	Otubain-2	Cathepsin G
ADAM12		Chymase
ADAM15	KLKs, *e.g.*,	coagulation factor proteases
ADAM17/TACE	KLK4	(*e.g.*, FVIIa, FIXa, FXa, FXIa, FXIIa)
ADAMDEC1	KLK5	
ADAMTS1	KLK6	Elastase
ADAMTS4	KLK7	Granzyme B
ADAMTS5	KLK8	Guanidinobenzoatase
	KLK10	HtrA1
Aspartate proteases, *e.g.*,	KLK11	Human Neutrophil Elastase
BACE	KLK13	Lactoferrin
Renin	KLK14	Marapsin
		NS3/4A
Aspartic cathepsins, *e.g.*,	Metallo proteinases, *e.g.*,	PACE4
Cathepsin D	Meprin	Plasmin
Cathepsin E	Neprilysin	PSA
	PSMA	tPA
Caspases, *e.g.*,	BMP-1	Thrombin
Caspase 1		Tryptase
Caspase 2	MMPs, *e.g.*,	uPA
Caspase 3	MMP1	
Caspase 4	MMP2	Type II Transmembrane
Caspase 5	MMP3	Serine Proteases (TTSPs), *e.g.*,
Caspase 6	MMP7	DESC1
Caspase 7	MMP8	DPP-4
Caspase 8	MMP9	FAP
Caspase 9	MMP10	Hepsin
Caspase 10	MMP11	Matriptase-2
Caspase 14	MMP12	MT-SP1/Matriptase
	MMP13	TMPRSS2
Cysteine cathepsins, *e.g.*,	MMP14	TMPRSS3
Cathepsin B	MMP15	TMPRSS4
Cathepsin C	MMP16	
Cathepsin K	MMP17	
Cathepsin L	MMP19	
Cathepsin S	MMP20	
Cathepsin V/L2	MMP23	

Cathepsin X/Z/P	MMP24
	MMP26
	MMP27

[0021] Provided herein are activatable anti-CTLA-4 antibodies that further comprise one or more linker peptides. In some embodiments, the linker peptide is between the MM and the CM. In some embodiments, the linker peptide is between the CM and the VL. In some embodiments, the activatable antibody comprises a first linker peptide (LP1) and a second linker peptide (LP2). In some embodiments, the activatable antibody comprises a heavy chain and a light chain such that the light chain has the structural arrangement, from N-terminus to C-terminus of the light chain, MM-LP1-CM-LP2-VL. In some embodiments, the LP1 and the LP2 are not identical to each other. In some embodiments, the LP1 and the LP2 are identical to each other. In some embodiments, the prodomain comprises MM-LP1-CM-LP2.

[0022] In some embodiments, the LP1 and/or the LP2 comprise a glycine-serine polymer. In some embodiments, the LP1 and/or the LP2 comprise an amino acid sequence selected from the group consisting of $(GS)_n$ (SEQ ID NO: 532), $(GGS)_n$ (SEQ ID NO: 533), $(GSGGS)_n$ (SEQ ID NO: 534), and $(GGGS)_n$ (SEQ ID NO: 535), where n is an integer of at least one. In some embodiments, the LP1 comprises the amino acid sequence GGGSSGGS (SEQ ID NO: 542). In some embodiments, the LP2 comprises the amino acid sequence GGGS (SEQ ID NO: 543).

[0023] Provided herein are activatable anti-CTLA-4 antibodies that also comprise a spacer. In some embodiments, the spacer is joined directly to the MM and has the structural arrangement from N-terminus to C-terminus as follows: spacer-MM-CM-VL. In some embodiments, the spacer comprises an amino acid sequence selected from the group consisting of QGQSGQG (SEQ ID NO: 544), GQSGQG (SEQ ID NO: 545), QGQSGS (SEQ ID NO: 546), QGQSGQ (SEQ ID NO: 547), QSGQG (SEQ ID NO: 548), GQSGS (SEQ ID NO: SEQ ID NO: 549), QGQSG (SEQ ID NO: 550), SGQG (SEQ ID NO: 551), QSGS (SEQ ID NO: 552), QGQS (SEQ ID NO: 553), GQG, SGS, QGQ, QG, GS, G, S, and Q. In some embodiments, the spacer and the MM comprise the amino acid sequence QGQSGSCRTQLYGYNLCPY (SEQ ID NO: 556).

[0024] Also provided herein are activatable antibodies that comprise a toxic agent, such as a dolastatin, an auristatin, an auristatin E, a monomethyl auristatin E (MMAE), a maytansinoid, a duocarmycin, a calicheamicin, a pyrrolobenzodiazepine, or a derivative

thereof. In some embodiments, the toxic agent is conjugated to the activatable antibody via a linker. In some embodiments, the linker is a cleavable linker. In some embodiments, the linker is a non-cleavable linker.

[0025] Provided herein are activatable anti-CTLA-4 antibodies that comprises a detectable moiety. In some embodiments, the detectable moiety is a diagnostic agent.

[0026] Provided herein are pharmaceutical compositions comprising an activatable anti-CTLA-4 antibody described herein. In some embodiments, the pharmaceutical composition comprises an additional therapeutic agent.

[0027] Also provided herein are isolated nucleic acid molecules encoding the heavy and/or light chains of the activatable anti-CTLA-4 antibodies described herein, vectors that comprise one or more of the isolated nucleic acid molecules, and methods of producing an activatable antibody by culturing a cell comprising the vector or vectors under conditions that lead to expression of the activatable antibody.

[0028] Provided herein are methods of manufacturing an activatable antibody, the methods comprising: (a) culturing a cell comprising a nucleic acid construct that encodes the activatable antibody described herein under conditions that lead to expression of the activatable antibody, and (b) recovering the activatable antibody.

[0029] Provided herein are methods of reducing CTLA-4 activity comprising administering an effective amount of the activatable antibody described herein or pharmaceutical compositions comprising an activatable anti-CTLA-4 antibody described herein to a subject in need thereof.

[0030] Provided herein are methods of blocking binding of a natural ligand to CTLA-4 comprising administering an effective amount of the activatable antibodies described herein or pharmaceutical compositions comprising an activatable anti-CTLA-4 antibody described herein to a subject in need thereof.

[0031] Provided herein are methods of treating, alleviating a symptom of, or delaying the progression of a CTLA-4-related disorder comprising administering a therapeutically effective amount of the activatable antibodies described herein or the pharmaceutical compositions comprising an activatable anti-CTLA-4 antibody described herein to a subject in need thereof. In some embodiments, the CTLA-4 related disorder is a cancer. In some embodiments, the cancer is a melanoma, such as unresectable or metastatic melanoma, breast cancer, colorectal cancer, gastric cancer, glioblastoma, head and neck

cancer, lung cancer, ovarian cancer, endometrial cancer, pancreatic cancer, prostate cancer, renal cancer, sarcoma, or skin cancer. In some embodiments, the CTLA-4 related disorder is a disorder known to be treatable with ipilimumab.

[0032] Where aspects or embodiments of the invention are described in terms of a Markush group or other grouping of alternatives, the present invention encompasses not only the entire group listed as a whole, but also each member of the group individually and all possible subgroups of the main group, and also the main group absent one or more of the group members. The present invention also envisages the explicit exclusion of one or more of any of the group members in the claimed invention.

BRIEF DESCRIPTION OF THE DRAWINGS/FIGURES

[0033] FIGs. 1A to 1C show tumor volumes as a function of days post tumor implantation in mice (n = 10) treated with (i) an unrelated mouse IgG2a antibody (FIG. 1A), (ii) a mouse anti-CTLA-4 (9D9) IgG2a antibody (FIG. 2B), or (iii) an activatable 9D9 antibody (FIG. 1C). All antibodies and activatable antibodies were dosed at 25 µg/mouse. The activatable 9D9 antibody comprises MY11 (SEQ ID NO: 294) as the masking moiety and 2001 (SEQ ID NO: 297) as the cleavable moiety. "TF" indicates the number of tumor free mice at the end of each experiment. The unrelated mouse IgG2a antibody and the mouse anti-CTLA-4 (9D9) IgG2a antibody were used as controls.

[0034] FIGs. 2A to 2C show the frequency of regulatory T cells in the tumor (FIG. 2A) and proliferation and activation of regulatory T cells in the spleen (FIGs. 2B and 2C) of mice treated with different activatable mouse anti-CTLA-4 (9D9) IgG2a antibodies. The different activatable 9D9 antibodies comprise (i) either MY03 (SEQ ID NO: 293) or MY11 (SEQ ID NO: 294) as the masking moiety and (2) 0003 (SEQ ID NO: 320), 1004 (SEQ ID NO: 323), or 2001 (SEQ ID NO: 297) as the cleavable moiety. The unrelated mouse IgG2a antibody ("DT 1D12 mg2a") and the mouse anti-CTLA-4 (9D9) IgG2a antibody ("9D9 mg2a") were used as controls. In FIG. 2A, the frequency of regulatory T cells is shown as a percentage of total CD4+ T cells that are Foxp3+ in the tumor. FIGs. 2B and 2C show the frequency of proliferating (Ki-67+) and activated (ICOS+) regulatory T cells, as a percentage of Foxp3+ T cells, in the spleen, respectively.

[0035] FIGs. 3A to 3E show the ability of different anti-CTLA-4 activatable antibodies (human IgG1 isotype) to bind to human CTLA-4, as measured *in vitro* with an ELISA

binding assay. Ipilimumab ("YV1") was used as a control in all experiments. In FIG. 3A, the anti-CTLA-4 activatable antibodies comprise YV04 (SEQ ID NO: 4), YV06 (SEQ ID NO: 6), YV09 (SEQ ID NO: 9), or YV23 (SEQ ID NO: 23) as the masking moiety. In FIG. 3B, the anti-CTLA-4 activatable antibodies comprise YV27 (SEQ ID NO: 27), YV29 (SEQ ID NO: 29), YV32 (SEQ ID NO: 32), or YV33 (SEQ ID NO: 33) as the masking moiety. In FIG. 3C, the anti-CTLA-4 activatable antibodies comprise YV35 (SEQ ID NO: 35) or YV41 (SEQ ID NO: 41) as the masking moiety. In FIG. 3D, the anti-CTLA-4 activatable antibodies comprise YV24 (SEQ ID NO: 24), YV39 (SEQ ID NO: 39), YV51 (SEQ ID NO: 51), YV52 (SEQ ID NO: 52), or YV53 (SEQ ID NO: 53) as the masking moiety. In FIG. 3E, the anti-CTLA-4 activatable antibodies comprise YV54 (SEQ ID NO: 54), YV55 (SEQ ID NO: 55), YV56 (SEQ ID NO: 56), YV57 (SEQ ID NO: 57), or YV58 (SEQ ID NO: 58) as the masking moiety. In FIGs. 3A to 3E, all the anti-CTLA-4 activatable antibodies comprise 2001 (SEQ ID NO: 297) as the cleavable moiety.

[0036] FIGs. 4A to 4D show the ability of additional anti-CTLA-4 activatable antibodies (human IgG1 isotype) to bind to human CTLA-4, as measured *in vitro* with an ELISA binding assay. Ipilimumab ("YV1") was used as a control in all experiments. In FIG. 4A, the anti-CTLA-4 activatable antibodies comprise YV04, YV06, YV09, YV23, YV27, or YV29 as the masking moiety. In FIG. 4B, the anti-CTLA-4 activatable antibodies comprise YV32, YV33, YV35, or YV41 as the masking moiety. In FIG. 4C, the anti-CTLA-4 activatable antibodies comprise YV24, YV39, YV51, YV52, or YV53 as the masking moiety. In FIG. 4D, the anti-CTLA-4 activatable antibodies comprise YV54, YV55, YV56, YV57, or YV58 as the masking moiety. In FIGs. 4A to 4D, all the anti-CTLA-4 activatable antibodies comprise 3001 as the cleavable moiety.

[0037] FIGs. 5A to 5F show the ability of several anti-CTLA-4 activatable antibodies (mouse IgG2a isotype) to bind to human CTLA-4, as measured *in vitro* with an ELISA binding assay. Ipilimumab ("YV1") was used as a control. In FIG. 5A, the anti-CTLA-4 activatable antibodies comprise YV04 as the masking moiety and 2001 (SEQ ID NO: 297), 2006 (SEQ ID NO: 300), 2007 (SEQ ID NO: 301), 2008 (SEQ ID NO: 302), or 2009 (SEQ ID NO: 303) as the cleavable moiety. In FIG. 5B, the anti-CTLA-4 activatable antibodies comprise YV04 or YV23 as the masking moiety, and 2001, 2006, 2007, 2008, or 2009 as the cleavable moiety. In FIG. 5C, the anti-CTLA-4 activatable

antibodies comprise YV39 as the masking moiety and 2001, 2006, 2008, or 2009 as the cleavable moiety. In FIG. 5D, the anti-CTLA-4 activatable antibodies comprise YV61 (SEQ ID NO: 60), YV62 (SEQ ID NO: 61), YV63 (SEQ ID NO: 62), YV64 (SEQ ID NO: 63), or YV39 (SEQ ID NO: 39) as the masking moiety and 2001 or 2012 as the cleavable moiety. In FIG. 5E, the anti-CTLA-4 activatable antibodies comprise YV65 (SEQ ID NO: 64), YV66 (SEQ ID NO: 65), YV01 (SEQ ID NO: 1), YV02 (SEQ ID NO: 2), or YV39 (SEQ ID NO: 39) as the masking moiety and 2001 or 2012 as the cleavable moiety. In FIG. 5F, the anti-CTLA-4 activatable antibodies comprise YV39 or YV03 (SEQ ID NO: 3) as the masking moiety and 2001 or 2012 as the cleavable moiety.

[0038] FIGs. 6A and 6B compares the ability of anti-CTLA-4 activatable antibodies having either a mouse IgG2a isotype (FIG. 6A) or human IgG1 isotype (FIG. 6B) to bind to human CTLA-4, as measured *in vitro* with an ELISA binding assay. Ipilimumab ("YV1") was used as a control. In both FIGs. 6A and 6B, the anti-CTLA-4 activatable antibodies comprise YV39 as the masking moiety and 2001, 2008, 2011, or 2012 as the cleavable moiety. In a modified antibody of the disclosure (YV39-NSUB), the cleavable moiety was replaced with a protease resistant linker ("NSUB") comprising the amino acid sequence GGSGGSGGGSGGGS (SEQ ID NO: 570).

[0039] FIGs. 7A to 7D show the ability of different anti-CTLA-4 activatable antibodies to bind 58 $\alpha^-\beta^-$ cells overexpressing human CTLA-4, as measured via flow cytometry. Binding is presented as arbitrary fluorescence units (mean fluorescence intensity, MFI, or geometric mean fluorescence intensity, gMFI) as a function of the concentration of anti-CTLA-4 antibody added. In FIG. 7A, the anti-CTLA-4 activatable antibodies comprise YV04, YV23, YV24, or YV39 as the masking moiety and 2001 as the cleavable moiety. In FIG. 7B, the anti-CTLA-4 activatable antibodies comprise YV61, YV62, YV64, or YV39 as the masking moiety and 2001 or 2011 as the cleavable moiety. In FIG. 7C, the anti-CTLA-4 activatable antibodies comprise YV39 as the masking moiety and for the cleavable moiety, 2011 ("Ipi YV39 2011") or three variants of Ipi YV39 2011: (i) mono-clipped ("Ipi YV39 MMP monoclipped"), (ii) fully clipped by MMP ("Ipi YV39 MMP"), or (iii) fully clipped by uPA ("Ipi YV39 2011 uPA"). FIG. 7D provides the EC50 values for the different activatable antibodies shown in FIG. 7C. Ipilimumab was used as a control for FIGs. 7A to 7D.

[0040] FIG. 8 shows the activity of the anti-CTLA-4 activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("Ipi YV39 2011") (square) at different concentrations, as measured *in vitro* with an SEB (Staphylococcal enterotoxin B) assay. Antibody activity is shown via IL-2 production by the human PBMCs after SEB stimulation. An unrelated human IgG1 isotype (triangle), ipilimumab (circle), and SEB only stimulation (x-mark) were used as controls.

[0041] FIGs. 9A to 9F show tumor volume as a function of days post tumor implantation in human CTLA-4 knock-in mice (n = 10) treated with different anti-human CTLA-4 activatable antibodies (mouse IgG2a isotype) dosed once at 10 mg/kg. An unrelated mouse IgG2a antibody (FIG. 9A) and ipilimumab with a mouse IgG2a isotype (FIG. 9B) were used as controls. In FIGs. 9C to 9F, the activatable antibodies comprise YV04, YV23, YV24, and YV39, respectively, as the masking moiety and 2001 as the cleavable moiety.

[0042] FIGs. 10A to 10F show tumor volume as a function of days post tumor implantation in human CTLA-4 knock-in mice (n = 10) treated with different anti-human CTLA-4 activatable antibodies (human IgG1 isotype). The antibodies were dosed once at 200 μg/mouse on day 7 post-implantation. An unrelated human IgG1 antibody (FIG. 10A) and ipilimumab with a human IgG1 isotype (FIG. 10B) were used as controls. In FIGs. 10C to 10F, the activatable antibodies comprise YV39 as the masking moiety and 2001, 2012, 2011, or 2008 as the cleavable moiety. Cleavable moieties 2012, 2011, and 2008 have been modified to overcome a deamidation site in 2001.

[0043] FIGs. 11A to 11G show tumor volume as a function of days post tumor implantation in human CTLA-4 knock-in mice (n = 16) treated with different doses of an anti-CTLA activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("Ipi YV39 2011") (FIGs. 11E to 11G). The antibody was dosed once at 10 mg/kg (FIG. 11E), 3 mg/kg (FIG. 11F), or 1 mg/kg (FIG. 11G) on day 7 post tumor implantation. Control animals were treated with ipilimumab (10 mg/kg, 3 mg/kg, or 1 mg/kg; FIGs. 11B to 11D, respectively) or an unrelated human IgG1 antibody (FIG. 11A).

[0044] FIGs. 12A to 12D show the frequency of regulatory T cells in the tumor (FIGs. 12A and 12B) or the spleen (FIGs. 12C and 12D) in human CTLA-4 knock-in mice (n = 10) treated with different anti-human CTLA-4 activatable antibodies with a mouse IgG2a

isotype. All antibodies were dosed once at 10 mg/kg. The activatable antibodies comprise YV04, YV23, YV24, or YV39 as the masking moiety and 2001 as the cleavable moiety. The labels on the abscissas of FIGs. 12C and 12D also apply to FIGs. 12A and 12B, respectively. An unrelated human IgG1 antibody and ipilimumab with a mouse IgG2a isotype were used as controls. In FIGs. 12A and 12C, the frequency of regulatory T cells is shown as a percentage of total CD4+ T cells that are Foxp3+. In FIGs. 12B and 12D, the frequency of regulatory T cells is shown as a percentage of total CD45+ T cells that are Foxp3+. FIGs. 12E and 12F show the frequency of activated (ICOS+) cells and proliferating (Ki-67+) cells is shown as a percentage of regulatory T cells in the spleen.

[0045] FIGs. 13A to 13C show the frequency of regulatory T cells in the tumor (FIGs. 13A and 13B) or the spleen (FIG. 13C) in human CTLA-4 knock-in mice treated with anti-CTLA-4 activatable antibody. The activatable antibody used comprises YV39 as the masking moiety and were either a mouse IgG2a isotype or human IgG1 isotype. An unrelated human IgG1 antibody and ipilimumab with a human IgG1 isotype were used as controls. In FIGs. 13A and 13C, the frequency of regulatory T cells is shown as a percentage of total CD4+ T cells that are Foxp3+. In FIG. 13B, the frequency of regulatory T cells is shown as a percentage of total CD45+ T cells that are Foxp3+. FIGs. 13D and 13E show the frequency of proliferating (Ki-67+) and activated (ICOS+) cells as a percentage of regulatory T cells in the spleen.

[0046] FIGs. 14A to 14C show the frequency of regulatory T cells (FIGs. 14A and 14B) or CD4+ effector T cells (FIG. 14C) in the tumors of mice treated with different anti-CTLA-4 activatable antibodies. FIGs. 14D and 14E show the regulatory T cells in the spleen. The anti-CTLA-4 activatable antibodies comprise YV39 as the masking moiety and 2012, 2011, 2008, or 2001 as the cleavable moiety. An unrelated human IgG1 antibody and ipilimumab with a human IgG1 isotype were used as controls. In FIGs. 14A and 14D, the frequency of regulatory T cells is shown as a percentage of total CD4+ T cells that are Foxp3+. In FIGs. 14B and 14E, the frequency of regulatory T cells is shown as a percentage of total CD45+ T cells that are Foxp3+. FIG. 14C shows the frequency of CD4+ effector T cells as a percentage of the total CD45+ T cells in the tumor. FIGs. 14F and 14G show the percentages of proliferating (Ki-67+) and activated (ICOS+) regulatory T cells in the spleen

[0047] FIG. 15 shows the frequency of regulatory T cells in the tumors of human CTLA-4 knock-in mice (n = 8) treated with different doses of either ipilimumab or an anti-CTLA-4 activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("Ipi YV39 2011"). The antibodies were dosed once at 10 mg/kg, 3 mg/kg, or 1 mg/kg on day 7 post tumor implantation. An unrelated human IgG1 antibody was used as a control.

[0048] FIGs. 16A and 16B show the percentages of activated (ICOS+) and proliferating (Ki-67+) regulatory T cells in the spleen of human CTLA-4 knock-in mice (n = 8) treated with different doses of either ipilimumab or an anti-CTLA-4 activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("Ipi YV39 2011"). The antibodies were dosed once at 10 mg/kg, 3 mg/kg, or 1 mg/kg on day 7 post tumor implantation. An unrelated human IgG1 antibody was used as a control.

[0049] FIGs. 17A to 17D show tumor volume as a function of days post tumor implantation in human CTLA-4 knock-in mice (n = 10) treated with different doses of ipilimumab ("Ipi") (FIG. 17B), a nonfucosylated version of ipilimumab ("Ipi NF") (FIG. 17C), or a nonfucosylated version of an anti-CTLA-4 activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("Ipi YV39 2011 NF") (FIG. 17D). The antibodies were dosed once at 10 mg/kg, 3 mg/kg, or 1 mg/kg (left panel, middle panel, and right panel, respectively, in FIGs. 17B to 17D). Control animals received an unrelated human IgG1 antibody (FIG. 17A).

[0050] FIG. 18 shows the frequency of regulatory T cells in the tumors of human CTLA-4 knock-in mice (n = 5) treated with either the nonfucosylated version of ipilimumab ("Ipi NF") or a nonfucosylated version of the anti-CTLA-4 activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("NF Ipi YV39 2011"). The antibodies were dosed once at 200 μg/mouse on day 7 post tumor implantation. An unrelated human IgG1 antibody was used as a control.

[0051] FIG. 19 shows the binding affinities (Kd) for both ipilimumab ("Ipi") and a nonfucosylated version of ipilimumab ("Ipi NF") to various human, cyno, and mouse Fc receptors.

[0052] FIG. 20 shows the median percentage of Ki67+ CD4+ T cells in the blood of cynomolgus monkeys after treatment with an anti-CTLA-4 activatable antibody. The anti-

CTLA-4 activatable antibody comprises YV39 as the masking moiety and 2001 as the cleavable moiety. Vehicle and ipilimumab were used as controls.

DETAILED DESCRIPTION OF INVENTION

[0053] In order that the present description can be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

[0054] It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a nucleotide sequence," is understood to represent one or more nucleotide sequences. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0055] Furthermore, "and/or" where used herein is to be taken as specific disclosure of each of the two specified features or components with or without the other. Thus, the term "and/or" as used in a phrase such as "A and/or B" herein is intended to include "A and B," "A or B," "A" (alone), and "B" (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following aspects: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0056] It is understood that wherever aspects are described herein with the language "comprising," otherwise analogous aspects described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[0057] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure is related. For example, the Concise Dictionary of Biomedicine and Molecular Biology, Juo, Pei-Show, 2nd ed., 2002, CRC Press; The Dictionary of Cell and Molecular Biology, 3rd ed., 1999, Academic Press; and the Oxford Dictionary Of Biochemistry And Molecular Biology, Revised, 2000, Oxford University Press, provide one of skill with a general dictionary of many of the terms used in this disclosure.

[0058] Units, prefixes, and symbols are denoted in their Système International de Unites (SI) accepted form. Numeric ranges are inclusive of the numbers defining the range. Unless otherwise indicated, nucleotide sequences are written left to right in 5' to 3' orientation. Amino acid sequences are written left to right in amino to carboxy orientation. The headings provided herein are not limitations of the various aspects of the

disclosure, which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification in its entirety.

[0059] The term "cytotoxic T-lymphocyte antigen 4" or "CTLA-4" as used herein refers to a receptor that is a member of the immunoglobulin superfamily that is expressed by activated T cells and transmits an inhibitory signal to T cells. CTLA-4 is homologous to the T-cell co-stimulatory protein, CD28, and both molecules bind to CD80 and CD86, also called B7-1 and B7-2 respectively, on antigen-presenting cells. CTLA4 is also found in regulatory T cells and contributes to its inhibitory function. CTLA-4 is also referred to as cytotoxic T-lymphocyte-associated protein 4, CD152, Insulin-dependent Diabetes Mellitus 12 (IDDM12), Celiac Disease 3 (CELIAC3), GRD4, and GSE. The term "CTLA-4" includes any variants or isoforms of CTLA-4 which are naturally expressed by cells.

[0060] The term "T cell" as used herein is defined as a thymus-derived lymphocyte that participates in a variety of cell-mediated immune reactions. The term "regulatory T cell" as used herein refers to a $CD4^+CD25^+FoxP3^+$ T cell with suppressive properties. "Treg" is the abbreviation used herein for a regulatory T cell.

[0061] The term "helper T cell" as used herein refers to a $CD4^+$ T cell; helper T cells recognize antigen bound to MHC Class II molecules. There are at least two types of helper T cells, Th1 and Th2, which produce different cytokines. Helper T cells become $CD25^+$ when activated, but only transiently become $FoxP3^+$.

[0062] The term "cytotoxic T cell" as used herein refers to a $CD8^+$ T cell; cytotoxic T cells recognize antigen bound to MHC Class I molecules.

[0063] The term "antibody" refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. By "specifically bind" or "immunoreacts with" or "immunospecifically bind" is meant that the antibody reacts with one or more antigenic determinants of the desired antigen and does not react with other polypeptides or binds at much lower affinity ($Kd > 10^{-6}$). Antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, domain antibody, single chain, Fab, and F(ab′)2 fragments, scFvs, and a Fab expression library.

[0064] The basic antibody structural unit is known to comprise a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. In general, antibody molecules obtained from humans relate to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG1, IgG2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain.

[0065] As used herein, the term “activatable antibody” refers to an antibody that also comprises a masking moiety (MM) and a cleavable moiety (CM), wherein the MM is joined to the VL of the antibody via the CM, which is cleavable by a protease. As used herein, a "prodomain" comprises the N-terminal fragment that is joined to the VL domain of the anti-human CTLA-4 activatable antibodies and, as such, comprises the MM and CM. In some embodiments, the light chain of the activatable antibody has the structural arrangement from N-terminus to C-terminus as follows: MM-CM-VL. In some embodiments, the prodomain is joined to the VH domain of the anti-human CTLA-4 antibody. An activatable antibody is designed to be cleaved by upregulated proteolytic activity present in most if not all cancers. Such proteolytic cleavage, or activation, removes the prodomain and releases an active antibody, i.e., an activated activatable antibody. Protease activation of activatable antibodies in normal tissue is significantly reduced due to the tight control of proteolytic activity in normal tissues. As such, activatable antibodies remain largely inert in circulation and in normal tissues.

[0066] An activatable antibody, in view of its prodomain masking the antigen binding domain thereby inhibiting the ability of the antigen binding domain to bind to its target, has a lower affinity for binding to the target than does an activated activatable antibody, in which the MM has been removed by proteolytic cleavage of the CM thereby releasing an active antibody. Such released antibody exhibits higher affinity for binding to its target. In some embodiments, the MM interacts specifically with the antigen binding domain of ipilimumab to reduce the antibody’s ability to bind to its target. When the MM

is removed by proteolytic cleavage of the activatable antibody, the released antibody binds to its target with an affinity similar to the parental ipilimumab.

[0067] Schematic representations of activatable antibodies of the present invention, *e.g.* MM-CM-VL, are not intended to be exclusive. Other sequence elements, such as linkers, spacers and signal sequences, may be present before, after, or between the listed sequence elements in such schematic representations. It is also to be appreciated that a prodomain comprising a MM and a CM can be joined to a VH of an antibody instead of to a VL of an antibody such that the heavy chain has the structural arrangement from N-terminus to C-terminus as follows: MM-CM-VH.

[0068] The term "monoclonal antibody" (mAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs contain an antigen binding site, or domain, capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it. Monoclonal antibody molecules will typically comprise two heavy chains and two light chains.

[0069] The term "antigen binding domain" refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains, referred to as "hypervariable regions," are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus, the term "FR" refers to amino acid sequences which are naturally found between, and adjacent to, hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs." The assignment of amino acids to each domain is in accordance with the definitions of Kabat Sequences of Proteins of

Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 and 1991)), or Chothia & Lesk *J. Mol. Biol.* 196:901-917 (1987), Chothia *et al. Nature* 342:878-883 (1989).

[0070] As used herein, the term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin, an scFv, or a T-cell receptor. The term "epitope" includes any protein determinant capable of specific binding to an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. For example, antibodies may be raised against N-terminal or C-terminal peptides of a polypeptide. An antibody is said to specifically bind an antigen when the dissociation constant is $\leqq$1 μM; preferably $\leqq$100 nM and most preferably $\leqq$10 nM.

[0071] As used herein, the terms "specific binding," "immunological binding," and "immunological binding properties" refer to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (k_{on}) and the "off rate constant" (k_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. (*See Nature* 361:186-87 (1993)). The ratio of k_{off}/k_{on} enables the cancellation of all parameters not related to affinity, and is equal to the dissociation constant K_d. (*See*, generally, Davies *et al.* (1990) *Annual Rev Biochem* 59:439-473). An antibody of the present invention is said to specifically bind to CTLA-4, when the equilibrium binding constant (K_d) is $\leqq$1 μM, preferably $\leqq$100 nM, more preferably $\leqq$10 nM, and most preferably $\leqq$100 pM to about 1 pM, as measured by assays such as radioligand binding assays or similar assays known to those skilled in the art.

[0072] The term "isolated polynucleotide" as used herein refers to a polynucleotide of genomic, cDNA, or synthetic origin or some combination thereof, which by virtue of its origin the "isolated polynucleotide" (1) is not associated with all or a portion of a polynucleotide in which the "isolated polynucleotide" is found in nature, (2) is operably linked to a polynucleotide which it is not linked to in nature, or (3) does not occur in nature as part of a larger sequence. Polynucleotides in accordance with the invention include the nucleic acid molecules encoding the heavy chain immunoglobulin molecules shown herein, and nucleic acid molecules encoding the light chain immunoglobulin molecules shown herein.

[0073] The term "isolated protein" referred to herein means a protein of cDNA, recombinant RNA, or synthetic origin or some combination thereof, which by virtue of its origin, or source of derivation, the "isolated protein" (1) is not associated with proteins found in nature, (2) is free of other proteins from the same source, e.g., free of murine proteins, (3) is expressed by a cell from a different species, or (4) does not occur in nature.

[0074] The term "polypeptide" is used herein as a generic term to refer to native protein, fragments, or analogs of a polypeptide sequence. Hence, native protein fragments, and analogs are species of the polypeptide genus. Polypeptides in accordance with the invention comprise the heavy chain immunoglobulin molecules shown herein, and the light chain immunoglobulin molecules shown herein, as well as antibody molecules formed by combinations comprising the heavy chain immunoglobulin molecules with light chain immunoglobulin molecules, such as kappa light chain immunoglobulin molecules, and vice versa, as well as fragments and analogs thereof.

[0075] The term "naturally-occurring" as used herein as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory or otherwise is naturally-occurring.

[0076] The term "operably linked" as used herein refers to positions of components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that

expression of the coding sequence is achieved under conditions compatible with the control sequences.

[0077] The term "control sequence" as used herein refers to polynucleotide sequences which are necessary to effect the expression and processing of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism in prokaryotes, such control sequences generally include promoter, ribosomal binding site, and transcription termination sequence in eukaryotes, generally, such control sequences include promoters and transcription termination sequence. The term "control sequences" is intended to include, at a minimum, all components whose presence is essential for expression and processing, and can also include additional components whose presence is advantageous, for example, leader sequences and fusion partner sequences. The term "polynucleotide" as referred to herein means nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide. The term includes single and double stranded forms of DNA.

[0078] The term “oligonucleotide” referred to herein includes naturally occurring, and modified nucleotides linked together by naturally occurring, and non-naturally occurring oligonucleotide linkages. Oligonucleotides are a polynucleotide subset generally comprising a length of 200 bases or fewer. Preferably oligonucleotides are 10 to 60 bases in length and most preferably 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 bases in length. Oligonucleotides are usually single stranded, e.g., for probes, although oligonucleotides may be double stranded, e.g., for use in the construction of a gene mutant. Oligonucleotides of the invention are either sense or antisense oligonucleotides.

[0079] The term "naturally occurring nucleotides" referred to herein includes deoxyribonucleotides and ribonucleotides. The term "modified nucleotides" referred to herein includes nucleotides with modified or substituted sugar groups and the like. The term "oligonucleotide linkages" referred to herein includes oligonucleotide linkages such as phosphorothioate, phosphorodithioate, phosphoroselerloate, phosphorodiselenoate, phosphoroanilothioate, phoshoraniladate, phosphoronmidate, and the like. *See e.g.*, LaPlanche *et al. Nucl. Acids Res.* 14:9081 (1986); Stec *et al. J. Am. Chem. Soc.* 106:6077 (1984), Stein *et al. Nucl. Acids Res.* 16:3209 (1988), Zon *et al. Anti Cancer Drug Design* 6:539 (1991); Zon *et al.* Oligonucleotides and Analogues: A Practical Approach, pp. 87-108 (F. Eckstein, Ed., Oxford University Press, Oxford England (1991)); Stec *et al.* U.S.

Pat. No. 5,151,510; Uhlmann and Peyman *Chemical Reviews* 90:543 (1990). An oligonucleotide can include a label for detection, if desired.

[0080] As used herein, the twenty conventional amino acids and their abbreviations follow conventional usage. See Immunology—A Synthesis (2nd Edition, E. S. Golub and D. R. Gren, Eds., Sinauer Associates, Sunderland Mass. (1991)). Stereoisomers (e.g., D-amino acids) of the twenty conventional amino acids, unnatural amino acids such as α-, α-disubstituted amino acids, N-alkyl amino acids, lactic acid, and other unconventional amino acids may also be suitable components for polypeptides of the present invention. Examples of unconventional amino acids include: 4 hydroxyproline, γ-carboxyglutamate, ε-N,N,N-trimethyllysine, ε-N-acetyllysine, O-phosphoserine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, σ-N-methylarginine, and other similar amino acids and imino acids (e.g., 4-hydroxyproline). In the polypeptide notation used herein, the left-hand direction is the amino terminal direction and the right-hand direction is the carboxy-terminal direction, in accordance with standard usage and convention.

[0081] As applied to polypeptides, the term "substantial identity" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80 percent sequence identity, preferably at least 90 percent sequence identity, more preferably at least 95 percent sequence identity, and most preferably at least 99 percent sequence identity.

[0082] As discussed herein, minor variations in the amino acid sequences of antibodies or immunoglobulin molecules are contemplated as being encompassed by the present invention, providing that the variations in the amino acid sequence maintain at least 75%, more preferably at least 80%, 90%, 95%, and most preferably 99% sequence identity. In particular, conservative amino acid replacements are contemplated. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids are generally divided into families: (1) acidic amino acids are aspartate, glutamate; (2) basic amino acids are lysine, arginine, histidine; (3) non-polar amino acids are alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and (4) uncharged polar amino acids are glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. The hydrophilic amino acids include arginine, asparagine, aspartate, glutamine, glutamate, histidine, lysine, serine, and

threonine. The hydrophobic amino acids include alanine, cysteine, isoleucine, leucine, methionine, phenylalanine, proline, tryptophan, tyrosine and valine. Other families of amino acids include (i) serine and threonine, which are the aliphatic-hydroxy family; (ii) asparagine and glutamine, which are the amide containing family; (iii) alanine, valine, leucine and isoleucine, which are the aliphatic family; and (iv) phenylalanine, tryptophan, and tyrosine, which are the aromatic family. In the case of an antibody, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the binding or properties of the resulting molecule, especially if the replacement does not involve an amino acid within a CDR or framework region. Whether an amino acid change results in a functional peptide can readily be determined by assaying the specific activity of the polypeptide derivative. Assays are described in detail herein. Fragments or analogs of antibodies or immunoglobulin molecules can be readily prepared by those of ordinary skill in the art. Preferred amino- and carboxy-termini of fragments or analogs occur near boundaries of functional domains. Structural and functional domains can be identified by comparison of the nucleotide and/or amino acid sequence data to public or proprietary sequence databases. Preferably, computerized comparison methods are used to identify sequence motifs or predicted protein conformation domains that occur in other proteins of known structure and/or function. Methods to identify protein sequences that fold into a known three-dimensional structure are known. Bowie *et al. Science* 253:164 (1991). Thus, the foregoing examples demonstrate that those of skill in the art can recognize sequence motifs and structural conformations that may be used to define structural and functional domains in accordance with the invention.

[0083] Preferred amino acid substitutions are those which: (1) reduce susceptibility to proteolysis in regions of the activatable antibody other than in the cleavable linker comprising the CM, (2) reduce susceptibility to oxidation, (3) alter binding affinity for forming protein complexes, (4) alter binding affinities, and (4) confer or modify other physicochemical or functional properties of such analogs. Analogs can include various muteins of a sequence other than the naturally-occurring peptide sequence. For example, single or multiple amino acid substitutions (preferably conservative amino acid substitutions) may be made in the naturally-occurring sequence (preferably in the portion

of the polypeptide outside the domain(s) forming intermolecular contacts). A conservative amino acid substitution should not substantially change the structural characteristics of the parent sequence (e.g., a replacement amino acid should not tend to break a helix that occurs in the parent sequence, or disrupt other types of secondary structure that characterizes the parent sequence). Examples of art-recognized polypeptide secondary and tertiary structures are described in Proteins, Structures and Molecular Principles (Creighton, Ed., W. H. Freeman and Company, New York (1984)); Introduction to Protein Structure (C. Branden and J. Tooze, eds., Garland Publishing, New York, N.Y. (1991)); and Thornton *et al. Nature* 354:105 (1991).

[0084] The term "polypeptide fragment" as used herein refers to a polypeptide that has an amino terminal and/or carboxy-terminal deletion and/or one or more internal deletion(s), but where the remaining amino acid sequence is identical to the corresponding positions in the naturally-occurring sequence deduced, for example, from a full length cDNA sequence. Fragments typically are at least 5, 6, 8 or 10 amino acids long, preferably at least 14 amino acids long′ more preferably at least 20 amino acids long, usually at least 50 amino acids long, and even more preferably at least 70 amino acids long. The term "analog" as used herein refers to polypeptides which comprise a segment of at least 25 amino acids that has substantial identity to a portion of a deduced amino acid sequence and which has specific binding to CTLA-4, under suitable binding conditions. Typically, polypeptide analogs comprise a conservative amino acid substitution (or addition or deletion) with respect to the naturally-occurring sequence. Analogs typically are at least 20 amino acids long, preferably at least 50 amino acids long or longer, and can often be as long as a full-length naturally-occurring polypeptide.

[0085] The term "agent" is used herein to denote a chemical compound, a mixture of chemical compounds, a biological macromolecule, or an extract made from biological materials.

[0086] As used herein, the terms "label" or "labeled" refers to incorporation of a detectable marker, e.g., by incorporation of a radiolabeled amino acid or attachment to a polypeptide of biotinyl moieties that can be detected by marked avidin (e.g., streptavidin containing a fluorescent marker or enzymatic activity that can be detected by optical or calorimetric methods). In certain situations, the label or marker can also be therapeutic. Various methods of labeling polypeptides and glycoproteins are known in the art and may

be used. Examples of labels for polypeptides include, but are not limited to, the following: radioisotopes or radionuclides (e.g., ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I) fluorescent labels (e.g., FITC, rhodamine, lanthanide phosphors), enzymatic labels (e.g., horseradish peroxidase, p-galactosidase, luciferase, alkaline phosphatase), chemiluminescent, biotinyl groups, predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, labels are attached by spacer arms of various lengths to reduce potential steric hindrance.

[0087] Other chemistry terms herein are used according to conventional usage in the art, as exemplified by The McGraw-Hill Dictionary of Chemical Terms (Parker, S., Ed., McGraw-Hill, San Francisco (1985)).

[0088] As used herein, "substantially pure" means an object species is the predominant species present (i.e., on a molar basis it is more abundant than any other individual species in the composition), and preferably a substantially purified fraction is a composition wherein the object species comprises at least about 50 percent (on a molar basis) of all macromolecular species present. Generally, a substantially pure composition will comprise more than about 80 percent of all macromolecular species present in the composition, more preferably more than about 85%, 90%, 95%, and 99%. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

[0089] As used herein, "treatment" is an approach for obtaining beneficial or desired clinical results. Beneficial or desired clinical results may include, but are not limited to, any one or more of: alleviation of one or more symptoms, diminishment of extent of disease, stabilized (i.e., not worsening) state of disease, preventing or delaying spread (e.g., metastasis) of disease, preventing or delaying occurrence or recurrence of disease, delay or slowing of disease progression, amelioration of the disease state, and remission (whether partial or total). Also encompassed by "treatment" is a reduction of pathological consequence of a proliferative disease such as cancer. The methods provided herein contemplate any one or more of these aspects of treatment.

[0090] The term "effective amount" used herein refers to an amount of a compound or composition, when used alone or in combination with a second therapy, is sufficient to

treat a specified disorder, condition or disease such as ameliorate, palliate, lessen, and/or delay one or more of its symptoms. In reference to cancers or other unwanted cell proliferation, an effective amount comprises an amount sufficient to cause a tumor to shrink and/or to decrease the growth rate of the tumor (such as to suppress tumor growth) or to prevent or delay other unwanted cell proliferation. An effective amount can be administered in one or more administrations.

[0091] As used herein, by "combination therapy" is meant that a first agent be administered in conjunction with another agent. "In conjunction with" refers to administration of one treatment modality in addition to another treatment modality. As such, "in conjunction with" refers to administration of one treatment modality before, during, or after delivery of the other treatment modality to the individual.

[0092] The term "pharmaceutical agent or drug" as used herein refers to a chemical compound or composition capable of inducing a desired therapeutic effect when properly administered to a subject.

[0093] As used herein, by "pharmaceutically acceptable" or "pharmacologically compatible" is meant a material that is not biologically or otherwise undesirable, e.g., the material may be incorporated into a pharmaceutical composition administered to an individual or subject without causing any significant undesirable biological effects or interacting in a deleterious manner with any of the other components of the composition in which it is contained. Pharmaceutically acceptable carriers or excipients have for example met the required standards of toxicological and manufacturing testing and/or are included on the Inactive Ingredient Guide prepared by the U.S. Food and Drug administration.

[0094] The terms "cancer", "cancerous", or "malignant" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, for example, melanoma, such as unresectable or metastatic melanoma, leukemia, lymphoma, blastoma, carcinoma and sarcoma. More particular examples of such cancers include chronic myeloid leukemia, acute lymphoblastic leukemia, Philadelphia chromosome positive acute lymphoblastic leukemia (Ph+ ALL), squamous cell carcinoma, small-cell lung cancer, non-small cell lung cancer, glioma, gastrointestinal cancer, renal cancer, ovarian cancer, liver cancer, colorectal cancer, endometrial cancer, kidney cancer, prostate cancer, thyroid cancer,

neuroblastoma, pancreatic cancer, glioblastoma multiforme, cervical cancer, stomach cancer, bladder cancer, hepatoma, breast cancer, colon carcinoma, and head and neck cancer, gastric cancer, germ cell tumor, pediatric sarcoma, sinonasal natural killer, multiple myeloma, acute myelogenous leukemia (AML), and chronic lymphocytic leukemia (CML).

[0095] "Leukemia" refers to progressive, malignant diseases of the blood-forming organs and is generally characterized by a distorted proliferation and development of leukocytes and their precursors in the blood and bone marrow. Leukemia is generally clinically classified on the basis of (1) the duration and character of the disease--acute or chronic; (2) the type of cell involved; myeloid (myelogenous), lymphoid (lymphogenous), or monocytic; and (3) the increase or non-increase in the number of abnormal cells in the blood--leukemic or aleukemic (subleukemic). Leukemia includes, for example, acute nonlymphocytic leukemia, chronic lymphocytic leukemia, acute granulocytic leukemia, chronic granulocytic leukemia, acute promyelocytic leukemia, adult T-cell leukemia, aleukemic leukemia, a leukocythemic leukemia, basophylic leukemia, blast cell leukemia, bovine leukemia, chronic myelocytic leukemia, leukemia cutis, embryonal leukemia, eosinophilic leukemia, Gross' leukemia, hairy-cell leukemia, hemoblastic leukemia, hemocytoblastic leukemia, histiocytic leukemia, stem cell leukemia, acute monocytic leukemia, leukopenic leukemia, lymphatic leukemia, lymphoblastic leukemia, lymphocytic leukemia, lymphogenous leukemia, lymphoid leukemia, lymphosarcoma cell leukemia, mast cell leukemia, megakaryocytic leukemia, micromyeloblastic leukemia, monocytic leukemia, myeloblastic leukemia, myelocytic leukemia, myeloid granulocytic leukemia, myelomonocytic leukemia, Naegeli leukemia, plasma cell leukemia, plasmacytic leukemia, promyelocytic leukemia, Rieder cell leukemia, Schilling's leukemia, stem cell leukemia, subleukemic leukemia, and undifferentiated cell leukemia. In certain aspects, the present invention provides treatment for chronic myeloid leukemia, acute lymphoblastic leukemia, and/or Philadelphia chromosome positive acute lymphoblastic leukemia (Ph+ ALL).

I. Anti-CTLA-4 Activatable Antibodies

[0096] The present invention provides improved anti-CTLA-4 antibodies that are as efficacious as the traditional anti-CTLA-4 antibodies (e.g., ipilimumab) but with a

greater, i.e., improved, safety profile. Specifically, the improved anti-CTLA-4 antibodies are activatable monoclonal antibodies (mAbs) that specifically bind human CTLA-4 when activated. These improved anti-CTLA-4 antibodies, also referred to herein as activatable anti-CTLA-4 antibodies or CTLA-4 activatable antibodies, are used in methods of treating, preventing, delaying the progression of, ameliorating and/or alleviating a symptom of a disease or disorder, including but not limited to, a disease or disorder associated with aberrant CTLA-4 expression and/or activity. For example, the activatable anti-CTLA-4 antibodies are used in methods of treating, preventing, delaying the progression of, ameliorating and/or alleviating a symptom of a cancer or other neoplastic condition. Activatable antibodies are described in, for example, US Pat. Nos. 8,513,390, 8,518,404; 9,120,853; 9,127,053 and International Publ. No. WO 2016/149201.

[0097] In some embodiments, the activatable anti-CTLA-4 antibodies provided herein comprise (i) ipilimumab or antigen binding domain thereof (AB), such as an ipilimumab variable light chain (VL), (ii) a cleavable moiety (CM), and (iii) a masking moiety (MM). In some embodiments, the VL is coupled to the MM, such that coupling of the MM reduces the ability of the ipilimumab to bind to CTLA-4. In some embodiments, the MM is coupled to the VL via a cleavable moiety (CM) (also known as a substrate linker) that includes a substrate for a protease, for example, a protease that is over-expressed in the tumor microenvironment.

Antibody or Antigen Binding Fragment Thereof

[0098] In some embodiments, the antibody or antigen binding domain thereof (AB) comprises the complementarity determining regions (CDRs) of the anti-CTLA-4 antibody ipilimumab, identified as 10D1 in U.S. Patent Nos. 6,984,720 and 7,605,238, which are hereby incorporated by reference in their entireties. Ipilimumab (also formerly known as MDX-010 and BMS-734016) is marketed as YERVOY® and has been approved for the treatment of metastatic melanoma and is in clinical testing in other cancers. *See* Hoos *et al.* (2010) *Semin. Oncol.* 37:533; Hodi *et al.* (2010) *N. Engl. J. Med.* 363:711; Pardoll (2012) *Nat. Immunol.* 13(12): 1129.

[0099] Ipilimumab has a human IgG1 isotype, which binds best to most human Fc receptors (Bruhns *et al.* (2009) *Blood* 113: 3716) and is considered equivalent to murine

IgG2a with respect to the types of activating Fc receptors that it binds. Since IgG1 binds to the activating receptor CD16 (FcγRIIIa) expressed by human NK cells and monocytes, ipilimumab can mediate ADCC. The IgG1-isotype ipilimumab was originally isolated directly from a hybridoma but was subsequently cloned and expressed in Chinese hamster ovary (CHO) cells. Notwithstanding the consideration that an isotype that mediates ADCC and/or CDC might be undesirable in an antibody targeting a receptor on T cells that seeks to upregulate an immune response, the IgG1 isotype of the antibody was retained, in part, because it enhanced vaccine response in cynomolgus monkey and was considered functional. Ipilimumab has been shown to increase the numbers of activated T cells in the blood, as evidenced, for example, by a significant increase in the expression of HLA-DR on the surface of post-treatment $CD4^+$ and $CD8^+$ cells as well as increases in absolute lymphocyte count (Ku *et al.* (2010) *Cancer* 116:1767; Attia *et al.* (2005) *J. Clin. Oncol.* 23:6043; Maker *et al.* (2005) *J. Immunol.* 175:7746; Berman *et al.* (2009) *J. Clin. Oncol.* 27(suppl):15s.3020; Hamid *et al.* (2009) *J. Clin. Oncol.* 27(suppl): 15s.9008), indicating that depletion of T cells does not occur in the periphery in man. Ipilimumab demonstrated only modest levels of ADCC of activated T cells using IL-2-activated PBMCs as effector cells; however, use of T_{regs} as targets was not tested. Minor changes in peripheral T_{reg} frequency in the blood of patients treated with ipilimumab have been observed (Maker *et al.* (2005) *J. Immunol.* 175:7746), but little information of the effect of ipilimumab on intratumoral T_{regs} is available. However, a positive correlation between a high $CD8^+$ to T_{reg} ratio and tumor necrosis in biopsies from metastatic melanoma lesions from patients treated with ipilimumab have been described. Hodi *et al.* (2008) *Proc. Nat'l Acad. Sci. (USA)* 105:3005. In addition, tumor tissue from ipilimumab-treated bladder cancer patients had lower percentages of $CD4^+$ $Foxp3^+$ T cells than tumors from untreated bladder cancer patients. Liakou *et al.* (2008) *Proc. Nat'l Acad. Sci. (USA)* 105:14987.

[0100] In some embodiments, the activatable anti-CTLA-4 antibody comprises a combination of a variable heavy chain CDR1 (VH CDR1, also referred to herein as CDRH1), CDR2 (VH CDR2, also referred to herein as CDRH2), and CDR3 (VH CDR3, also referred to herein as CDRH3), and a variable light chain CDR1 (VL CDR1, also referred to herein as CDRL1), CDR2 (VL CDR2, also referred to herein as CDRL2), and

CDR3 (VL CDR3, also referred to herein as CDRL3). These CDR sequences are provided at Table 2.

Table 2: CDR Sequences of heavy and light chains for Ipilimumab

CHAIN	CDR1	CDR2	CDR3
LIGHT	RASQSVGSSYLA (SEQ ID NO: 560)	GAFSRAT (SEQ ID NO: 561)	QQYGSSPWT (SEQ ID NO: 562)
HEAVY	SYTMH (SEQ ID NO: 557)	FISYDGNNKYYADSVKG (SEQ ID NO: 558)	TGWLGPFDY (SEQ ID NO: 559)

[0101] Ipilimumab-VL chain
EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK (SEQ ID NO: 344)

[0102] Ipilimumab-VH chain
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYD GNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDY WGQGTLVTVSS (SEQ ID NO: 345)

[0103] Various other sequences, as indicated, are provided below.

[0104] Human Kappa constant LC
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 346)

[0105] Mouse Kappa constant light chain
RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC (SEQ ID NO: 347)

[0106] Ipilimumab—Human Kappa LC
EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTVA

APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 348)

[0107] Ipilimumab—Mouse Kappa LC

EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRA TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRADA APTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC (SEQ ID NO: 349)

[0108] Human IgG1 constant HC

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP G (SEQ ID NO: 350)

[0109] Mouse IgG1 constant HC

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PG (SEQ ID NO: 351)

[0110] Mouse IgG2a constant HC

AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPA VLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKC PAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVH TAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPK

GSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKN
TEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
(SEQ ID NO: 352)

[0111] Ipilimumab-VH—Human IgG1 constant HC
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYD
GNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDY
WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH
YTQKSLSLSPG (SEQ ID NO: 353)

[0112] Ipilimumab-VH—Mouse IgG1 constant HC
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYD
GNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDY
WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
NHYTQKSLSLSPG (SEQ ID NO: 354)

[0113] Ipilimumab-VH—Mouse IgG2a constant HC
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYD
GNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDY
WGQGTLVTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNS
GSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEP
RGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDV
QISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNK

DLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEW TNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHN HHTTKSFSRTPGK (SEQ ID NO: 355)

[0114] In some embodiments, the antibody comprises a combination of a VH CDR1 sequence, a VH CDR2 sequence, a VH CDR3 sequence, a VL CDR1 sequence, a VL CDR2 sequence, and a VL CDR3 sequence, wherein at least one CDR sequence comprises 1, 2, 3, 4 or more amino acid sequence differences compared with the CDR sequences shown in Table 2, including conservative amino acid differences.

[0115] In some embodiments, the activatable anti-CTLA-4 antibody comprises a heavy chain variable domain that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to the group consisting of SEQ ID NO: 345. In some embodiments, the activatable anti-CTLA-4 antibody comprises a light chain variable domain, not including any MM, CM, linker, spacer or other sequence added in creation of the activatable form of the antibody, that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identical to the group consisting of SEQ ID NOs: 563 to 565.

[0116] In some embodiments, the antibody or antigen-binding fragment thereof that binds CTLA-4 in the activatable antibodies can include modifications, particularly in the Fc region of the antibody or antigen-binding fragment thereof. For example, the interaction of antibodies with FcγRs can be enhanced by modifying the glycan moiety attached to each Fc fragment at the N297 residue. In particular, the absence of core fucose residues strongly enhances ADCC via improved binding of IgG to activating FcγRIIIA without altering antigen binding or CDC. Natsume *et al.* (2009) *Drug Des. Devel. Ther.* 3:7. There is convincing evidence that afucosylated tumor-specific antibodies translate into enhanced therapeutic activity in mouse models *in vivo*. Nimmerjahn & Ravetch (2005) *Science* 310:1510; Mossner *et al.* (2010) *Blood* 115:4393.

[0117] Modification of antibody glycosylation can be accomplished by, for example, expressing the antibody in a host cell with altered glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express recombinant antibodies of this disclosure to thereby produce an antibody with altered glycosylation. For example, the cell lines Ms704, Ms705, and Ms709 lack the fucosyltransferase gene, FUT8 (α-(1,6) fucosyltransferase) (see U.S. Pat.

App. Publication No. 20040110704; Yamane-Ohnuki *et al.* (2004) *Biotechnol. Bioeng.* 87: 614), such that antibodies expressed in these cell lines lack fucose on their carbohydrates. As another example, EP 1176195 also describes a cell line with a functionally disrupted FUT8 gene as well as cell lines that have little or no activity for adding fucose to the N-acetylglucosamine that binds to the Fc region of the antibody, for example, the rat myeloma cell line YB2/0 (ATCC CRL 1662). PCT Publication WO 03/035835 describes a variant CHO cell line, Lec13, with reduced ability to attach fucose to Asn (297)-linked carbohydrates, also resulting in hypofucosylation of antibodies expressed in that host cell. See also Shields *et al.* (2002) *J. Biol. Chem.* 277:26733. Antibodies with a modified glycosylation profile can also be produced in chicken eggs, as described in PCT Publication No. WO 2006/089231. Alternatively, antibodies with a modified glycosylation profile can be produced in plant cells, such as Lemna. *See e.g.* U.S. Publication No. 2012/0276086. PCT Publication No. WO 99/54342 describes cell lines engineered to express glycoprotein-modifying glycosyl transferases (e.g., beta(1,4)-N-acetylglucosaminyltransferase III (GnTIII)) such that antibodies expressed in the engineered cell lines exhibit increased bisecting GlcNac structures which results in increased ADCC activity of the antibodies. *See also* Umaña *et al.* (1999) *Nat. Biotech.* 17:176. Alternatively, the fucose residues of the antibody may be cleaved off using a fucosidase enzyme. For example, the enzyme alpha-L-fucosidase removes fucosyl residues from antibodies. Tarentino *et al.* (1975) *Biochem.* 14:5516. Core fucosylation may also be reduced by culturing antibody-producing cells in the presence of small molecule fucose analogs, such as those described at EP2282773B1, or in the presence of castanospermine, as described at WO 08/052030.

Cleavable Moiety

[0118] In some embodiments, the CM is specific for a protease, which is useful in leveraging the dysregulated protease activity in tumor cells for targeted activatable antibody activation at the site of treatment and/or diagnosis. Numerous studies have demonstrated the correlation of aberrant protease levels, e.g., uPA, legumain, MT-SP1, matrix metalloproteases (MMPs), in solid tumors. (*See e.g.*, Murthy R V, *et al.* "Legumain expression in relation to clinicopathologic and biological variables in colorectal cancer." *Clin Cancer Res.* 11 (2005): 2293-2299; Nielsen B S, *et al.*

"Urokinase plasminogen activator is localized in stromal cells in ductal breast cancer." *Lab Invest* 81 (2001): 1485-1501; Look O R, *et al.* "In situ localization of gelatinolytic activity in the extracellular matrix of metastases of colon cancer in rat liver using quenched fluorogenic DQ-gelatin." *J Histochem Cytochem.* 51 (2003): 821-829).

[0119] A general overview of this process is discussed in US Pat. Nos. 7,666,817, 8,513,390, and 9,120,853 and International Publication Nos. WO 2016/118629 and WO 2016/149201, which are hereby incorporated by reference in their entireties. The cleavable moiety selection process is used to identify cleavable moieties that have a number of desirable characteristics. For example, the selected cleavable moieties are systemically stable (i.e., stable in the systemic circulation of a subject), are generally not susceptible to cleavage by circulating proteases such as plasmin, thrombin, tissue plasminogen activator (tPA) or a kallikrein (KLK) such as KLK-5 and/or KLK-7, are non-toxic, are generally not susceptible to cleavage at potential sites of toxicity such as the skin by proteases such as ADAM 9, ADAM 10, ADAM 17 and/or kallikreins, such as KLK-5 and KLK-7, and are active at an intended site of treatment and/or diagnosis. In some embodiments, the identified cleavable moieties are selected for proteases that are overexpressed at an intended site of therapy and/or diagnosis but are not typically expressed at or in normal, healthy or otherwise non-diseased or non-damaged tissue, and then the selected substrates are subsequently counter-screened against proteases expressed in normal, e.g., non-diseased, tissue. Exemplary proteases and/or enzymes are provided in Table 1 as indicated earlier.

[0120] In some embodiments, the cleavable moiety is selected from the group consisting of 2001 and 3001, and derivatives thereof. In some embodiments, the cleavable moiety is selected from the group consisting of 2001 (SEQ ID NO: 297), 2006 (SEQ ID NO: 300), 2007 (SEQ ID NO: 301), 2008 (SEQ ID NO: 302), 2009 (SEQ ID NO: 303), 2012 (SEQ ID NO: 305), 2011 (SEQ ID NO: 304), 2003 (SEQ ID NO: 298), 3001 (SEQ ID NO: 306), 3006 (SEQ ID NO: 313), 3007 (SEQ ID NO: 308), 3008 (SEQ ID NO: 309), 3009 (SEQ ID NO: 310), 3012 (SEQ ID NO: 312), 3011 (SEQ ID NO: 311), and 2005 (SEQ ID NO: 299). Table 3 provides additional cleavable moieties that may be used with the activatable anti-CTLA-4 antibodies disclosed herein.

Table 3. Anti-CTLA-4 Activatable Cleavable Moieties

SEQUENCE IDENTIFIER	CM Sequence
313	LSGRSDNH
314	LSGRSANPRG
315	TGRGPSWV
316	PLTGRSGG
317	TARGPSFK
318	NTLSGRSENHSG
319	NTLSGRSGNHGS
320	TSTSGRSANPRG
321	TSGRSANP
322	VHMPLGFLGP
306	AVGLLAPPGGLSGRSDNH
307	AVGLLAPPGGLSGRSDDH
308	AVGLLAPPGGLSGRSDIH
309	AVGLLAPPGGLSGRSDQH
310	AVGLLAPPGGLSGRSDTH
338	AVGLLAPPGGLSGRSDYH
339	AVGLLAPPGGLSGRSANI
340	AVGLLAPPGGLSGRSDNI
312	AVGLLAPPGGLSGRSANP
311	AVGLLAPPGGLSGRSDNP
299	AVGLLAPPSGRSANPRG
323	AVGLLAPP
324	AQNLLGMV
325	QNQALRMA
326	LAAPLGLL
327	STFPFGMF
328	ISSGLLSS
329	PAGLWLDP
330	VAGRSMRP
331	VVPEGRRS
332	ILPRSPAF
333	MVLGRSLL
334	VAGRSMRP
335	QGRAITFI
336	SPRSIMLA
337	SMLRSMPL
297	ISSGLLSGRSDNH
300	ISSGLLSGRSDDH
301	ISSGLLSGRSDIH
302	ISSGLLSGRSDQH
303	ISSGLLSGRSDTH
341	ISSGLLSGRSDYH

342	ISSGLLSGRSANI
343	ISSGLLSGRSDNI
305	ISSGLLSGRSANP
304	ISSGLLSGRSDNP
298	ISSGLLSGRSANPRG

Masking Moiety

[0121] The activatable anti-CTLA-4 antibodies provided herein comprise a masking moiety (MM). In some embodiments, the MM is an amino acid sequence that is coupled, or otherwise attached, to the anti-CTLA-4 antibody and is positioned within the activatable anti-CTLA-4 antibody construct such that the MM reduces the ability of the anti-CTLA-4 antibody to specifically bind CTLA-4. In some embodiments, the MM binds specifically to the antigen binding domain. Suitable MMs are identified using any of a variety of known techniques. For example, peptide MMs are identified using the methods described in U.S. Patent Application Publication Nos. 2009/0062142 by Daugherty *et al.* and 2012/0244154 by Daugherty *et al.*, the contents of which are hereby incorporated by reference in their entirety.

[0122] In some embodiments, the MM is selected from the group consisting of YV01 to YV66 and comprises an amino acid sequence selected from Table 4 below.

Table 4: Anti-CTLA4 Masking Moieties (MM)

SEQUENCE IDENTIFIER	MM SEQUENCE	SEQUENCE IDENTIFIER	MM SEQUENCE
1	DFSCLHSMYNVCLDP	147	EHCDVWMFGFNLCPY
2	QPCAQMYGYSMCPHT	148	EPCDYWMFGVNLCPY
3	LHCRTQMYGYNLCPY	149	EQCTMWMYGFNLCPY
4	LHCRTQLYGYNLCPY	150	ESACSLRMYEVCLQP
5	CTYSFFNVC	151	ESCASMYGYSMCPRT
6	CAQMYGYSMC	152	ESCSYWMFGYNLCPY
7	CPNHPMC	153	FSNTCPHHPMCYDYR
8	GTACTYSFFNVCLDP	154	FWNTCPHHPMCHDYK
9	FGTACPNHPMCHDWQ	155	FYQNCYPPTWCSMFS
10	SACAYWMFGVNLCPY	156	GECSYWMFGYNLCPY
11	CRTQLYGYNLC	157	GGSCMYSFFNICLDP
12	CRTQIYGYNLC	158	GGSCVYVMYNVCLDP
13	LHCRTQIYGYNLCPY	159	GHCLMHMYGYNLCPK
14	CPNHPMCHDWQ	160	GHCRMSMYEMTLCPR
15	GTACPNHPMCHDWQ	161	GISCVHIMFNFCLDP
16	CAYWMFGVNLCPY	162	GLCVMYMFGVNLCPY
17	QECHLYMYGVNLCPY	163	GSCDYWMFGYNLCPY

18	CHLYMYGVNLCPY	164	GSYCMYVMYNVCLDP
19	GQCQFYMFGYNLCPY	165	GTKCIYSFYNVCLDP
20	LSTCMYSFFNVCLDP	166	GTSTCPYHPMCHDYR
21	CLHSMYNVCLDP	167	GTTCTYSFFNVCLDP
22	CLHSMYNVC	168	GVCHFFMYGVSMCPA
23	CLHSLYNVCLDP	169	GVPCWYSMYNVCLDP
24	CLHSAYNVCLDP	170	GVSCMYSMFNICLDP
25	CMYSFFNVCLDP	171	HAKCVYSFFNVCLDP
26	CMYSFFNVC	172	HDSCMYSMYNFCLDP
27	QPCAQMYGYSMC	173	HGNTCPNHPMCHDYQ
28	CAQLYGYSMCPHT	174	HKGCLYSFYNICLDP
29	CAQMYGYSMCAHT	175	HKGCLYSFYNVCLDP
30	CAQMYGYSMCPAT	176	HLSCMYIMYNVCLDP
31	CAQMYGYSMCPHT	177	HSSCIYSMFNVCLDP
32	CPNHPLCHDWQ	178	HTNMCPYHPMCYDYK
33	CPNHPMCADWQ	179	HTPCTYSFFNVCLDP
34	CPNHPMCHAWQ	180	IMNTCPYHPMCHDYQ
35	CPNHPMCHDAQ	181	IVPCTYMMFGVCLQP
36	CPNHPMCHDWA	182	KKCDYWFYGVNLCPY
37	GTACPNHPMC	183	KNTCVYSFFNVCLDP
38	LHCRTQLYGYNLC	184	KPCAQMYGYSMCPHP
39	CRTQLYGYNLCPY	185	KPSCMYSFFNVCLDP
40	CRTQLYGYNLCAY	186	KRPCMYSFYNVCLDP
41	CRTQLYGYNLCPA	187	KTSCMYSFYNICLDP
42	FGTACPNHPLCHDWQ	188	KTTCTYSFFNVCLDP
43	CPNHPLCHDFQ	189	LDCQMYWWFGACGDM
44	CPNHPLCHDYQ	190	LHCAIYMYGYNLCPF
45	CPNHPLCPY	191	LHCPFQMYGYNLCPH
46	CPNHPLCPA	192	LHCSMYMYGFNLCPN
47	CMYSFFNVCYP	193	RECMAYMYGYNLCPY
48	CMYSFFNVCYA	194	RHCQMHMFGYDLCPY
49	CLYSFFNVCYP	195	LIHCRYVMYGMCLEP
50	CLYSFFNVCYA	196	LLPCEVMGPSRCKHD
51	FGAACPNHPICHDWQ	197	LPCHAYMYGYSLCPY
52	FGAACPNHPLCHDWQ	198	LPCLAYMYGVNLCPN
53	FGAACPNHPMCHDAQ	199	LPCMAYMFGFNLCPH
54	CLHSAYNACLDP	200	LPCNFHMFGFNLCPY
55	CAHSAYNVCLDP	201	LQCAMYMYGYNLCPY
56	CLHSAYNVCADP	202	LSSCTYSFFNVCLDP
57	CLHSAYNVCLAP	203	LTCPFQMYGYNLCPY
58	CLHSAYNVCLDA	204	LTSQCSPWYWCQIYD
59	KNTCTYVMYNVCLDP	205	LYCPYMMYGYNLCPY
60	YISDCPYHPMCHDYQ	206	LYHCTYSFYNVCLDP
61	FRNTCPYHPMCHDYR	207	LYRCIYSFYNVCLDP
62	RECHMWMFGVNLCPY	208	MGCSMRMWGMELCPE
63	AVCHMYMYGYNLCPF	209	MKCDYWLYGYNLCPY
64	RSCPQMYGYSMCPHT	210	MNHCTLHMYNICMDP
65	QPCAQMFGYSMCPHT	211	MNPECPHHPMCHNSN
66	TAKCTYSFFNVCLDP	212	MPACTYSFFNICLDP
67	DFSCLYSMYNVCLDP	213	MPQCHVIMYNLCLDP
68	DVSCMYMMYNFCLDP	214	MSTCTYSFFNVCLDP

69	CPNHPMC	215	MTCNYWFYGVNLCPY
70	CMYSFFNVCPY	216	MYCHQSMFGFRMCPD
71	CMYSFFNVCPA	217	NACAQMYGYSMCPHT
72	CTYSFFNVCPY	218	NDCDISMFDQSLCPY
73	CTYSFFNVCPA	219	NFSCVYVMFNVCLDP
74	GFPCMYSMFNVCLDP	220	NFTCALTMYEVCLDP
75	GLSCMYSMYGYCLDP	221	NLCHAFMFGFNLCPY
76	IPCDYWMFGVNLCPY	222	NLNNCPHHPMCHDYQ
77	QVCHAYMYGYNLCPY	223	NPPCMYSFFNICLDP
78	RMYCTYSFYNVCLDP	224	NSACTYSFFNVCLDP
79	ALSCMYIMYNVCLDP	225	NVCTVSMFGVMLCPS
80	DFSCMYVMFNVCLDP	226	PACATLMYSVPLCPA
81	DFSCVYSMFNVCLDP	227	PAPCMYSFYNVCLDP
82	DMNTCPNHPMCYDYR	228	PLCAEMYGYSMCPHN
83	DMNTCPRHPMCHDYH	229	PQCHLYMYGYNLCPY
84	DSRCMYVMYNVCLDP	230	PRPCMYSFYNVCLDP
85	EHLCTYSFYNVCLDP	231	QHCPFQMYGYNLCPY
86	ELSCVYSMFGFCLDP	232	QHCQMHMFGYNLCPY
87	FTNNCPYHPMCHDYL	233	QHSCMYSFFNVCLDP
88	GFSCTYIMYDVCLDP	234	QKCHSYLYGVNLCPY
89	GSSCMYSMYNVCLDP	235	QKCNMFMFGYNLCPY
90	HFSCMYIMYNVCLDP	236	QMNDCPNHPMCHDYH
91	LHCGMWMFGVNLCPK	237	QPCAQMYGYSMCPAT
92	LPCQMWMFGHNLCPH	238	QPCAQMYGYSMCPRT
93	LPCTMYMYGYNLCPY	239	RECHFFFYGVNLCPY
94	LTCHHWMFGVNLCPY	240	LNCGMFMYGYNLCPY
95	NFSCMYSMFNVCLDP	241	RLCTSYMFGYNLCPQ
96	NNHCMYSFFNICLDP	242	RLSCMYSMFNVCLDP
97	NRSCMYIMYNVCLDP	243	RNCPFVMFGVNLCPY
98	NSCTMFMFGVNLCPY	244	RNGCMYSFFNVCLDP
99	NTCELYMFGVNLCPY	245	RNGCVYSFFNVCLDP
100	QHCDMWMFGYNLCPY	246	RPCHLYMFGYNLCPD
101	QHCPMYMFGYNLCPF	247	RPCHSYMYGINLCPY
102	QVCHIQMYGFDLCPH	248	RSCDMIMFGFNLCPY
103	RACDYWMYGVNLCPY	249	RSCPMWFYGVNLCPY
104	RQCHMQMFGYDLCPF	250	RSTVCFYDFCGPWER
105	SGSCLYSFYNVCLDP	251	RTCHFYMYGVNLCPY
106	SNGCTYSFFNVCLDP	252	RTCSMVMFGVNLCPY
107	STCAQMYGYSMCPH	253	SGKCTYSFFNVCLDP
108	SYKCLYSFYNVCLDP	254	SIVCDLYWEATCLRP
109	VLYCTYVMYNVCLDP	255	SLSCTYSFFNICLDP
110	VNCGMWMFGYNLCPK	256	SMNTCPYHPMCFDYK
111	YGSCLYSFYNICLDP	257	SQCWMWMYGYNLCPK
112	YPCAQMYGYSMCPHT	258	SSSCMYSFFNVCLDP
113	AACDLWMFGVNLCPY	259	STACTYSFYNVCLDP
114	AFCTLAPYNQACIAN	260	STCAQMYGYSMCPHT
115	AGSCLYSMYNVCLDP	261	STRCVYSFYNVCLDP
116	ALCENTMYGYHLCPW	262	TACGAWMFGVNLCPY
117	ALSCMYIMYGVCLDP	263	TGACMYSFYNVCLDP
118	APVCDVLMFGFCMQP	264	TLSCMYSMYNVCLDP
119	AQVCSIMMYGTCLMP	265	TSCTVTMYQISMCPY

120	ASTCMYSFYNVCLDP	266	VGGCRHSFYNVCLDP
121	AVCEFWMFGFNLCPY	267	VHCQMYMYGYNLCPY
122	DANTCPNHPMCYDYH	268	VHNCMYSFFNVCLDP
123	DFSCIYIMFDVCLDP	269	VMCKLHMYGIPVCPK
124	DFSCMYVMYGFCLDP	270	VNFCNYSMYGICLLP
125	DFTCMYSMYNVCLDP	271	VNFCYACYCMSCVFS
126	DFTCTYSMYNVCLDP	272	VNQCTYSFFNVCLDP
127	DHYCTYIMYSICLDP	273	VPCPFHMFGYNLCPY
128	DICTNFMFGVNLCPY	274	VRCQMWMYGFNLCPH
129	DINTCPYHPMCHDYH	275	VRPCTYSFFNVCLDP
130	DKNTCPLHPMCHDYR	276	VSGCTYSFFNICLDP
131	DMNMCPNHPMCHDWH	277	YCSSWDTMTIPACNN
132	DMNSCPNHPMCHDYH	278	YDCDLSMFGIEMCPQ
133	DMNSCPNHPMCYDYR	279	YGNTCPFHPMCHDYK
134	DMNTCPNHPMCFDYR	280	YGYCMYSFFNVCLDP
135	DMNTCPNHPMCHDFQ	281	YHCTMHMFGYNLCPF
136	DMNTCPNHPMCHDYR	282	YMNTCPNHPMCFDYQ
137	DMNTCPNHPMCYDYH	283	YMNTCPYHPMCHDYL
138	DMNTCPNHPMCYDYK	284	YMNTCPYHPMCHDYR
139	DMSTCPNHPMCHDYM	285	YNNCTYSFFNVCLDP
140	DRNMCPYHPMCYDYR	286	YPGCQYSFFNVCLDP
141	DSCAFMMFGVNLCPY	287	YRSCTHIMYNVCLDP
142	DSCRSVFDMVWNCWN	288	YSFCDMLMYDVCLVP
143	DTPNCPHHPMCHNHM	289	YSIDCGLSWWCGGMT
144	DVSCLYVMYSVCLDP	290	YSTTCPYHPMCHDYH
145	DWCASMMFGYNLCPY	291	YVNTCPHHPMCHDYH
146	EFSCMYSMFNVCLDP	292	YVNTCPYHPMCHDYN

[0123] In some embodiments, the K_d of the activatable anti-CTLA-4 antibody, comprising a MM disclosed herein, towards the target is at least 2, 3, 4, 5, 10, 25, 50, 100, 250, 500, 1,000 times greater than, or between 5-10, 10-100, 10-200, 10-500, 10-1,000 times greater than the K_d of the AB not modified with a MM or of the parental AB towards the target.

[0124] In some embodiments, the MM is not a natural binding partner of the activatable antibody. In some embodiments, the MM contains no or substantially no homology to any natural binding partner of the activatable antibody. In some embodiments, the MM is no more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or 80% identical to any natural binding partner of the activatable antibody. In some embodiments, the MM is no more than 50%, 25%, 20%, or 10% identical to any natural binding partner of the activatable antibody. In some embodiments, the MM is no more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or 80% identical to human CTLA-4. In some embodiments, the MM is no more than 50%, 25%, 20%, or 10% identical to human CTLA-4.

Exemplary Activatable anti-CTLA-4 Antibodies

[0125] Particular antibodies described herein are activatable anti-CTLA-4 antibodies comprising any combination of the masking moieties, cleavable moieties, light chain variable domains (VL) (or the corresponding CDRs), and heavy chain variable domains (VH) (or the corresponding CDRs) provided in Tables 2-6. In some embodiments, the activatable anti-CTLA-4 antibody comprises a light chain comprising YV01 (SEQ ID NO: 1) as the masking moiety, LSGRSDNH (SEQ ID NO: 313) as the cleavable moiety, and the light chain variable domain (VL) of ipilimumab (SEQ ID NO: 344). In some embodiments, the activatable anti-CTLA-4 antibody comprises a light chain comprising YV01 (SEQ ID NO: 1) as the masking moiety, ISSGLLSGRSDNH (2001) (SEQ ID NO: 297) as the cleavable moiety, and the CDRs of the light chain variable domain (VL) of ipilimumab (SEQ ID NOs: 560, 561, and 562, respectively). In some embodiments, the activatable anti-CTLA-4 antibody comprises the heavy chain variable domain (VH) of ipilimumab (SEQ ID NO: 345) or just the corresponding CDRs (SEQ ID NOs: 557, 558, and 559).

[0126] In some embodiments, the activatable anti-CTLA-4 comprises YV39 (SEQ ID NO: 39) as the masking moiety, and ISSGLLSGRSDNP ("2011") (SEQ ID NO: 304) as the cleavable moiety, and the heavy and light chain variable domains of ipilimumab ((SEQ ID NOs: 345 and 344, respectively), wherein the MM and CM are linked to the VL in the arrangement MM-CM-VL.

[0127] In some embodiments, the activatable anti-CTLA-4 antibody includes a signal peptide. The signal peptide can be linked to the activatable anti-CTLA-4 antibody by a spacer. In some embodiments, the spacer is conjugated to the activatable antibody in the absence of a signal peptide. In some embodiments, the spacer is joined directly to the MM of the activatable antibody. In some embodiments, the spacer has amino acid sequence QGQSGS (SEQ ID NO: 546). In some embodiments, an activatable antibody comprises a spacer of sequence QGQSGS (SEQ ID NO: 546) joined directly to a MM sequence CRTQLYGYNLCPY (YV39) (SEQ ID NO: 39) in the structural arrangement from N-terminus to C-terminus of "spacer-MM-CM-VL" or "spacer-MM-CM-AB."

[0128] In some embodiments, the activatable anti-CTLA-4 antibody comprises a linker peptide (LP) between the MM and the CM. In some embodiments, the activatable anti-CTLA-4 antibody comprises a linker peptide between the CM and the antibody or antigen

binding domain thereof (AB). In some embodiments, the activatable anti-CTLA-4 antibody comprises a first linker peptide (LP1) and a second linker peptide (LP2), and wherein the activatable anti-CTLA-4 antibody has the structural arrangement from N-terminus to C-terminus as follows: MM-LP1-CM-LP2-AB. In some embodiments, the light chain of the activatable anti-CTLA-4 antibody has the structural arrangement from N-terminus to C-terminus as follows: MM-LP1-CM-LP2-VL. In some embodiments, the two linker peptides need not be identical to each other. Examples of linker peptides that may be used with the activatable anti-CTLA-4 antibodies as disclosed herein are provided in U.S. Patent Publication No. 2016/0193332 and International Publication No. WO 2016/149201, *ibid.*

[0129] The disclosure also comprises a modified anti-CTLA-4 antibody that comprises a MM that is joined to the light chain of the antibody via a non-protease cleavable linker. In some embodiments, the non-protease cleavable linker comprises the amino acid sequence set forth in SEQ ID NO: 570. In some embodiments, such a modified anti-CTLA-4 antibody has a light chain comprising YV39 and a non-protease cleavable linker. In some embodiments, the light chain of the modified anti-CTLA-4 antibody comprises the amino acid sequence:

QGQSGSCRTQLYGYNLCPYGGGSSGGSGGSGGSGGGSGGGSGGSEIVLT
QSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSR
ATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKV
EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC (SEQ ID NO: 530) or

CRTQLYGYNLCPYGGGSSGGSGGSGGSGGGSGGGSGGSEIVLTQSPGTL
SLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPD
RFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTV
AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC (SEQ ID NO: 531).

[0130] Linkers suitable for use in compositions described herein are generally ones that provide flexibility of the activatable anti-CTLA-4 antibody to facilitate the inhibition of the binding of the activatable antibody to the target. Such linkers are generally referred to as flexible linkers (also referred to as linker peptides herein). Suitable linkers can be readily selected and can be of any of a suitable of different lengths, such as from 1 amino acid (e.g. , Gly) to 20 amino acids, from 2 amino acids to 15 amino acids, from 3 amino acids to 12 amino acids, including 4 amino acids to 10 amino acids, 5 amino acids to 9 amino acids, 6 amino acids to 8 amino acids, or 7 amino acids to 8 amino acids, and may

be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids in length.

[0131] Exemplary flexible linkers include glycine polymers (G)n, glycine-serine polymers (including, for example, (GS)n, (GSGGS)n (GSGGS is SEQ ID NO: 534) and (GGGS)n (GGGS is SEQ ID NO: 535), where n is an integer of at least one), glycine-alanine polymers, alanine- serine polymers, and other flexible linkers known in the art. Glycine and glycine-serine polymers are relatively unstructured, and therefore may be able to serve as a neutral tether between components. Glycine accesses significantly more phi-psi space than even alanine, and is much less restricted than residues with longer side chains (*see* Scheraga, *Rev. Computational Chem.* 11173-142 (1992)). Exemplary flexible linkers include, but are not limited to Gly-Gly-Ser-Gly (SEQ ID NO: 536), Gly-Gly-Ser-Gly-Gly (SEQ ID NO: 537), Gly-Ser-Gly-Ser-Gly (SEQ ID NO: 538), Gly-Ser-Gly-Gly-Gly (SEQ ID NO: 539), Gly- Gly-Gly-Ser-Gly (SEQ ID NO: 540), Gly-Ser-Ser-Ser-Gly (SEQ ID NO: 541), and the like. The ordinarily skilled artisan will recognize that design of an activatable antibodies can include linkers that are all or partially flexible, such that the linker can include a flexible linker as well as one or more portions that confer less flexible structure to provide for a desired activatable antibodies structure.

[0132] In some embodiments, the activatable anti-CTLA-4 antibodies comprise the VL and VH (or the corresponding CDRs) of ipilimumab and a combination of MMs and CMs provided in Table 5 below, such that any MM in column 2 can be combined with any CM in column 4.

Table 5. Activatable anti-CTLA-4 Antibody Combinations

SEQ ID NO.	Masking Moiety (MM)	SEQ ID NO.	Cleavable Moiety (CM)
1	(YV01) DFSCLHSMYNVCLDP	313	LSGRSDNH
2	(YV02) QPCAQMYGYSMCPHT	314	LSGRSANPRG
3	(YV03) LHCRTQMYGYNLCPY	315	TGRGPSWV
4	(YV04) LHCRTQLYGYNLCPY	316	PLTGRSGG
5	(YV05) CTYSFFNVC	317	TARGPSFK
6	(YV06) CAQMYGYSMC	318	NTLSGRSENHSG
7	(YV07) CPNHPMC	319	NTLSGRSGNHGS
8	(YV08) GTACTYSFFNVCLDP	320	TSTSGRSANPRG
9	(YV09) FGTACPNHPMCHDWQ	321	TSGRSANP
10	(YV10) SACAYWMFGVNLCPY	322	VHMPLGFLGP
11	(YV11) CRTQLYGYNLC	323	AVGLLAPP
12	(YV12) CRTQIYGYNLC		
13	(YV13) LHCRTQIYGYNLCPY		

14	(YV14) CPNHPMCHDWQ	324	AQNLLGMV
15	(YV15) GTACPNHPMCHDWQ	325	QNQALRMA
16	(YV16) CAYWMFGVNLCPY	326	LAAPLGLL
17	(YV17) QECHLYMYGVNLCPY	327	STFPFGMF
18	(YV18) CHLYMYGVNLCPY	328	ISSGLLSS
19	(YV19) GQCQFYMFGYNLCPY	329	PAGLWLDP
20	(YV20) LSTCMYSFFNVCLDP	330	VAGRSMRP
21	(YV21) CLHSMYNVCLDP	331	VVPEGRRS
22	(YV22) CLHSMYNVC	332	ILPRSPAF
23	(YV23) CLHSLYNVCLDP	333	MVLGRSLL
24	(YV24) CLHSAYNVCLDP	334	VAGRSMRP
25	(YV25) CMYSFFNVCLDP	335	QGRAITFI
26	(YV26) CMYSFFNVC	336	SPRSIMLA
27	(YV27) QPCAQMYGYSMC	337	SMLRSMPL
28	(YV28) CAQLYGYSMCPHT	297	ISSGLLSGRSDNH
29	(YV29) CAQMYGYSMCAHT	300	ISSGLLSGRSDDH
30	(YV30) CAQMYGYSMCPAT	301	ISSGLLSGRSDIH
31	(YV31) CAQMYGYSMCPHT	302	ISSGLLSGRSDQH
32	(YV32) CPNHPLCHDWQ	303	ISSGLLSGRSDTH
33	(YV33) CPNHPMCADWQ	341	ISSGLLSGRSDYH
35	(YV34) CPNHPMCHAWQ	342	ISSGLLSGRSANI
35	(YV35) CPNHPMCHDAQ	343	ISSGLLSGRSDNI
36	(YV36) CPNHPMCHDWA	305	ISSGLLSGRSANP
37	(YV37) GTACPNHPMC	304	ISSGLLSGRSDNP
38	(YV38) LHCRTQLYGYNLC	298	ISSGLLSGRSANPRG
39	(YV39) CRTQLYGYNLCPY	306	AVGLLAPPGGLSGRSDNH
40	(YV40) CRTQLYGYNLCAY	307	AVGLLAPPGGLSGRSDDH
41	(YV41) CRTQLYGYNLCPA	308	AVGLLAPPGGLSGRSDIH
42	(YV42) FGTACPNHPLCHDWQ	309	AVGLLAPPGGLSGRSDQH
43	(YV43) CPNHPLCHDFQ	310	AVGLLAPPGGLSGRSDTH
44	(YV44) CPNHPLCHDYQ	338	AVGLLAPPGGLSGRSDYH
45	(YV45) CPNHPLCPY	339	AVGLLAPPGGLSGRSANI
46	(YV46) CPNHPLCPA	340	AVGLLAPPGGLSGRSDNI
47	(YV47) CMYSFFNVCYP	312	AVGLLAPPGGLSGRSANP
48	(YV48) CMYSFFNVCYA	311	AVGLLAPPGGLSGRSDNP
49	(YV49) CLYSFFNVCYP	299	AVGLLAPPSGRSANPRG
50	(YV50) CLYSFFNVCYA		
51	(YV51) FGAACPNHPICHDWQ		
52	(YV52) FGAACPNHPLCHDWQ		
53	(YV53) FGAACPNHPMCHDAQ		
54	(YV54) CLHSAYNACLDP		
55	(YV55) CAHSAYNVCLDP		
56	(YV56) CLHSAYNVCADP		
57	(YV57) CLHSAYNVCLAP		
58	(YV58) CLHSAYNVCLDA		
59	(YV60) KNTCTYVMYNVCLDP		
60	(YV61) YISDCPYHPMCHDYQ		
61	(YV62) FRNTCPYHPMCHDYR		
62	(YV63) RECHMWMFGVNLCPY		
63	(YV64) AVCHMYMYGYNLCPF		
64	(YV65) RSCPQMYGYSMCPHT		
65	(YV66) QPCAQMFGYSMCPHT		

[0133] In some embodiments, the activatable anti-CTLA-4 antibodies comprise the specific combination of MMs and CMs provided in Table 6 below.

Table 6. Exemplary Activatable Anti-CTLA-4 Antibody Combination

Comb. No.	Masking Moiety (MM)	Cleavable Moiety (CM)
1	CRTQLYGYNLCPY (SEQ ID NO: 39)	ISSGLLSGRSDNH (SEQ ID NO: 297)
2	CRTQLYGYNLCPY (SEQ ID NO: 39)	ISSGLLSGRSDNP (SEQ ID NO: 304)
3	CRTQLYGYNLCPY (SEQ ID NO: 39)	ISSGLLSGRSANP (SEQ ID NO: 305)
4	CRTQLYGYNLCPY (SEQ ID NO: 39)	ISSGLLSGRSDQH (SEQ ID NO: 302)
5	CRTQLYGYNLCPY (SEQ ID NO: 39)	ISSGLLSGRSDDH (SEQ ID NO: 300)
6	CRTQLYGYNLCPY (SEQ ID NO: 39)	ISSGLLSGRSDTH (SEQ ID NO: 303)
7	LHCRTQMYGYNLCPY (SEQ ID NO: 3)	ISSGLLSGRSDNH (SEQ ID NO: 297)
8	LHCRTQMYGYNLCPY (SEQ ID NO: 3)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
9	LHCRTQMYGYNLCPY (SEQ ID NO: 3)	ISSGLLSGRSDDH (SEQ ID NO: 300)
10	LHCRTQMYGYNLCPY (SEQ ID NO: 3)	ISSGLLSGRSDIH (SEQ ID NO: 301)
11	LHCRTQMYGYNLCPY (SEQ ID NO: 3)	ISSGLLSGRSDQH (SEQ ID NO: 302)
12	LHCRTQMYGYNLCPY (SEQ ID NO: 3)	ISSGLLSGRSDTH (SEQ ID NO: 303)
13	CAQMYGYSMC (SEQ ID NO: 06)	ISSGLLSGRSDNH (SEQ ID NO: 297)
14	CAQMYGYSMC (SEQ ID NO: 06)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
15	FGTACPNHPMCHDWQ (SEQ ID NO: 09)	ISSGLLSGRSDNH (SEQ ID NO: 297)
16	FGTACPNHPMCHDWQ (SEQ ID NO: 09)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
17	CLHSLYNVCLDP (SEQ ID NO: 23)	ISSGLLSGRSDNH (SEQ ID NO: 297)
18	CLHSLYNVCLDP (SEQ ID NO: 23)	ISSGLLSGRSDDH (SEQ ID NO: 300)
19	CLHSLYNVCLDP (SEQ ID NO: 23)	ISSGLLSGRSDIH (SEQ ID NO: 301)
20	CLHSLYNVCLDP (SEQ ID NO: 23)	ISSGLLSGRSDQH (SEQ ID NO: 302)

21	CLHSLYNVCLDP (SEQ ID NO: 23)	ISSGLLSGRSDTH (SEQ ID NO: 303)
22	CLHSLYNVCLDP (SEQ ID NO: 23)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
23	CLHSAYNVCLDP (SEQ ID NO: 24)	ISSGLLSGRSDNH (SEQ ID NO: 297)
24	CLHSAYNVCLDP (SEQ ID NO: 24)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
25	QPCAQMYGYSMC (SEQ ID NO: 27)	ISSGLLSGRSDNH (SEQ ID NO: 297)
26	QPCAQMYGYSMC (SEQ ID NO: 27)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
27	CAQMYGYSMCAHT (SEQ ID NO: 29)	ISSGLLSGRSDNH (SEQ ID NO: 297)
28	CAQMYGYSMCAHT (SEQ ID NO: 29)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
29	CPNHPLCHDWQ (SEQ ID NO: 32)	ISSGLLSGRSDNH (SEQ ID NO: 297)
30	CPNHPLCHDWQ (SEQ ID NO: 32)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
31	CPNHPMCADWQ (SEQ ID NO: 33)	ISSGLLSGRSDNH (SEQ ID NO: 297)
32	CPNHPMCADWQ (SEQ ID NO: 33)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
33	CPNHPMCHDAQ (SEQ ID NO: 35)	ISSGLLSGRSDNH (SEQ ID NO: 297)
34	CPNHPMCHDAQ (SEQ ID NO: 35)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
35	CRTQLYGYNLCPY (SEQ ID NO: 39)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
36	CRTQLYGYNLCPA (SEQ ID NO: 41)	ISSGLLSGRSDNH (SEQ ID NO: 297)
37	CRTQLYGYNLCPA (SEQ ID NO: 41)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
38	FGAACPNHPICHDWQ (SEQ ID NO: 51)	ISSGLLSGRSDNH (SEQ ID NO: 297)
39	FGAACPNHPICHDWQ (SEQ ID NO: 51)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
40	FGAACPNHPLCHDWQ (SEQ ID NO: 52)	ISSGLLSGRSDNH (SEQ ID NO: 297)
41	FGAACPNHPLCHDWQ (SEQ ID NO: 52)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
42	FGAACPNHPMCHDAQ (SEQ ID NO: 53)	ISSGLLSGRSDNH (SEQ ID NO: 297)
43	FGAACPNHPMCHDAQ (SEQ ID NO: 53)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
44	CLHSAYNACLDP (SEQ ID NO: 54)	ISSGLLSGRSDNH (SEQ ID NO: 297)

45	CLHSAYNACLDP (SEQ ID NO: 54)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
46	CAHSAYNVCLDP (SEQ ID NO: 55)	ISSGLLSGRSDNH (SEQ ID NO: 297)
47	CAHSAYNVCLDP (SEQ ID NO: 55)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
48	CLHSAYNVCADP (SEQ ID NO: 56)	ISSGLLSGRSDNH (SEQ ID NO: 297)
49	CLHSAYNVCADP (SEQ ID NO: 56)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
50	CLHSAYNVCLAP (SEQ ID NO: 57)	ISSGLLSGRSDNH (SEQ ID NO: 297)
51	CLHSAYNVCLAP (SEQ ID NO: 57)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
52	CLHSAYNVCLDA (SEQ ID NO: 58)	ISSGLLSGRSDNH (SEQ ID NO: 297)
53	CLHSAYNVCLDA (SEQ ID NO: 58)	AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306)
54	YISDCPYHPMCHDYQ (SEQ ID NO: 60)	ISSGLLSGRSDNH (SEQ ID NO: 297)
55	FRNTCPYHPMCHDYR (SEQ ID NO: 61)	ISSGLLSGRSDNH (SEQ ID NO: 297)
56	AVCHMYMYGYNLCPF (SEQ ID NO: 63)	ISSGLLSGRSDNH (SEQ ID NO: 297)
57	RSCPQMYGYSMCPHT (SEQ ID NO: 64)	ISSGLLSGRSANP (SEQ ID NO: 305)
58	QPCAQMFGYSMCPHT (SEQ ID NO: 65)	ISSGLLSGRSANP (SEQ ID NO: 305)

[0134] In some embodiments, the activatable anti-CTLA-4 antibodies described herein also include an agent conjugated to the activatable antibody. In some embodiments, the conjugated agent is a therapeutic agent, such as an anti-neoplastic agent. In some embodiments, the agent is conjugated to a carbohydrate moiety of the activatable antibody, preferably where the carbohydrate moiety is located outside the antigen-binding region of the antibody or antigen-binding fragment in the activatable antibody. In some embodiments, the agent is conjugated to a sulfhydryl group of the antibody or antigen-binding fragment in the activatable antibody. In some embodiments, the agent is conjugated to an amino group of the antibody or antigen-binding fragment of the activatable antibody. In some embodiments, the agent is conjugated to a carboxylic acid group of the antibody or antigen-binding fragment of the activatable antibody.

[0135] In some embodiments, the agent is a cytotoxic agent such as a toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

[0136] In some embodiments, the conjugated activatable antibody can be modified for site-specific conjugation through modified amino acid sequences inserted or otherwise included in the activatable antibody sequence. These modified amino acid sequences are designed to allow for controlled placement and/or dosage of the conjugated agent within a conjugated activatable anti-CTLA-4 antibody. For example, the activatable antibody can be engineered to include cysteine substitutions at positions on light and heavy chains that provide reactive thiol groups and do not negatively impact protein folding and assembly, nor alter antigen binding. In some embodiments, the activatable antibody can be engineered to include or otherwise introduce one or more non-natural amino acid residues within the activatable antibody to provide suitable sites for conjugation. In some embodiments, the activatable antibody can be engineered to include or otherwise introduce enzymatically activatable peptide sequences within the activatable antibody sequence.

[0137] In some embodiments, the agent is a detectable moiety such as, for example, a label or other marker. For example, the agent is or includes a radiolabeled amino acid, one or more biotinyl moieties that can be detected by marked avidin (e.g., streptavidin containing a fluorescent marker or enzymatic activity that can be detected by optical or calorimetric methods), one or more radioisotopes or radionuclides, one or more fluorescent labels, one or more enzymatic labels, and/or one or more chemiluminescent agents. In some embodiments, detectable moieties are attached by linker molecules.

[0138] Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 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.*, *Science* 238: 1098 (1987).

Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. (See WO94/11026).

[0139] Those of ordinary skill in the art will recognize that a large variety of possible moieties can be coupled to the resultant antibodies of the invention. (*See, e.g.*, "Conjugate Vaccines", Contributions to Microbiology and Immunology, J. M. Cruse and R. E. Lewis, Jr (eds), Carger Press, New York, (1989), the entire contents of which are incorporated herein by reference).

II. Uses of Anti-CTLA-4 Activatable Antibodies

[0140] Therapeutic formulations of the invention, which include an activatable anti-CTLA-4 antibody, are used to prevent, treat or otherwise ameliorate a disease or disorder, including but not limited to, a disease or disorder associated with aberrant CTLA-4 expression and/or activity. For example, therapeutic formulations of the invention, which include an activatable anti-CTLA-4 antibody, are used as cancer immunotherapy, e.g., potentiating an endogenous immune response in a subject afflicted with a cancer so as to thereby treat the subject, which method comprises administering to the subject therapeutically effective amount of any of the activatable anti-CTLA-4 antibodies described herein.

[0141] Examples of cancers that may be treated using the immunotherapeutic methods of the disclosure include bone cancer, pancreatic cancer, skin cancer, cancer of the head or neck, breast cancer, lung cancer, cutaneous or intraocular malignant melanoma, unresectable or metastatic melanoma, renal cancer, uterine cancer, ovarian cancer, colorectal cancer, colon cancer, rectal cancer, cancer of the anal region, stomach cancer, testicular cancer, uterine cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system, cancer of the thyroid gland, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, a hematological malignancy, solid tumors of childhood, lymphocytic lymphoma, cancer of the bladder, cancer of the kidney or ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor,

brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, environmentally induced cancers including those induced by asbestos, metastatic cancers, and any combinations of said cancers. In some embodiments, the cancer is selected from MEL, RCC, squamous NSCLC, non-squamous NSCLC, CRC, CRPC, squamous cell carcinoma of the head and neck, and carcinomas of the esophagus, ovary, gastrointestinal tract and breast. The present methods are also applicable to treatment of metastatic cancers.

[0142] Other cancers include hematologic malignancies including, for example, multiple myeloma, B-cell lymphoma, Hodgkin lymphoma/primary mediastinal B-cell lymphoma, non-Hodgkin's lymphomas, acute myeloid lymphoma, chronic myelogenous leukemia, chronic lymphoid leukemia, follicular lymphoma, diffuse large B-cell lymphoma, Burkitt's lymphoma, immunoblastic large cell lymphoma, precursor B-lymphoblastic lymphoma, mantle cell lymphoma, acute lymphoblastic leukemia, mycosis fungoides, anaplastic large cell lymphoma, T-cell lymphoma, and precursor T-lymphoblastic lymphoma, and any combinations of said cancers.

[0143] Increased proteolysis is known to be a hallmark of cancer. (*See e.g.*, Affara N I, *et al.* "Delineating protease functions during cancer development." *Methods Mol Biol.* 539 (2009): 1-32). Progression, invasion and metastasis of tumors result from several interdependent processes in which proteases are implicated. This process is described generally in U.S. Publication No. 2016/0193332 A1, which is incorporated in its entirety.

[0144] In some embodiments of these methods for treating a cancer subject, the activatable antibodies of the present invention, e.g. activatable ipilimumab, is administered to the subject as monotherapy. In some embodiments, stimulation or blockade of immunomodulatory targets may be effectively combined with standard cancer treatments, including chemotherapeutic regimes, radiation, surgery, hormone deprivation and angiogenesis inhibitors. The activatable anti-CTLA-4 antibody can be linked to an anti-neoplastic agent (as an immunoconjugate) or can be administered separately from the agent. In the latter case (separate administration), the antibody can be administered before, after or concurrently with the agent or can be co-administered with other known therapeutic agents. Chemotherapeutic drugs include, among others, doxorubicin (ADRIAMYCIN®), cisplatin, carboplatin, bleomycin sulfate, carmustine, chlorambucil (LEUKERAN®), cyclophosphamide (CYTOXAN®; NEOSAR®),

lenalidomide (REVLIMID®), bortezomib (VELCADE®), dexamethasone, mitoxantrone, etoposide, cytarabine, bendamustine (TREANDA®), rituximab (RITUXAN®), ifosfamide, vincristine (ONCOVIN®), fludarabine (FLUDARA®), thalidomide (THALOMID®), alemtuzumab (CAMPATH®, ofatumumab (ARZERRA®), everolimus (AFINITOR®, ZORTRESS®), and carfilzomib (KYPROLISTM). Co-administration of anti-cancer agents that operate via different mechanisms can help overcome the development of resistance to drugs or changes in the antigenicity of tumor cells.

[0145] Activatable anti-CTLA-4 antibodies of the present invention, such as the activatable ipilimumab, may also be used in combination with other immunomodulatory agents, such as antibodies against other immunomodulatory receptors or their ligands. Several other co-stimulatory and inhibitory receptors and ligands that regulate T cell responses have been identified. Examples of stimulatory receptors include Inducible T cell Co-Stimulator (ICOS), CD137 (4-1BB), CD134 (OX40), CD27, Glucocorticoid-Induced TNFR-Related protein (GITR), and Herpes Virus Entry Mediator (HVEM), whereas examples of inhibitory receptors include Programmed Death-1 (PD-1), Programmed Death Ligand-1 (PD-L1), B and T Lymphocyte Attenuator (BTLA), T cell Immunoglobulin and Mucin domain-3 (TIM-3), Lymphocyte Activation Gene-3 (LAG-3), adenosine A2a receptor (A2aR), Killer cell Lectin-like Receptor G1 (KLRG-1), Natural Killer Cell Receptor 2B4 (CD244), CD160, T cell Immunoreceptor with Ig and ITIM domains (TIGIT), and the receptor for V-domain Ig Suppressor of T cell Activation (VISTA). Mellman *et al.* (2011) *Nature* 480:480; Pardoll (2012) *Nat. Rev. Cancer* 12: 252; Baitsch *et al.* (2012) *PloS One* 7:e30852.

[0146] Anti-PD-1 antibodies OPDIVO® (nivolumab) and KEYTRUDA® (pembrolizumab), as well as anti-PD-L1 antibody TECENTRIQ® (atezolizumab), have been approved for use in treating cancer, and may be combined with the activatable anti-CLTA-4 antibodies of the present invention, e.g. activatable ipilimumab. These receptors and their ligands provide targets for therapeutics designed to stimulate, or prevent the suppression, of an immune response so as to thereby attack tumor cells. Weber (2010) *Semin. Oncol.* 37:430; Flies *et al.* (2011) *Yale J. Biol. Med.* 84:409; Mellman *et al.* (2011) *Nature* 480:480; Pardoll (2012) Nat. Rev. Cancer 12:252. Stimulatory receptors or receptor ligands are targeted by agonist agents, whereas inhibitory receptors or receptor ligands are targeted by blocking agents. Among the most promising approaches to

enhancing immunotherapeutic anti-tumor activity is the blockade of so-called "immune checkpoints," which refer to the plethora of inhibitory signaling pathways that regulate the immune system and are crucial for maintaining self-tolerance and modulating the duration and amplitude of physiological immune responses in peripheral tissues in order to minimize collateral tissue damage. *See e.g.* Weber (2010) *Semin. Oncol.* 37:430; Pardoll (2012) *Nat. Rev. Cancer* 12:252. Because many of the immune checkpoints are initiated by ligand-receptor interactions, they can be readily blocked by antibodies or modulated by recombinant forms of ligands or receptors.

Anti-PD-1 Antibodies Useful for the Invention

[0147] Any anti-PD-1 antibody that is known in the art can be used in the presently described methods. In particular, various human monoclonal antibodies that bind specifically to PD-1 with high affinity have been disclosed in U.S. Patent No. 8,008,449. Each of the anti-PD-1 humanized antibodies disclosed in U.S. Patent No. 8,008,449 has been demonstrated to exhibit one or more of the following characteristics: (a) binds to human PD-1 with a K_D of 1 x 10^{-7} M or less, as determined by surface plasmon resonance using a Biacore biosensor system; (b) does not substantially bind to human CD28, CTLA-4 or ICOS; (c) increases T-cell proliferation in a Mixed Lymphocyte Reaction (MLR) assay; (d) increases interferon-γ production in an MLR assay; (e) increases IL-2 secretion in an MLR assay; (f) binds to human PD-1 and cynomolgus monkey PD-1; (g) inhibits the binding of PD-L1 and/or PD-L2 to PD-1; (h) stimulates antigen-specific memory responses; (i) stimulates antibody responses; and (j) inhibits tumor cell growth *in vivo*. Anti-PD-1 antibodies usable in the present invention include monoclonal antibodies that bind specifically to human PD-1 and exhibit at least one, in some embodiments, at least five, of the preceding characteristics.

[0148] Other anti-PD-1 monoclonal antibodies have been described in, for example, U.S. Patent Nos. 6,808,710, 7,488,802, 8,168,757 and 8,354,509, US Publication No. 2016/0272708, and PCT Publication Nos. WO 2012/145493, WO 2008/156712, WO 2015/112900, WO 2012/145493, WO 2015/112800, WO 2014/206107, WO 2015/35606, WO 2015/085847, WO 2014/179664, WO 2017/020291, WO 2017/020858, WO 2016/197367, WO 2017/024515, WO 2017/025051, WO 2017/123557, WO 2016/106159, WO 2014/194302, WO 2017/040790, WO 2017/133540, WO

2017/132827, WO 2017/024465, WO 2017/025016, WO 2017/106061, each of which is incorporated by reference in its entirety.

[0149] In some embodiments, the anti-PD-1 antibody is selected from the group consisting of nivolumab (also known as "OPDIVO®"; formerly designated 5C4, BMS-936558, MDX-1106, or ONO-4538), pembrolizumab (Merck, also known as "KEYTRUDA®", lambrolizumab, and MK-3475. *See* WO2008156712A1), PDR001 (Novartis; *see* WO 2015/112900), MEDI-0680 (AstraZeneca; AMP-514; *see* WO 2012/145493), REGN-2810 (Regeneron; *see* WO 2015/112800), JS001 (TAIZHOU JUNSHI PHARMA; *see* Si-Yang Liu et al., *J. Hematol. Oncol. 10*:136 (2017)), BGB-A317 (Beigene; *see* WO 2015/35606 and US 2015/0079109), INCSHR1210 (SHR-1210; Jiangsu Hengrui Medicine; *see* WO 2015/085847; Si-Yang Liu et al., *J. Hematol. Oncol. 10*:136 (2017)), TSR-042 (ANB011; Tesaro Biopharmaceutical; *see* WO2014/179664), GLS-010 (WBP3055; Wuxi/Harbin Gloria Pharmaceuticals; *see* Si-Yang Liu et al., *J. Hematol. Oncol. 10*:136 (2017)), AM-0001 (Armo), STI-1110 (Sorrento Therapeutics; *see* WO 2014/194302), AGEN2034 (Agenus; *see* WO 2017/040790), and MGD013 (Macrogenics).

[0150] In one embodiment, the anti-PD-1 antibody is nivolumab. Nivolumab is a fully human IgG4 (S228P) PD-1 immune checkpoint inhibitor antibody that selectively prevents interaction with PD-1 ligands (PD-L1 and PD-L2), thereby blocking the down-regulation of antitumor T-cell functions (U.S. Patent No. 8,008,449; Wang et al., 2014 *Cancer Immunol Res. 2(9)*:846-56).

[0151] In another embodiment, the anti-PD-1 antibody is pembrolizumab. Pembrolizumab is a humanized monoclonal IgG4 antibody directed against human cell surface receptor PD-1 (programmed death-1 or programmed cell death-1). Pembrolizumab is described, for example, in U.S. Patent Nos. 8,354,509 and 8,900,587; see also www.cancer.gov/drugdictionary?cdrid=695789 (last accessed: December 14, 2014). Pembrolizumab has been approved by the FDA for the treatment of relapsed or refractory melanoma.

[0152] Anti-PD-1 antibodies usable in the disclosed methods also include isolated antibodies that bind specifically to human PD-1 and cross-compete for binding to human PD-1 with any anti-PD-1 antibody disclosed herein, e.g., nivolumab (*see, e.g.*, U.S. Patent No. 8,008,449 and 8,779,105; WO 2013/173223). In some embodiments, the anti-PD-1

antibody binds the same epitope as any of the anti-PD-1 antibodies described herein, e.g., nivolumab. The ability of antibodies to cross-compete for binding to an antigen indicates that these monoclonal antibodies bind to the same epitope region of the antigen and sterically hinder the binding of other cross-competing antibodies to that particular epitope region. These cross-competing antibodies are expected to have functional properties very similar those of the reference antibody, *e.g.*, nivolumab, by virtue of their binding to the same epitope region of PD-1. Cross-competing antibodies can be readily identified based on their ability to cross-compete with nivolumab in standard PD-1 binding assays such as Biacore analysis, ELISA assays or flow cytometry (*see, e.g.*, WO 2013/173223).

[0153] In certain embodiments, the antibodies that cross-compete for binding to human PD-1 with, or bind to the same epitope region of human PD-1 antibody, nivolumab, are monoclonal antibodies. For administration to human subjects, these cross-competing antibodies are chimeric antibodies, engineered antibodies, or humanized or human antibodies. Such chimeric, engineered, humanized or human monoclonal antibodies can be prepared and isolated by methods well known in the art.

[0154] Anti-PD-1 antibodies usable in the methods of the disclosed invention also include antigen-binding portions of the above antibodies. It has been amply demonstrated that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody.

[0155] Anti-PD-1 antibodies suitable for use in the disclosed methods or compositions are antibodies that bind to PD-1 with high specificity and affinity, block the binding of PD-L1 and or PD-L2, and inhibit the immunosuppressive effect of the PD-1 signaling pathway. In any of the compositions or methods disclosed herein, an anti-PD-1 "antibody" includes an antigen-binding portion or fragment that binds to the PD-1 receptor and exhibits the functional properties similar to those of whole antibodies in inhibiting ligand binding and up-regulating the immune system. In certain embodiments, the anti-PD-1 antibody or antigen-binding portion thereof cross-competes with nivolumab for binding to human PD-1.

Anti-PD-L1 Antibodies Useful for the Invention

[0156] Any anti-PD-L1 antibody can be used in the methods of the present disclosure. Examples of anti-PD-L1 antibodies useful in the methods of the present disclosure include the antibodies disclosed in US Patent No. 9,580,507. Each of the anti-PD-L1

human monoclonal antibodies disclosed in U.S. Patent No. 9,580,507 have been demonstrated to exhibit one or more of the following characteristics: (a) binds to human PD-L1 with a K_D of 1 x 10^{-7} M or less, as determined by surface plasmon resonance using a Biacore biosensor system; (b) increases T-cell proliferation in a Mixed Lymphocyte Reaction (MLR) assay; (c) increases interferon-γ production in an MLR assay; (d) increases IL-2 secretion in an MLR assay; (e) stimulates antibody responses; and (f) reverses the effect of T regulatory cells on T cell effector cells and/or dendritic cells. Anti-PD-L1 antibodies usable in the present invention include monoclonal antibodies that bind specifically to human PD-L1 and exhibit at least one, in some embodiments, at least five, of the preceding characteristics.

[0157] In certain embodiments, the anti-PD-L1 antibody is selected from the group consisting of BMS-936559 (formerly 12A4 or MDX-1105; *see, e.g.,* U.S. Patent No. 7,943,743 and WO 2013/173223), MPDL3280A (also known as RG7446, atezolizumab, and TECENTRIQ®; US 8,217,149; *see, also*, Herbst et al. (2013) J Clin Oncol 31(suppl):3000), durvalumab (IMFINZI™; MEDI-4736; AstraZeneca; *see* WO 2011/066389), avelumab (Pfizer; MSB-0010718C; BAVENCIO®; *see* WO 2013/079174), STI-1014 (Sorrento; *see* WO2013/181634), CX-072 (CytomX; *see* WO2016/149201), KN035 (3D Med/Alphamab; *see* Zhang et al., *Cell Discov. 7*:3 (March 2017), LY3300054 (Eli Lilly Co.; *see, e.g.*, WO 2017/034916), and CK-301 (Checkpoint Therapeutics; *see* Gorelik et al., AACR:Abstract 4606 (Apr 2016)).

[0158] In certain embodiments, the PD-L1 antibody is atezolizumab (TECENTRIQ®). Atezolizumab is a fully humanized IgG1 monoclonal anti-PD-L1 antibody.

[0159] In certain embodiments, the PD-L1 antibody is durvalumab (IMFINZI™). Durvalumab is a human IgG1 kappa monoclonal anti-PD-L1 antibody.

[0160] In certain embodiments, the PD-L1 antibody is avelumab (BAVENCIO®). Avelumab is a human IgG1 lambda monoclonal anti-PD-L1 antibody.

[0161] In other embodiments, the anti-PD-L1 monoclonal antibody is selected from the group consisting of 28-8, 28-1, 28-12, 29-8, 5H1, and any combination thereof.

[0162] Anti-PD-L1 antibodies usable in the disclosed methods also include isolated antibodies that bind specifically to human PD-L1 and cross-compete for binding to human PD-L1 with any anti-PD-L1 antibody disclosed herein, *e.g.*, atezolizumab and/or avelumab. In some embodiments, the anti-PD-L1 antibody binds the same epitope as any

of the anti-PD-L1 antibodies described herein, *e.g.*, atezolizumab and/or avelumab. The ability of antibodies to cross-compete for binding to an antigen indicates that these antibodies bind to the same epitope region of the antigen and sterically hinder the binding of other cross-competing antibodies to that particular epitope region. These cross-competing antibodies are expected to have functional properties very similar those of the reference antibody, *e.g.*, atezolizumab and/or avelumab, by virtue of their binding to the same epitope region of PD-L1. Cross-competing antibodies can be readily identified based on their ability to cross-compete with atezolizumab and/or avelumab in standard PD-L1 binding assays such as Biacore analysis, ELISA assays or flow cytometry (*see, e.g.*, WO 2013/173223).

[0163] In certain embodiments, the antibodies that cross-compete for binding to human PD-L1 with, or bind to the same epitope region of human PD-L1 antibody as, atezolizumab and/or avelumab, are monoclonal antibodies. For administration to human subjects, these cross-competing antibodies are chimeric antibodies, engineered antibodies, or humanized or human antibodies. Such chimeric, engineered, humanized or human monoclonal antibodies can be prepared and isolated by methods well known in the art.

[0164] Anti-PD-L1 antibodies usable in the methods of the disclosed invention also include antigen-binding portions of the above antibodies. It has been amply demonstrated that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody.

[0165] Anti-PD-L1 antibodies suitable for use in the disclosed methods or compositions are antibodies that bind to PD-L1 with high specificity and affinity, block the binding of PD-1, and inhibit the immunosuppressive effect of the PD-1 signaling pathway. In any of the compositions or methods disclosed herein, an anti-PD-L1 "antibody" includes an antigen-binding portion or fragment that binds to PD-L1 and exhibits the functional properties similar to those of whole antibodies in inhibiting receptor binding and up-regulating the immune system. In certain embodiments, the anti-PD-L1 antibody or antigen-binding portion thereof cross-competes with atezolizumab and/or avelumab for binding to human PD-L1.

[0166] Efficaciousness of prevention, amelioration or treatment is determined in association with any known method for diagnosing or treating the disease or disorder, including but not limited to, a disease or disorder associated with aberrant CTLA-4

expression and/or activity. Prolonging the survival of a subject or otherwise delaying the progression of the disease or disorder, including but not limited to, a disease or disorder associated with aberrant CTLA-4 expression and/or activity in a subject, indicates that the activatable antibody confers a clinical benefit.

[0167] It will be appreciated that therapeutic entities in accordance with the invention will be administered with suitable carriers, excipients, and other agents that are incorporated into formulations to provide improved transfer, delivery, tolerance, and the like. A multitude of appropriate formulations can be found in the formulary known to all pharmaceutical chemists: Remington's Pharmaceutical Sciences (15th ed, Mack Publishing Company, Easton, Pa. (1975)), particularly Chapter 87 by Blaug, Seymour, therein. These formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as Lipofectin™), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. Any of the foregoing mixtures may be appropriate in treatments and therapies in accordance with the present invention, provided that the active ingredient in the formulation is not inactivated by the formulation and the formulation is physiologically compatible and tolerable with the route of administration. *See also* Baldrick P. "Pharmaceutical excipient development: the need for preclinical guidance." *Regul. Toxicol Pharmacol.* 32(2):210-8 (2000), Wang W. "Lyophilization and development of solid protein pharmaceuticals." *Int. J. Pharm.* 203(1-2):1-60 (2000), Charman W N "Lipids, lipophilic drugs, and oral drug delivery-some emerging concepts." *J Pharm Sci.* 89(8):967-78 (2000), Powell *et al.* "Compendium of excipients for parenteral formulations" *PDA J Pharm Sci Technol.* 52:238-311 (1998) and the citations therein for additional information related to formulations, excipients and carriers well known to pharmaceutical chemists.

[0168] Activatable anti-CTLA-4 antibodies can be administered in the form of pharmaceutical compositions. Principles and considerations involved in preparing such compositions, as well as guidance in the choice of components are provided, for example, in Remington: The Science And Practice Of Pharmacy 19th ed. (Alfonso R. Gennaro, *et al.*, editors) Mack Pub. Co., Easton, Pa.: 1995; Drug Absorption Enhancement: Concepts, Possibilities, Limitations, And Trends, Harwood Academic Publishers, Langhorne, Pa.,

1994; and Peptide And Protein Drug Delivery (Advances In Parenteral Sciences, Vol. 4), 1991, M. Dekker, New York.

[0169] The formulation can also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition can comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0170] The active ingredients can 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, nano-particles, and nanocapsules) or in macroemulsions.

[0171] The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

[0172] Sustained-release preparations can be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, 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(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ 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. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

[0173] In some embodiments, the activatable antibody contains a detectable label. An intact antibody, or a fragment thereof (e.g., Fab, scFv, or F(ab)2) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity

with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. Included within the usage of the term "biological sample", therefore, is blood and a fraction or component of blood including blood serum, blood plasma, or lymph. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

III. Pharmaceutical Compositions

[0174] The activatable anti-CTLA-4 antibodies of the invention (also referred to herein as "active compounds"), and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the activatable antibody and a pharmaceutically acceptable carrier. As used herein, the term "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, ringer's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

[0175] A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (i.e., topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the

following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[0176] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringe ability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

[0177] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a

basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0178] For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

[0179] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

[0180] Activatable antibodies of the present invention may also be administered subcutaneously in conjunction with agents to facilitate injection of large volumes at a single site (insterstitial drug dispersion agents) such as soluble neutral-active hyaluronidase glycoproteins (sHASEGP), for example, human soluble PH-20 hyaluronidase glycoproteins, such as rHuPH20 (HYLENEX®, Baxter International, Inc.). Certain exemplary sHASEGPs and methods of use, including rHuPH20, are described in US Patent Publication Nos. 2005/0260186 and 2006/0104968. In one aspect, a sHASEGP is combined with one or more additional glycosaminoglycanases such as chondroitinases.

[0181] The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

[0182] In some embodiments, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid.

Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

[0183] It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

[0184] The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

[0185] Embodiments of the present disclosure can be further defined by reference to the following non-limiting examples, which describe in detail preparation of certain antibodies of the present disclosure and methods for using antibodies of the present disclosure. It will be apparent to those skilled in the art that many modifications, both to materials and methods, may be practiced without departing from the scope of the present disclosure.

[0186] The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example 1: Identification of Masking Moieties for the Activatable anti-CTLA-4 Antibody

[0187] In order to identify masking moieties (MM) that reduce the binding of anti-CTLA-4 antibodies to their target protein, anti-CTLA-4 antibody (i.e., ipilimumab) was used to

screen peptide libraries using methods similar to that described in PCT International Publication Nos. WO 2009/025846, WO 2010/081173, and WO 2016/149201, the contents of which are hereby incorporated by reference in their entireties. The screening consisted of two rounds of magnetic-activated cell sorting (MACS) purification followed by three rounds of fluorescence-activated cell sorting (FACS).

[0188] The initial MACS purification was done with protein-A Dynabeads® (Invitrogen) and anti-CTLA-4 antibody at a concentration of 100 nM. Approximately 10^{11} cells were screened for binding, and $6x10^6$ cells were collected. The second MACS purification was done with streptavidin DYNABEADS® (Thermo Fisher Scientific) and biotinylated anti-CTLA-4 antibody at a concentration of 100 nM. The eluate from the initial MACS purification was expanded, approximately 10^{11} cells were screened for binding, and approximately 10^7 cells were collected. The output of the previously described MACS purification was subjected to serial rounds of FACS sorting with decreasing concentrations of anti-CTLA-4 labeled with Alexa Fluor® 488 (Thermo Fisher Scientific). Labeled anti-CTLA4 antibody was used at concentrations of 10 nM, 1 nM, and 200 pM for the first, second, and third sorts, respectively. Individual peptide clones, from the third sort were identified by sequence analysis and subsequently verified for their ability to bind the anti-CTLA4 antibody. Two peptide consensus sequences were selected for affinity maturation: XXCXXXMYGYNLCPY (SEQ ID NO: 554) and XXXCXHSMYNVCLDP (SEQ ID NO: 555).

[0189] Affinity maturation libraries were built on these consensus sequences as described in Table 7. Rows 1 and 3 represent the consensus sequence and rows 2 and 4 represent the nucleotide sequences encoding the peptide libraries that were inserted into the display system using a method similar to that described in PCT International Publication Number WO 2010/081173, *ibid.*

Table 7: Maturation Libraries

1	X	X	C	X	X	X	M	Y	G	Y	N	L	C	P	Y
2	NNK	NNK	TGC	NNK	NNK	NNK	NTT	TWT	GGG	KWT	AAT	CTG	TGC	CCG	TAT
3	X	X	X	C	X	H	S	M	Y	N	V	C	L	D	P
4	NNK	NNK	NNK	TGC	NNK	NWT	AGT	NTT	TWT	AAT	NTT	TGC	CTT	GAT	CCT

[0190] The maturation libraries were screened in a manner similar to that described for the naïve libraries described above. The screening consisted of one round of MACS and

subsequent rounds of FACS sorting. The MACS was done with protein-A DYNABEADS® (Thermo Fisher Scientific) and the anti-CTLA-4 antibody at a concentration of 100 nM. For MACS, 10^{11} cells were screened for binding, and approximately 10^{8} cells were selected. The eluate from the MACS was expanded, and approximately 10^{11} cells were subjected to serial rounds of FACS sorting with decreasing concentrations of Alexa Fluor® 488-labeled anti-CTLA4 antibody. Labeled anti-CTLA4 antibody was used at concentrations of 100 nM, 20 nM, 5 nM, 1 nM, and 1 nM for the first, second, third, fourth and fifth sorts, respectively. Individual peptide clones from the fourth and fifth sorts were identified by sequence analysis and subsequently verified for their ability to bind the anti-CTLA4 antibody. The sequences of the anti-CTLA-4 masking moieties identified through the methods described above are provided in Tables 4 and 5. Four consensus sequences can be derived from the mask sequences listed in Tables 4 and 5:

Consensus 1. C(L/M/V/T)Y(S/V/I)(F/L/M/A)(Y/F)N(V/I)CLDP (SEQ ID NO: 566)

Consensus 2. CAQMYGYSMC(P/A)(H/R/A)T (SEQ ID NO: 567)

Consensus 3. CX(M/I/Y/L/N/F)(Y/W/F/Q/T)(M/Y)YG(Y/V/F)(N/D)LCP(Y/F) (SEQ ID NO: 568)

Consensus 4. (N/T)(S/T/M/A)CP(N/Y)HP(M/L)C(H/F/Y)D(Y/F/W) (SEQ ID NO: 569)

Example 2:
Construction and Characterization of Activatable Anti-muCTLA-4 Antibodies

[0191] In order to show a proof-of-concept that the activatable anti-CTLA-4 antibodies can be used to treat tumors, six activatable anti-mouse CTLA-4 antibodies (based on clone 9D9) were constructed using techniques similar to those disclosed in Examples 1 and 3 herein. These antibodies comprise either MY11 or MY03 as the masking moiety, and cleavable moiety “0003” having amino acid sequence TSTSGRSANPRG (SEQ ID NO: 320), “1004” having amino acid sequence AVGLLAPP (SEQ ID NO: 323), or “2001” having amino acid sequence ISSGLLSGRSDNH (SEQ ID NO: 297). The antibodies were all mouse IgG2a isotype. As controls, anti-mouse CTLA-4 monoclonal antibody (9D9) ("9D9 mg2a") and a human anti-diptheria toxin antibody with a mIgG2a isotype ("mg2a") were used.

[0192] On day 0, BALB/c mice were subcutaneously injected with 1 x 10^6 CT26 tumor cells. Administration of the different antibodies began on day 7 post tumor implantation. Prior to administration, tumor size was measured and the mice were randomized into different treatment groups, so as to have comparable mean tumor volumes (e.g., 39-44 mm^3). Tumors were measured with calipers two-dimensionally, and tumor volume was calculated as $L\times(W^2/2)$, L = length (the longer of the 2 measurements), W = width. The mice were then treated intraperitoneally (i.p.) with the designated antibody (e.g., 25 μg/dose). Tumor volume was measured twice weekly. At day 12 post tumor implantation, some of the mice from each group were sacrificed, and tumor and spleen were harvested for immunomonitoring to investigate the effects of the antibodies on the T cell populations. Some or all of the remaining mice from the different groups were used for subsequent pharmacokinetic (PK) and/or pharmacodynamics (PD) analysis.

[0193] As shown in FIG. 1A, mice that received the unrelated mouse IgG2a antibody (i.e., the human anti-diptheria toxin antibody) failed to control the tumor. In contrast, as shown in FIG. 1C, mice that received the activatable anti-mouse CTLA-4 antibody (comprising MY11 as the masking moiety and 2001 as the cleavable moiety) controlled tumor size almost as well as those mice that received the anti-mouse CTLA-4 mAb (9D9) (FIG. 1B). These data demonstrate that tumor-specific protease can cleave the cleavable moiety, resulting in the removal of the masking moiety and the binding of the released antibody to its target protein.

[0194] To determine whether or not activatable anti-mouse CTLA-4 antibodies are active in the periphery, proliferation and activity of Foxp3+ regulatory T cells were determined in the spleen, and regulatory T cell abundance was determined in tumor samples for comparison, as described in Example 5, *infra*. In agreement with the data from FIGs. 1B and 1C, all the activatable anti-CTLA-4 antibodies behaved similarly to the anti-mouse CTLA-4 mAb (9D9) in the tumor (FIG. 2A). In contrast, the activatable antibodies resembled the unrelated mouse IgG2a antibody in the spleen (FIGs. 2B and 2C). Such data suggest that the masking moiety-containing prodomain of the activatable anti-mouse CTLA-4 antibodies remains intact and attached to the antibody in the spleen, blocking the activity of the antibody, whereas the prodomain is cleaved off by tumor specific proteases to generate fully active anti-CTLA-4 antibody in the tumor.

Example 3:
Construction of Activatable Anti-human CTLA-4 Antibodies

[0195] Activatable anti-CTLA4 antibodies comprising an anti-CTLA4 masking moiety, a cleavable moiety, and an anti-CTLA4 antibody (e.g., ipilimumab) of the disclosure were produced according to methods similar to those described in PCT Publication Nos. WO 2009/025846 *ibid.* and WO 2010/081173 *ibid*, and WO 2016/118629, *ibid.* Activatable anti-CTLA4 antibodies were expressed in EXPI293™ cells (Thermo Fisher Scientific) and purified by protein A chromatography (MabSelect SuRe, GE Healthcare) as per manufacturers' protocols. Quality control of the resultant activatable antibodies indicated that most comprise at least 95% monomer.

[0196] To assess the feasibility of using the activatable anti-CTLA-4 antibodies disclosed herein in a human setting, the antibodies were produced as human IgG1 (hIgG1) heavy chain (Hc) and human kappa (hK) light chain (Lc) format. The activatable antibodies all comprise the antibody or antigen binding domain thereof of ipilimumab. The cleavable moiety was selected from the group consisting of a cleavable moiety referred to herein as "2001" and comprising the sequence ISSGLLSGRSDNH (SEQ ID NO: 297) and derivatives thereof and a cleavable moiety referred to herein as "3001" and comprising the sequence AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306) and derivatives thereof. In some embodiments, the cleavable moiety was selected from the group consisting of ISSGLLSGRSDNH (SEQ ID NO: 297), also referred to herein as "2001"; ISSGLLSGRSDDH (SEQ ID NO: 300), also referred to herein as "2006"; ISSGLLSGRSDIH (SEQ ID NO: 301), also referred to herein as "2007"; ISSGLLSGRSDQH (SEQ ID NO: 302), also referred to herein as "2008"; ISSGLLSGRSDTH (SEQ ID NO: 303), also referred to herein as "2009"; ISSGLLSGRSANP (SEQ ID NO: 305), also referred to herein as "2012"; ISSGLLSGRSDNP (SEQ ID NO: 304), also referred to herein as "2011"; ISSGLLSGRSANPRG (SEQ ID NO: 298), also referred to herein as "2003"; AVGLLAPPGGLSGRSDNH (SEQ ID NO: 306), also referred to herein as "3001"; AVGLLAPPGGLSGRSDDH (SEQ ID NO: 307), also referred to herein as "3006"; AVGLLAPPGGLSGRSDIH (SEQ ID NO: 308), also referred to herein as "3007"; AVGLLAPPGGLSGRSDQH (SEQ ID NO: 309), also referred to herein as "3008"; AVGLLAPPGGLSGRSDTH (SEQ ID NO: 310), also referred to herein as "3009";

AVGLLAPPGGLSGRSANP (SEQ ID NO: 312), also referred to herein as "3012"; AVGLLAPPGGLSGRSDNP (SEQ ID NO: 311), also referred to herein as "3011"; and AVGLLAPPSGRSANPRG (SEQ ID NO: 299), also referred to herein as "2005". The masking moiety was selected from the group of masking moieties provided in Tables 4 and 5. In some embodiments, the masking moiety was CRTQLYGYNLCPY (SEQ ID NO: 39), referred to herein as YV39. Some of the activatable anti-CTLA-4 antibodies also included spacer sequences and/or linker peptides.

Example 4:
In vitro Characterization of Activatable Anti-Human CTLA-4 Antibodies

[0197] In order to assess the ability of the activatable antibodies to bind to CTLA-4 in the absence of protease activity, an enzyme-linked immunosorbent assay (ELISA) was used to measure binding affinity. Briefly, Nunc MaxiSorp® plates were coated overnight at 40°C with 100 µL/well of a 1 µg/mL solution of human CTLA-4 protein (Sino Biological) in PBS, pH 7.4. Plates were then washed three times with PBST (PBS, pH 7.4, 0.05% Tween-20), and the wells were blocked with 200 µL/well, 10 mg/mL bovine serum albumin (BSA) in PBST for 2 hours at room temperature. Afterwards, the plates were washed three more times with PBST. The activatable antibodies were then serially diluted, as shown below in Table 8.

Table 8. Serial Dilution of Activatable Anti-CTLA-4 Antibodies for Binding Analysis

	[Antibody] = nM Columns 1-3	[activatable antibody 1] = nM Columns 4-6	[activatable antibody 2] = nM Columns 7-9	[activatable antibody 3] = nM Columns 10-12
A	10	1000	1000	1000
B	3.33	333	333	333
C	1.11	111	111	111
D	0.37	37	37	37
E	0.123	12.3	12.3	12.3
F	0.041	4.1	4.1	4.1
G	0.0137	1.34	1.34	1.34
H	.0046	0.45	0.45	Blank

[0198] In the current Example, the highest concentration used for the parental antibody and the activatable antibodies were 10 nM and 100 nM, respectively. However, the

concentrations can be increased or decreased to give full saturation binding curves for activatable antibodies with stronger or weaker masking.

[0199] The diluted antibodies were added to the plates and incubated for 1 hour at room temperature. Afterwards, the plates were washed three times with PBST. Then, 100 µL of goat-anti-human IgG (Fab specific, Sigma cat # A0293; diluted at 1:4,000 in 10 mg/mL BSA in PBST) was added to each well, and the plate was incubated for an additional 1 hour at room temperature. Next, the plates were developed with tetramethylbenzidine (TMB) and 1N HCl. Absorbance at 450 nm was then measured and reported as optical density (OD 450 nm).

[0200] As shown in FIGs. 3A to 3E, anti-CTLA-4 activatable antibodies typically had reduced binding to CTLA-4 as compared to ipilimumab ("YV1"). *See also* FIGs. 4A to 4D, FIGs. 5A to 5F, and FIGs. 6A to 6B. Such data demonstrate that the masking moieties effectively conceal the antigen binding domain on the anti-CTLA-4 activatable antibodies.

[0201] To further assess the binding ability, the activatable human anti-CTLA-4 antibodies were serially diluted (e.g., 60 µg/mL to 0.0003 µg/mL) and added to 58 α-β-CTLA-4/CD3ζ cells, which stably express human CTLA-4. After 30 minutes of incubation at 4°C, an allophycocyanin (APC)-labeled anti-human secondary antibody was added and binding of the activatable anti-human CTLA-4 antibodies to human CTLA-4 was assessed using a Canto flow cytometer. The geometric mean fluorescence intensity (GMFI) was determined using FlowJo® analysis software. Ipilimumab was used as a control. As shown in FIGs. 7A and 7B, the activatable human anti-CTLA-4 antibodies did not bind to human CTLA-4 as effectively as ipilimumab. These data further demonstrate that in the absence of specific proteases, the masking moiety of the activatable antibodies inhibits binding of such activatable antibodies to human CTLA-4.

[0202] To confirm that the reduced binding observed with the activatable anti-CTLA-4 antibodies was due to the masking moiety, studies were performed on mono-clippped, MMP fully-clipped and uPA fully-clipped forms of the activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety. The mono-clipped form of the antibody was produced by expressing a construct producing one intact light chain (including the mask moiety) and a second light chain truncated at the same position as if it had been cleaved by MMP14. The MMP or uPA fully clipped forms were expressed

from constructs with both light chains truncated as if they had been cleaved by MMP or μPA, respectively. As shown in FIGs. 7C and 7D, the mono-clipped activatable antibody had intermediate binding (EC50 = 2.8 nM) as compared to the non-clipped activatable antibody (EC50 = 22 nM) and ipilimumab (EC50 = 0.54 nM). In contrast, the MMP or uPA fully-clipped activatable antibodies behaved similarly to ipilimumab (MMP clipped: EC50 = 0.65 nM; μPA clipped: EC50 = 0.76). Such data confirm that the reduced binding observed with the activatable anti-CTLA-4 antibody is due to the masking moiety.

[0203] Next, to determine whether the observed reduced binding to CTLA-4 correlated with reduced activity, the activity of an activatable human anti-CTLA-4 antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("Ipi YV39 2011") was characterized in an *in vitro* functional assay using staphylococcal enterotoxin B (SEB). SEB is a superantigen that strongly activates T cells and stimulates cytokine secretion. Whole fresh peripheral blood mononuclear cells (PBMC) were isolated from healthy human donors using a standard Ficoll-Paque separation method. Serial dilution of the antibodies (e.g., 40 μg/mL to 0.01 μg/mL) were performed and plated in triplicate in a 96-well flat-bottom tissue culture plate. The antibodies used included (i) Ipi YV39 2011, (ii) ipilimumab, and (iii) an unrelated isotype control. Next, the isolated PBMC were resuspended in T-cell assay media (RPMI media + 10% heat-inactivated fetal bovine serum (HI-FBS) + 1% HEPES buffer + 1% MEM non-essential amino acid + 1% Na-pyruvate) and added to the plate at $1x10^5$ cells/well. The cells were stimulated with a suboptimal concentration (e.g., 85 ng/mL – determined by titrating SEB and observing the stimulation on T-cell proliferation) of SEB. The cells were incubated at 37°C for 3 days. Then, the IL-2 concentration in the supernatants was measured by homogeneous time-resolved fluorescence (HTRF). The HTRF data were analyzed using Softmax Pro and graphed using GraphPad Prism.

[0204] As shown in FIG. 8, ipilimumab enhanced the SEB-mediated IL-2 production by the PBMC in a dose-dependent manner. In contrast, the Ipi YV39 2011 activatable antibody had activity similar to that of the isotype control, suggesting that the masking moiety (YV39) is effective in blocking the functional activity of ipilimumab. These data are in agreement with the binding data described above and demonstrate that in the absence of specific proteases, the activatable anti-human CTLA-4 antibodies exhibit reduced activity.

Example 5:
In vivo Characterization of Activatable Anti-Human CTLA-4 Antibodies

[0205] In order to characterize the antibodies disclosed herein *in vivo*, four activatable human anti-human CTLA-4 antibodies (based on ipilimumab) were prepared using mouse IgG2a. The antibodies comprise YV04, YV23, YV24, or YV39 as the masking moiety, and 2001 as the cleavable moiety ("Ipi YV04 2001", "Ipi YV23 2001", "Ipi YV24 2001", and "Ipi YV39 2001", respectively). As controls, ipilimumab ("Ipi mg2a") and an unrelated human anti-diphtheria toxin ("control mg2a") were used. The activity of these activatable anti-CTLA-4 antibodies was assessed using the MC38 tumor model as described below.

[0206] Briefly, on day 0, human CTLA-4 knock-in C57BL/6 mice were subcutaneously injected with 2 x 10^6 MC38 colon adenocarcinoma cells into their left lower abdominal quadrant. Tumors were measured with calipers two-dimensionally, and tumor volume was calculated as $L \times (W^2/2)$, L = length (the longer of the 2 measurements), W = width. Next, the mice were randomized into different groups, so as to have similar mean tumor volumes (e.g., 37 mm^3). Administration of the antibodies began on day 7 post tumor implantation with the mice receiving a single dose (e.g., 200 μg/mouse) of the relevant antibody via intraperitoneal (i.p.) injection. At day 12 post tumor implantation, several of the mice from each group were sacrificed, and tumor and spleen were harvested for immunomonitoring to investigate the effect of the antibodies on the T cell populations. Some or all of the remaining mice from the different groups were used for subsequent pharmacokinetic (PK) and/or pharmacodynamics (PD) analysis.

Immunomonitoring of T Cell Populations

[0207] The harvested tumor and spleen were processed on a gentleMACS Octo Dissociator™ (Miltenyi, San Diego, CA). Single cell suspensions were stained with the following T cell markers: CD4, CD8, CD19, ICOS, CD45, FoxP3, CTLA-4, CD3, Ki-67, PD-1, Granzyme B, and LIVE/DEAD®.

PK/PD Analysis

[0208] The mice were checked daily for postural, grooming, and respiratory changes, as well as lethargy. Tumors and group body weights were recorded twice a week until death,

euthanasia, or end of the study period. The response to the treatments was measured as a function of tumor growth inhibition (TGI), which was calculated as follows: % TGI = {1-[(Tt-To)/(Ct-Co)]}×100, Tt = tumor volume of the treatment group on a given day, To = initial tumor volume, Ct = tumor volume of the control group on a given day, Co = initial tumor volume of the control group. Animals were euthanized if the tumor reached a volume greater than approximately 2500 mm^3 or appeared ulcerated.

Statistical Analysis

[0209] Microsoft Excel was used to calculate the mean, standard deviation (SD), and median values of tumor volumes and body weights. The mean and median values were calculated when 100% and at least 60% of the study animals remained in each treatment group, respectively. GraphPad Prism® v.4 software was used to plot data.

[0210] As expected, mice that received the unrelated control antibody failed to control tumor growth (FIG. 9A) whereas all the mice that received ipilimumab effectively controlled tumor growth (FIG. 9B). Mice that received the different activatable human anti-CTLA-4 antibodies controlled tumor growth comparably with ipilimumab (FIGs. 9C to 9F). Of the activatable antibodies, Ipi YV39 2001 most closely resembled the efficacy of ipilimumab in controlling tumor growth (FIG. 9F).

[0211] In regard to the frequency of regulatory T cells in the tumor and spleen of the treated mice, as observed earlier with the activatable anti-mouse CTLA-4 antibodies (*see* Example 2), activatable anti-human CTLA-4 antibodies (mouse IgG2a isotype) behaved similarly to ipilimumab in tumors (FIGs. 12A and 12B), but in the spleen, the activatable antibodies were more comparable to the unrelated control antibody (FIGs. 12C to 12F).

[0212] The data shown here collectively demonstrate that the activatable human anti-CTLA-4 antibodies disclosed herein can effectively control tumors like the traditional ipilimumab while exhibiting less risk of undesirable side effects.

Example 6:
In vivo Characterization of Activatable Anti-Human CTLA-4 Antibodies Comprising Modified Cleavable Moieties

[0213] To address a possible deamidation site in certain cleavable moiety sequences (see Example 10), activatable human anti-CTLA4 antibodies were prepared using a human

IgG1 and various CM sequences. The activatable antibodies comprise YV39 as the masking moiety and one of several variants of the 2001 cleavable moiety: WT (2001), ANP (2012), DNP (2011), or Q (2008) ("Ipi YV39 2001", "Ipi YV39 2012", "Ipi YV39 2011", and "Ipi YV39 2008", respectively). Ipilimumab and the unrelated human anti-diphtheria toxin were again used as controls.

[0214] To measure the activity of the activatable anti-CTLA-4 antibodies, the MC38 tumor model was used as described above in Example 5. For the dose titration study (FIGs. 11A to 11F), the mice were treated with ipilimumab or the activatable antibody comprising YV39 as the masking moiety and 2011 as the cleavable moiety ("Ipi YV39 2011") at doses of 200 μg/dose, 60 μg/dose, and 20 μg/dose.

[0215] As shown in FIGs. 10A and 10B, mice treated with the control antibody failed to control the tumor, whereas 6 out of 10 mice treated with ipilimumab were tumor-free at the end of the experiment. Mice treated with the different activatable antibodies were able to control tumor as observed with the traditional ipilimumab (FIGs. 10C to 10F). *See also* FIGs. 11B – 11G.

[0216] In regard to the frequency of regulatory T cells in the tumor and spleen of the treated mice, as observed earlier, tumor-specific protease was required to cleave the 2001 cleavable moiety variants. In the tumors, these activatable antibodies behaved like ipilimumab in reducing the frequency of Foxp3+ regulatory T cells (FIGs. 13A, 13B, 14A, and 14B). *See also* FIG. 15. In the spleen, the antibodies more closely mirrored the unrelated control antibody (FIGs. 13C to 13E, 14D to 14G, and 16A to 16B), demonstrating that the masking moiety remains coupled to the activatable antibody in the absence of the specific tumor-associated proteases.

Example 7:
In vivo Characterization of A Non-Fucosylated Version of Activatable Anti-Human CTLA-4 Antibodies

[0217] As described above, the absence of core fucose residues can strongly enhance ADCC via improved binding of IgG to activating FcγRIIIA without altering antigen binding or CDC. Natsume *et al.* (2009) *Drug Des. Devel. Ther.* 3:7. Non-fucosylated forms of ipilimumab ("Ipi NF") and ipi YV39 2011 ("Ipi YV39 2011 NF") were prepared. Binding of Ipi and Ipi NF were determined for various mouse, human and

cynomolgus monkey Fc receptors. Results are provided at FIG. 19. As expected, Ipi NF showed dramatically enhanced affinity (i.e., lower K_d) for activating receptors human CD16a (FcγRIIIa), cyno CD16 (FcγRIII) and mouse FcγRIV.

[0218] Ipi YV39 2011 NF and Ipi-NF were tested at various doses in the MC38 tumor model described in Example 5. Ipilimumab and an unrelated hIgG1 were used as controls. Results are provided at FIGs. 17A - D. Ipi NF was somewhat more effective at limiting or preventing tumor growth than ipilimumab (compare FIGs. 17B and 17C), and Ipi YV39 2011 NF was equivalent to Ipi NF (compare FIGs. 17C and 17D). In addition, FoxP3+ regulatory T cells were also similarly depleted in the tumors of mice treated with Ipi NF and Ipi YV39 2011 antibody (*see* FIG. 18). In both experiments, the Ipi YV39 2011 NF is shown to be fully activated in the tumor.

[0219] These results confirm that the methods of the present invention are equally applicable to non-fucosylated forms of ipilimumab, including non-fucosylated activatable CTLA-4 antibodies such as YV39 2011 NF.

Example 8:
In vivo Characterization of Activatable Anti-Human CTLA-4 Antibodies in Cynomolgus Monkeys

[0220] To assess the anti-CTLA-4 antibodies in a primate, cynomolgous monkeys were administered activatable antibody comprising YV39 as the masking moiety and 2001 as the cleavable moiety. Vehicle and ipilimumab were used as controls. Each monkey received 10 mg of antibody or anti-CTLA-4 activatable antibody, and blood was collected on days 0, 4, 8, 15, 22, 36, and 43 post-antibody administration. As shown in FIG. 20, in monkeys that received ipilimumab, there was a spike in CD4+ T cell proliferation as measured by Ki67-staining at around days 8-15 post antibody administration. In contrast, activatable anti-CTLA-4 antibody behaved similarly to the vehicle control and did not induce CD4+ T cell proliferation in the monkeys. These data demonstrate that even in primates, the activatable anti-CTLA-4 antibody shows little if any activation, indicating the absence of specific proteases.

[0221] Collectively, the data presented at FIGs. 1 - 20 demonstrate that the activatable anti-CTLA-4 antibodies described herein offer an improvement over ipilimumab. The

activatable antibodies control tumor growth just as effectively as ipilimumab while reducing the risk of serious adverse events often observed with ipilimumab treatment.

Example 9:
K_{app} and ME Values for Activatable CTLA-4 Antibodies

[0222] Table 9 provides the K_{app} and masking efficiency (ME) values for activatable antibodies, disclosed herein, comprising a variety of masking moieties and cleavable moieties in a human IgG1 format. The values provided in this Table were calculated from the data depicted in the Figures. K_{app} represents the binding affinity of the activatable antibody under the conditions of the measurement, in this example binding by ELISA; it is to be appreciated, however, that binding affinity can also be measured by binding to CTLA-4 expressed on primary or transfected cells or by other physical methods such as, but not limited to, surface plasmon resonance or equilibrium dialysis. Masking efficiency (ME) is calculated by dividing the K_{app} of the activatable antibody by the K_D of ipilimumab, measured under the same conditions.

Table 9: K_{app} and ME Values

	CM 2001		CM 3001		CM 2008		CM 2011		CM 2012		NSUB	
	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME
YV04-YV1	17.8	57										
YV06-YV1	0.6	2										
YV09-YV1	33.6	112	44.4	126								
YV23-YV1	11.4	38	13.8	39								
YV24-YV1			9.0	29								
YV27-YV1	0.7	2.3	0.8	2.3								
YV29-YV1	0.7	2.3	0.8	2.3								
YV32-YV1	0.9	3.0	1.2	3.4								
YV33-YV1	1.3	4.3	1.9	5								
YV35-YV1	3.7	12.3	5.3	15								
YV39-YV1	16.9	56	14.3	41	31.4	135	13.2	57	14.9	64	31.8	137
YV41-YV1	14.4	48	22.6	65								
YV51-YV1	4.4	15	4.9	14								
YV52-YV1	0.8	2.7	0.9	2.6								
YV53-YV1	4.1	14	5.3	15								
YV54-YV1	0.6	2	1.0	2.8								
YV55-YV1	4.8	16	6.0	18								
YV56-YV1	0.4	1.3	0.4	1								
YV57-YV1	0.4	1.3	1.6	4.6								
YV58-YV1	0.3	1	0.4	1								

[0223] Table 10 provides the K_{app} and ME values for the activatable antibodies disclosed herein, comprising a variety of masking moieties and cleavable moieties in a YV1 mouse Ig2a format. The values provided were calculated from the data depicted in the Figures.

Table 10: K_{app} and ME values

	CM 2001		CM 2006		CM 2007		CM 2008		CM 2009	
	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME
YV04-YV1	5.7	16.2	26.4	75	19.3	55	19.1	54	16.4	47
YV23-YV1			12.5	36	7.8	22	2.7	8	9.4	27
YV39-YV1	18.0	51	23.9	68			17.6	50	18.0	51

[0224] Table 11 provides K_{app} and ME values for the activatable antibodies comprising masking moieties having higher ME values and the 2012 cleavable moiety in aYV1 mouse IgG2a format. The values provided were calculated from the data depicted in the Figures.

Table 11: K_{app} and ME values

	CM 2001		CM 2011		CM 2012		NSUB	
	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME	K_{app} nM	ME
YV39-YV1	18.0	51	18.0	51	12.9	144	29.8	85
YV61-YV1					17.9	200		
YV62-YV1					15.5	173		
YV63-YV1					104	1170		
YV64-YV1					56.5	631		
YV65-YV1					12.3	156		
YV66-YV1					18.9	242		
YV01-YV1					38.6	493		
YV02-YV1					14.8	189		

Example 10:
Deamidation, Isomerization, and Stabilization Assessment for Activatable CTLA-4 Antibodies

[0225] As suggested in Example 6, to address a possible deamidation site in certain cleavable moiety (CM) sequences in certain activatable human anti-CTLA-4 antibodies, such activatable antibodies were prepared using various CM sequences (i.e., 2001, 2011, 2012, and 2008). In the cleavable moieties 2011, 2012, and 2008, the DNH sequence found in the 2001 cleavable moiety was replaced with DNP, ANP, and DQH, respectively.

[0226] These activatable CTLA-4 antibodies were produced by transient transfection of the relevant constructs in HEK 293 cells, and subjected to peptide mapping liquid chromatography - mass spectroscopy (LC-MS) to detect potential breakdown products. The 2001 (DNH) cleavable moiety, which was initially selected for use in the activatable

anti-CTLA-4 antibodies of the present invention, showed deamidation of the asparagine (N) residue (6.4%) after 7 days in PBS at 4°C. Forced stability studies showed an increase from 18.5% to 32.8% deamidation when stored at 25°C for 4 weeks, and to 36.5% and 66.6% when stored at 40°C for one week and four weeks, respectively.

[0227] Cleavable moieties 2008, 2011 and 2012 were selected to try to overcome the deamidation problem with 2001 in these activatable CTLA-4 antibodies. All of these had 0.1% or less deamidation when stored 40°C for one week in PBS, compared with 6.4% deamidation of 2001. However, further stability analysis (also by LC-MS) showed that while these activatable CTLA-4 antibodies comprising the 2008 (DQH) cleavable moiety exhibited minimal deamidation, it showed significant aspartate isomerization at the aspartate residue under various conditions (*see* Table 12). In contrast, 2011 (DNP) exhibited minimal aspartate isomerization. Aspartate isomerization was not relevant for 2012 (ANP), in which the aspartate residue is replaced with alanine.

Table 12: Isomerization values

Temperature	**Time**	**Cleavable Moiety – Isomerization Values**		
		2011 (DNP)	**2012 (ANP)**	**2008 (DQH)**
-80°C	0 days (T_0)	0.1%	N/A	1.8%
4°C	0 days (T_0)	0.1%	N/A	2.4%
25°C	3 months	0.2%	N/A	8.2%
40°C	3 months	0.2%	N/A	34.5%

[0228] However, *in vitro* stability studies in mouse, rat, and cynomolgus monkey serum showed substantial clipping between asparagine and proline residues for 2012 (ANP) (*see* Table 13) in these activatable CTLA-4 antibodies. 2011 (DNP) remained as the cleavable moiety with acceptably low levels of deamidation, aspartate isomerization, and light chain clipping.

Table 13: Degree of clipping observed between the asparagine and proline residues

Serum	**Cleavable Moiety – Clipping Between Asparagine and Proline Residues**	
	2011 (DNP)	**2012 (ANP)**
Mouse	-	++
Cyno	+/-	+++

[0229] All publications, patents, patent applications, internet sites, and accession numbers/database sequences (including both polynucleotide and polypeptide sequences)

cited herein are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, internet site, or accession number/database sequence were specifically and individually indicated to be so incorporated by reference.

What is claimed:

1. An activatable anti-human CTLA-4 antibody comprising:

(i) a heavy chain comprising a heavy chain variable domain (VH) comprising CDRH1: SYTMH (SEQ ID NO: 557); CDRH2: FISYDGNNKYYADSVKG (SEQ ID NO: 558); and CDRH3: TGWLGPFDY (SEQ ID NO: 559); and

(ii) a light chain comprising:

(a) a light chain variable domain (VL) comprising CDRL1: RASQSVGSSYLA (SEQ ID NO: 560); CDRL2: GAFSRAT (SEQ ID NO: 561); and CDRL3: QQYGSSPWT (SEQ ID NO: 562);

(b) a cleavable moiety (CM); and

(c) a masking moiety (MM),

wherein the light chain has the structural arrangement from N-terminus to C-terminus as follows: MM-CM-VL.

2. The activatable anti-human CTLA-4 antibody of Claim 1, wherein the MM is selected from the group consisting of YV01, YV02, YV03, YV04, YV09, YV23, YV24, YV35, YV39, YV51, YV61, YV62, YV63, YV64, YV65, and YV66.

3. The activatable anti-human CTLA-4 antibody of Claim 2, wherein the CM is a substrate for a protease selected from the group consisting of MMP1, MMP2, MMP3, MMP8, MMP9, MMP11, MMP13, MMP14, MMP17, legumain, matriptase, and uPA.

4. The activatable anti-human CTLA-4 antibody of Claim 3, wherein the CM is selected from a group consisting of 2001, 2003, 2005, 2006, 2007, 2008, 2009, 2011, 2012, 3001, 3006, 3007, 3008, 3009, 3011, and 3012.

5. The activatable anti-human CTLA-4 antibody of Claim 4, wherein the MM is YV04, YV23, YV24, YV39, YV61, YV62, YV63, or YV64.

6. The activatable anti-human CTLA-4 antibody of Claim 5, wherein the MM is YV39.

7. The activatable anti-human CTLA-4 antibody of Claim 6, wherein the CM is 2001, 2011, or 2012.

8. The activatable anti-human CTLA-4 antibody of claim 7, wherein the CM is 2011.

9. The activatable anti-human CTLA-4 antibody of any one of claims 1 to 8 comprising:

(i) a heavy chain comprising the amino acid sequence of SEQ ID NO: 345; and

(ii) a light chain comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 563, 564, and 565.

10. The activatable anti-human CTLA-4 antibody of claim 9 comprising:

(i) a heavy chain comprising the amino acid sequence of SEQ ID NO: 345; and

(ii) a light chain comprising the amino acid sequence of SEQ ID NO: 564.

11. The activatable anti-human CTLA-4 antibody of claim 10, wherein:

(i) the heavy chain further comprises the human IgG1 constant domain sequence of SEQ ID NO: 350; and

(ii) the light chain further comprises the human light chain kappa constant domain sequence of SEQ ID NO: 346.

12. The activatable anti-human CTLA-4 antibody of any one of claims 1 to 11 further comprising a second linker peptide (LP2) as disclosed herein, and wherein the activatable anti-human CTLA-4 antibody has the structural arrangement, from N-terminus to C-terminus, MM-LP1-CM-LP2-VL or MM-LP2-CM-LP1-VL.

13. The activatable anti-human CTLA-4 antibody of claim 12, wherein the LP1 and the LP2 are not identical to each other.

14. The activatable anti-human CTLA-4 antibody of any one of claims 1 to 13 further comprising a spacer, and having the structural arrangement, from N-terminus to C-terminus, spacer-MM-CM-VL.

15. The activatable anti-human CTLA-4 antibody of any one of claims 1 to 14 further comprising a toxic agent.

16. The activatable anti-human CTLA-4 antibody of claim 15, wherein the toxic agent is conjugated to the activatable antibody via a cleavable linker.

17. The activatable anti-human CTLA-4 antibody of any one of claims 1 to 14 further comprising a detectable moiety.

18. The activatable anti-human CTLA-4 antibody of claim 178, wherein the detectable moiety is a diagnostic agent.

19. A pharmaceutical composition comprising the activatable anti-human CTLA-4 antibody of any one of claims 1 to 18 and a carrier.

20. The pharmaceutical composition of claim 19 comprising an additional therapeutic agent.

21. An isolated nucleic acid molecule encoding the heavy chain and/or the light chain of the activatable anti-human CTLA-4 antibody of any one of claims 1 to 14.

22. A vector comprising the isolated nucleic acid molecule of claim 21.

23. A method of producing an activatable anti-human CTLA-4 antibody comprising:

(i) culturing a cell comprising the vector of claim 22 under conditions that lead to expression of the activatable antibody; and

(ii) recovering the activatable antibody.

24. A method of reducing CTLA-4 activity in a subject in need thereof comprising administering an effective amount of the pharmaceutical composition of claim 19 or 20 to the subject.

25. A method of treating, alleviating a symptom of, or delaying the progression of a cancer in a subject comprising administering a therapeutically effective amount of the pharmaceutical composition of claim 19 or 20 to the subject.

26. The method of claim 25, wherein the cancer is a bladder cancer, a bone cancer, a breast cancer, a carcinoid, a cervical cancer, a colon cancer, an endometrial cancer, a glioma, a

head and neck cancer, a liver cancer, a lung cancer, a lymphoma, a melanoma, an ovarian cancer, a pancreatic cancer, a prostate cancer, a renal cancer, a sarcoma, a skin cancer, a stomach cancer, a testis cancer, a thyroid cancer, a urogenital cancer, or a urothelial cancer.

27. The method of claim 26, wherein the cancer is melanoma.

FIG. 1A

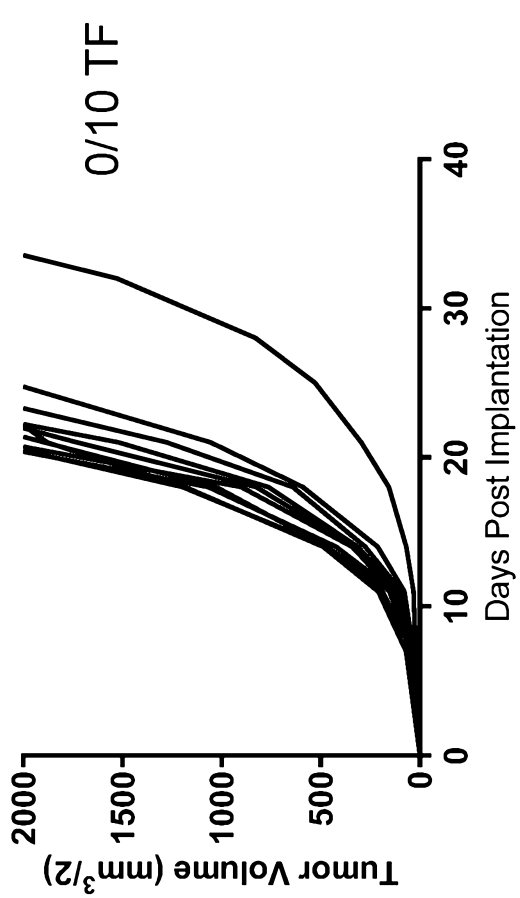


FIG. 1B

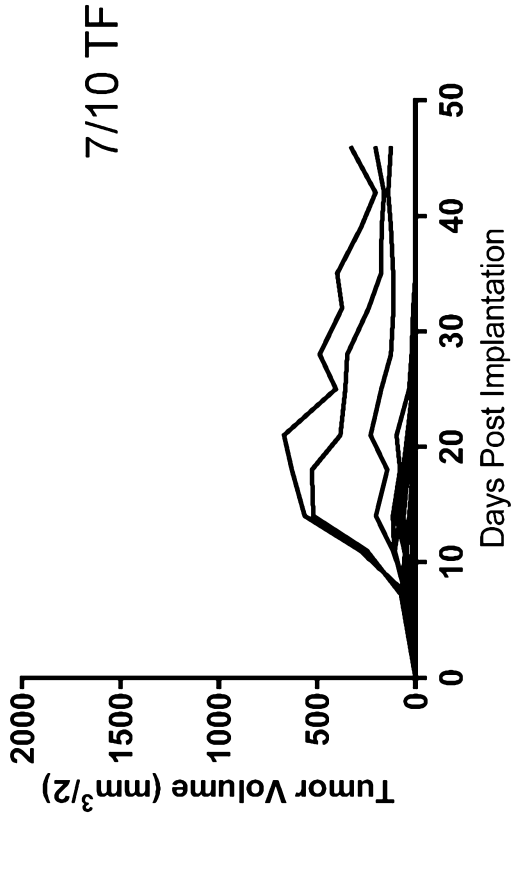


FIG. 1C

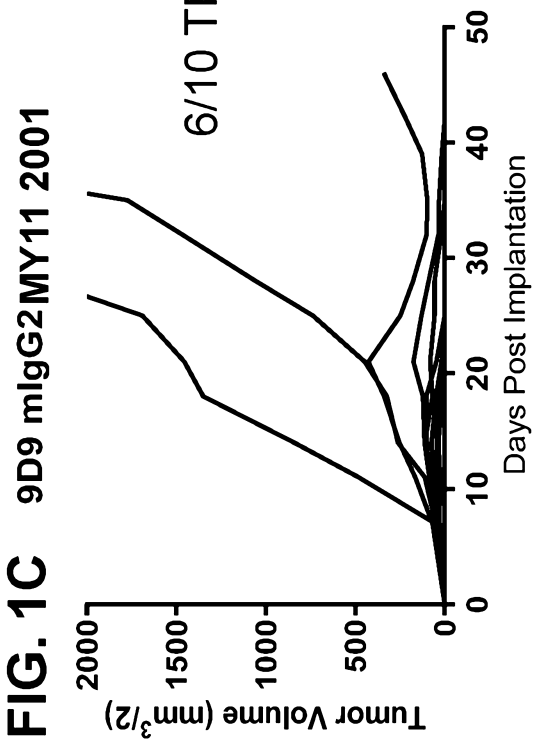


FIG. 2A Tumor Foxp3+ of CD4+

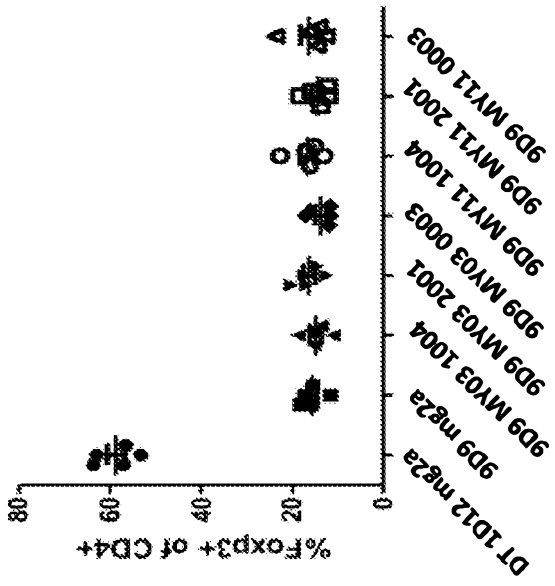


FIG. 2B Spleen Ki-67+ of Foxp3+

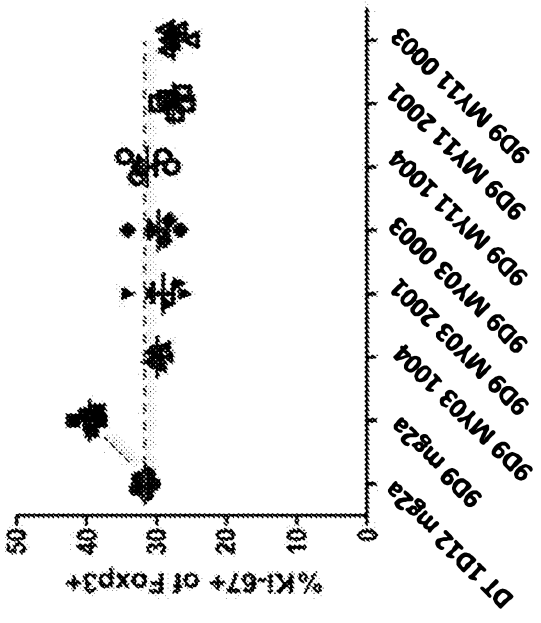
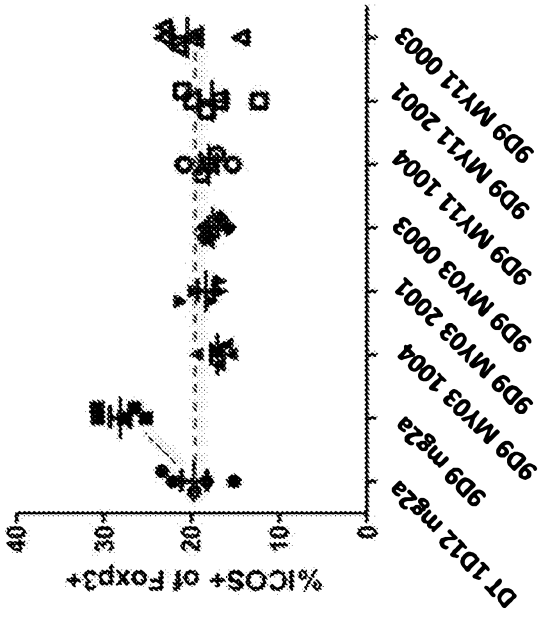


FIG. 2C Spleen ICOS+ of Foxp3+



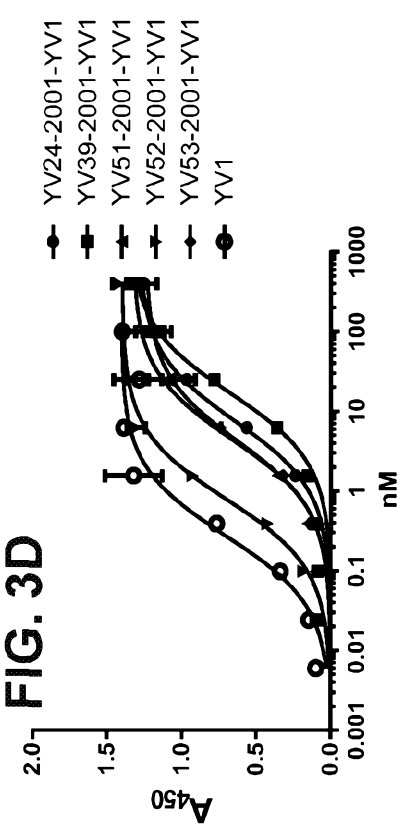


FIG. 3A

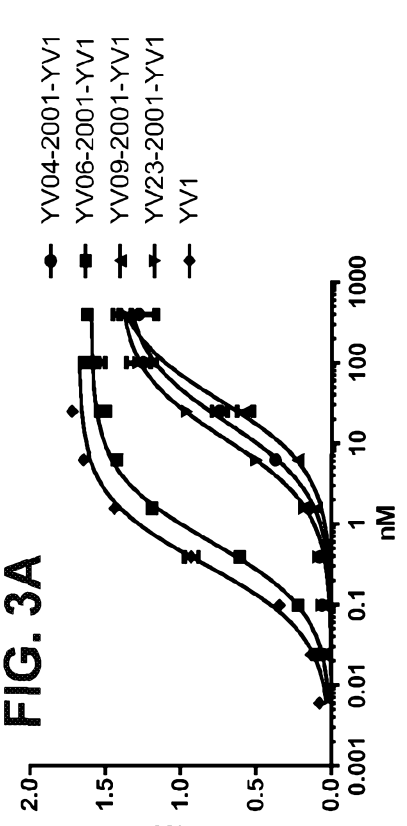


FIG. 3D

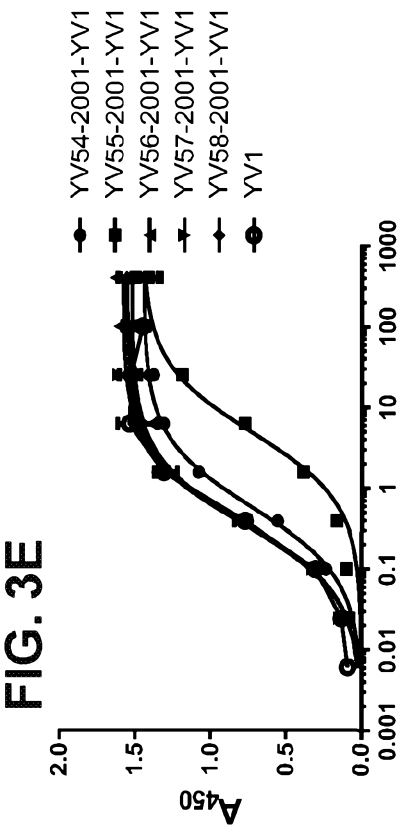


FIG. 3B

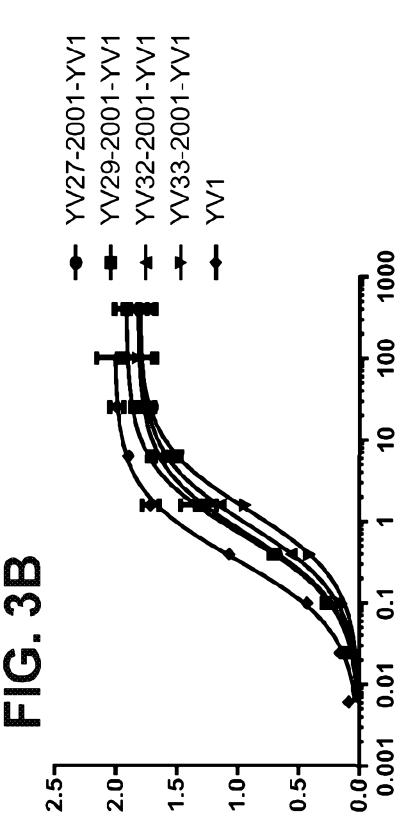


FIG. 3E

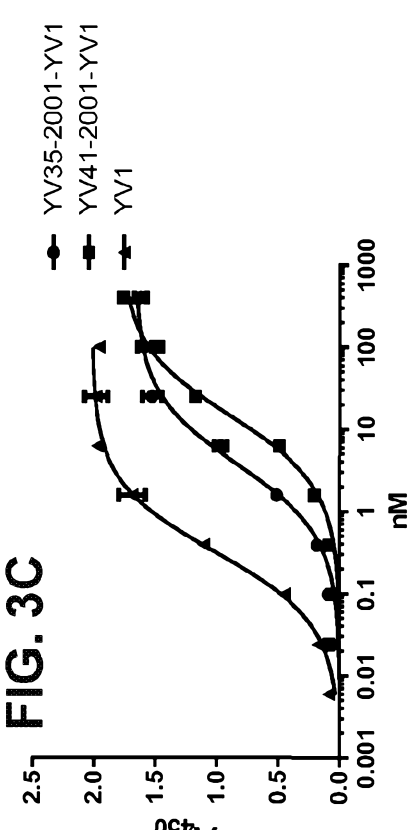


FIG. 3C

FIG. 4A

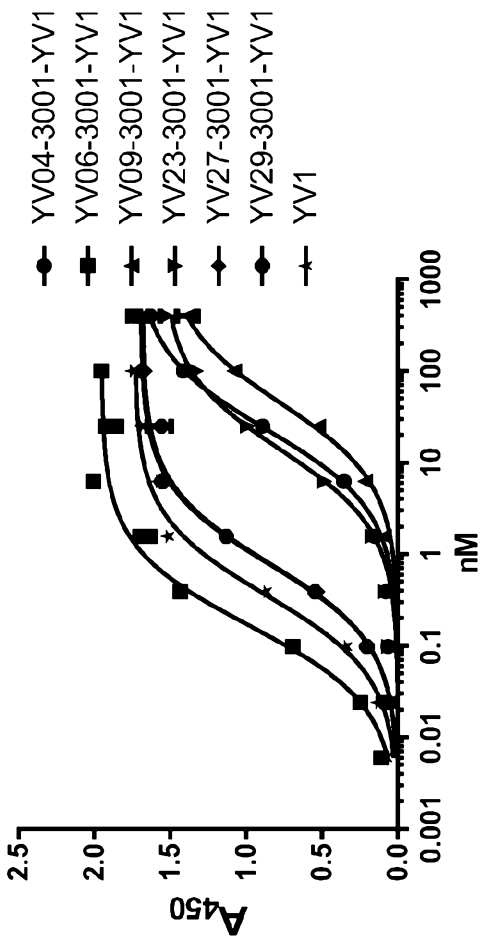


FIG. 4B

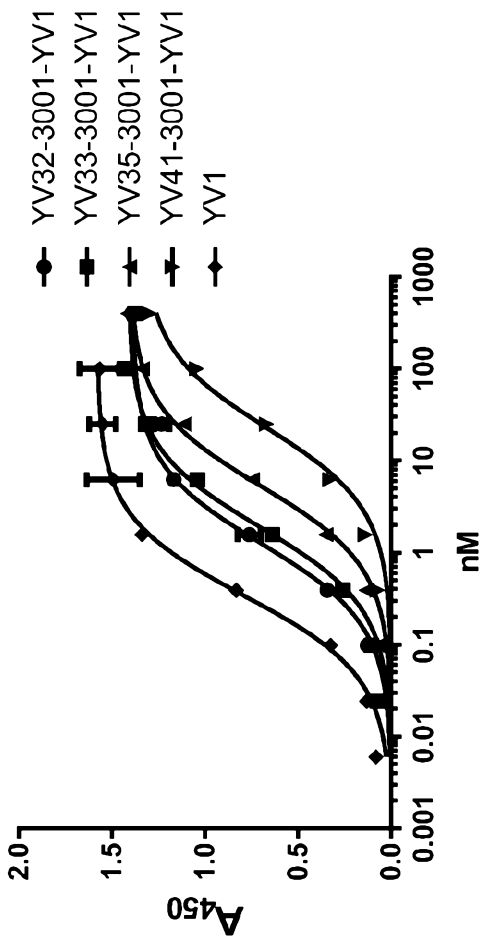


FIG. 4C

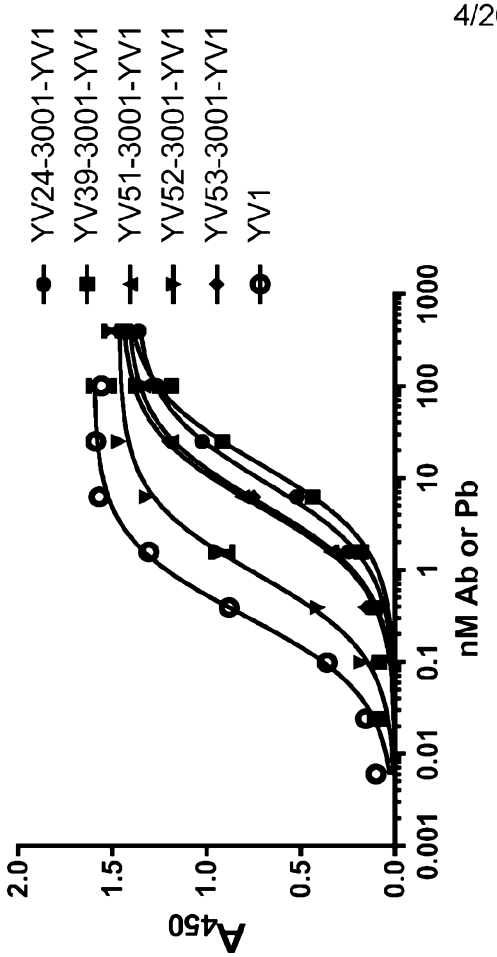


FIG. 4D

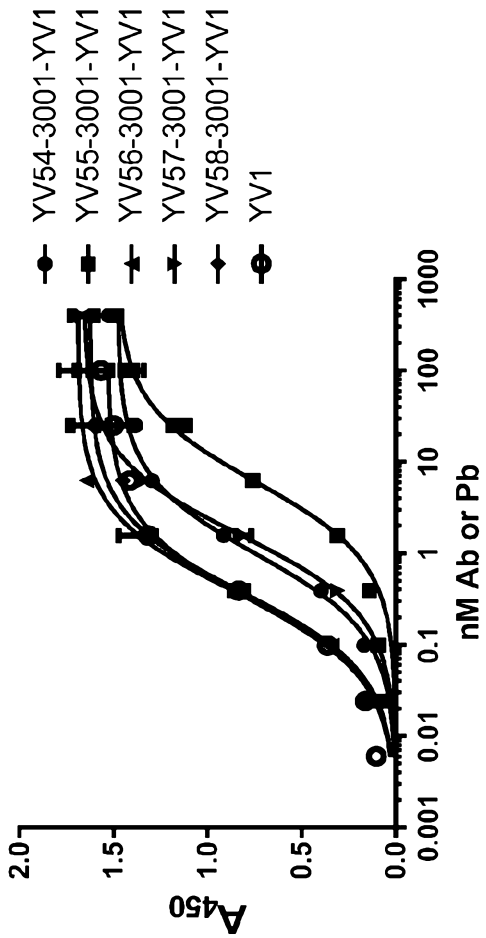


FIG. 5A

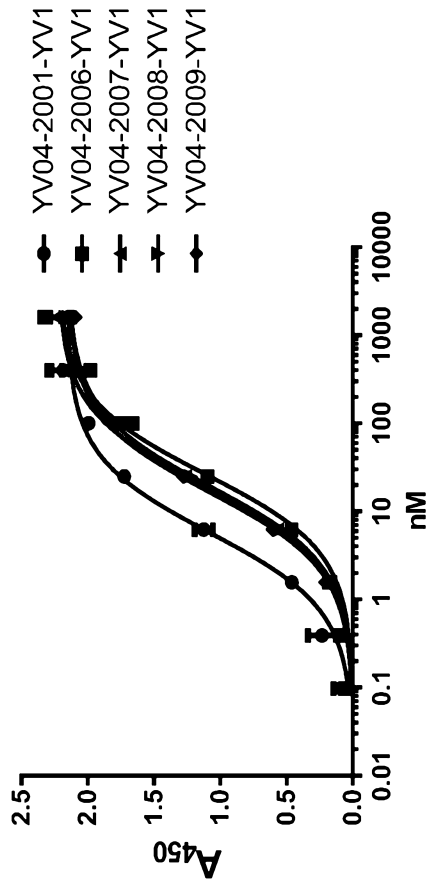


FIG. 5B

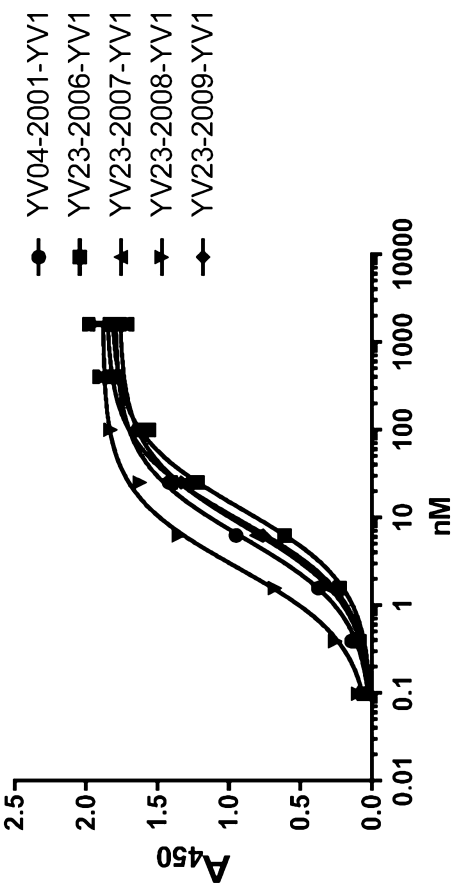


FIG. 5C

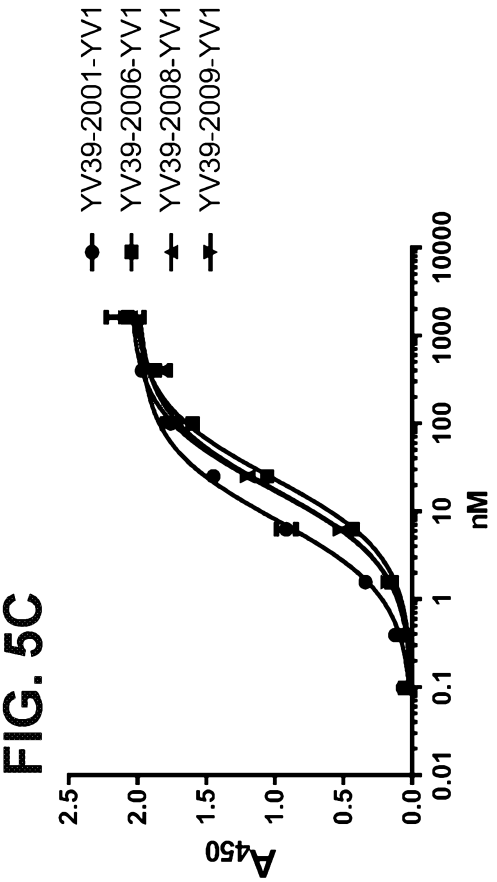


FIG. 5D

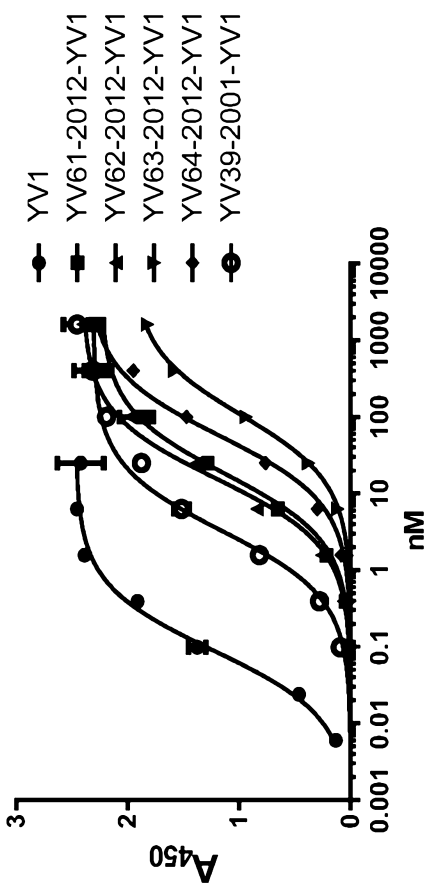


FIG. 5E

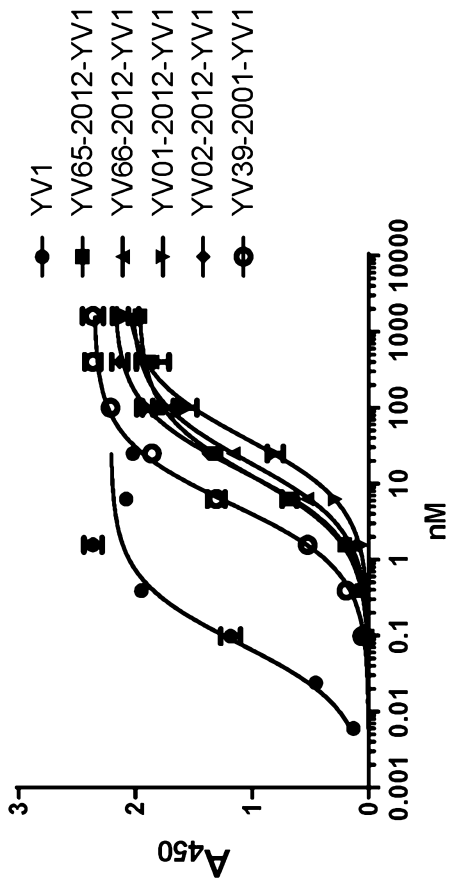


FIG. 5F

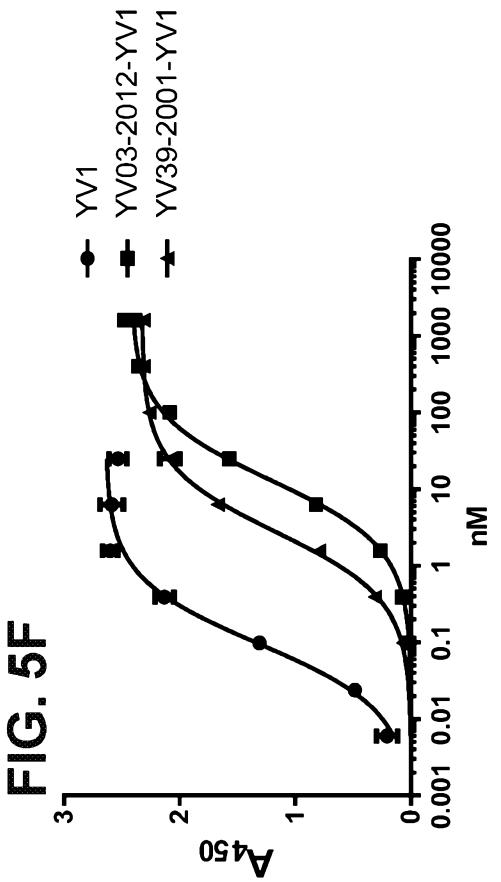


FIG. 6A

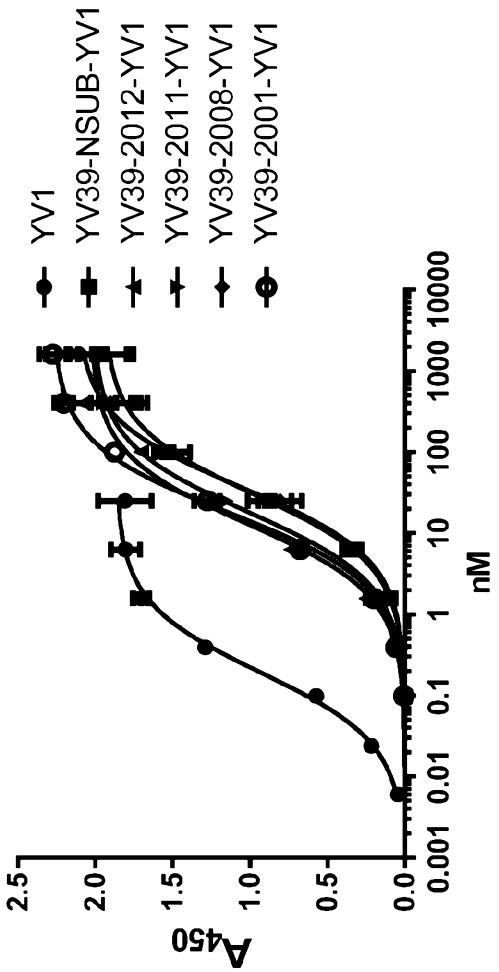

YV1
YV39-NSUB-YV1
YV39-2012-YV1
YV39-2011-YV1
YV39-2008-YV1
YV39-2001-YV1
A450
2.5
2.0
1.5
1.0
0.5
0.0
0.001
0.01
0.1
1
10
100
1000
10000
nM

FIG. 6B

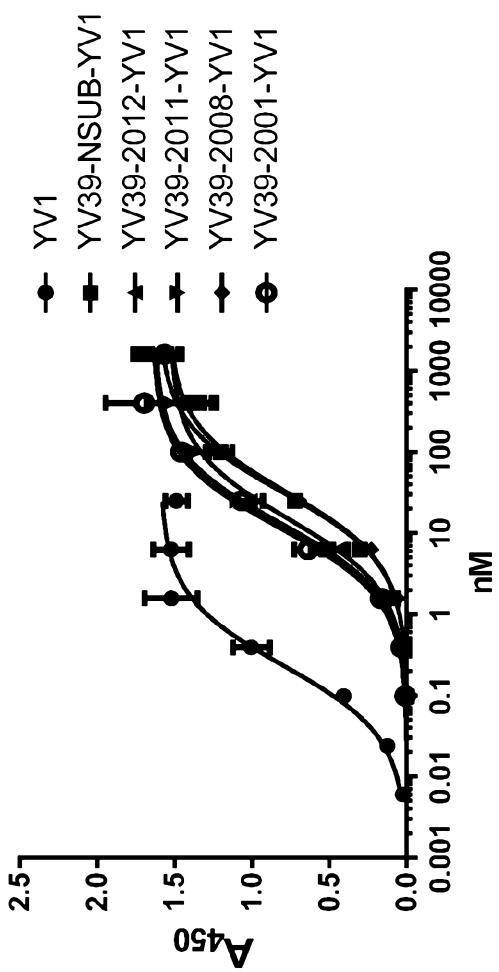

YV1
YV39-NSUB-YV1
YV39-2012-YV1
YV39-2011-YV1
YV39-2008-YV1
YV39-2001-YV1
A450
2.5
2.0
1.5
1.0
0.5
0.0
0.001
0.01
0.1
1
10
100
1000
10000
nM

FIG. 7A

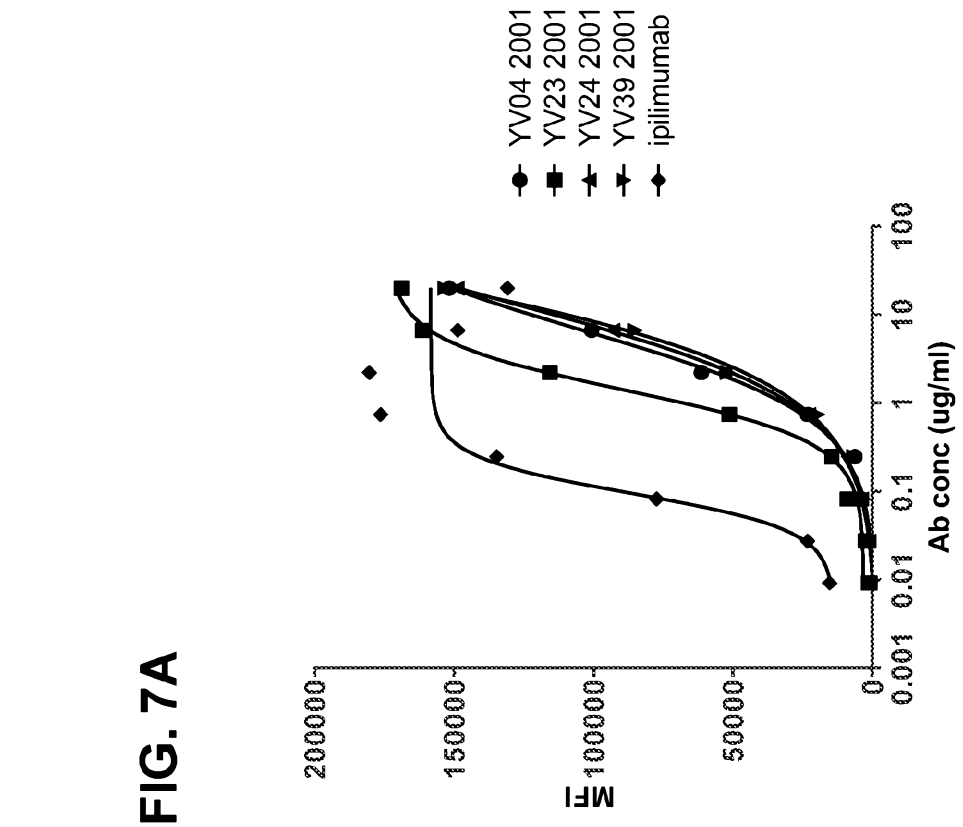

MFI
200000
150000
100000
50000
0
0.001
0.01
0.1
1
10
100
Ab conc (ug/ml)
YV04 2001
YV23 2001
YV24 2001
YV39 2001
ipilimumab

FIG. 7B

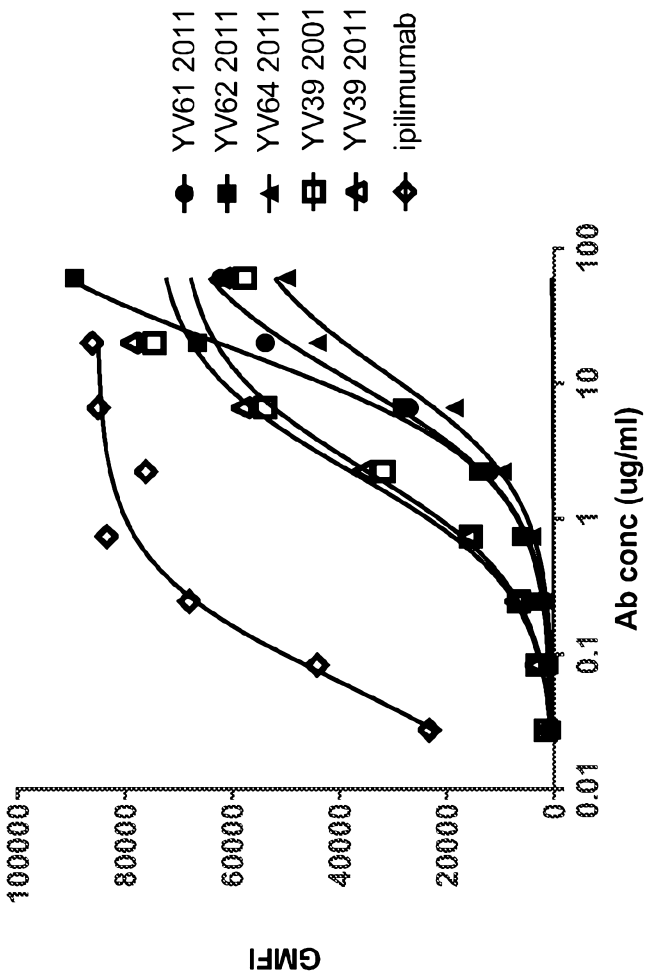

GMFI
100000
80000
60000
40000
20000
0
0.01
0.1
1
10
100
Ab conc (ug/ml)
YV61 2011
YV62 2011
YV64 2011
YV39 2001
YV39 2011
ipilimumab

FIG. 7C

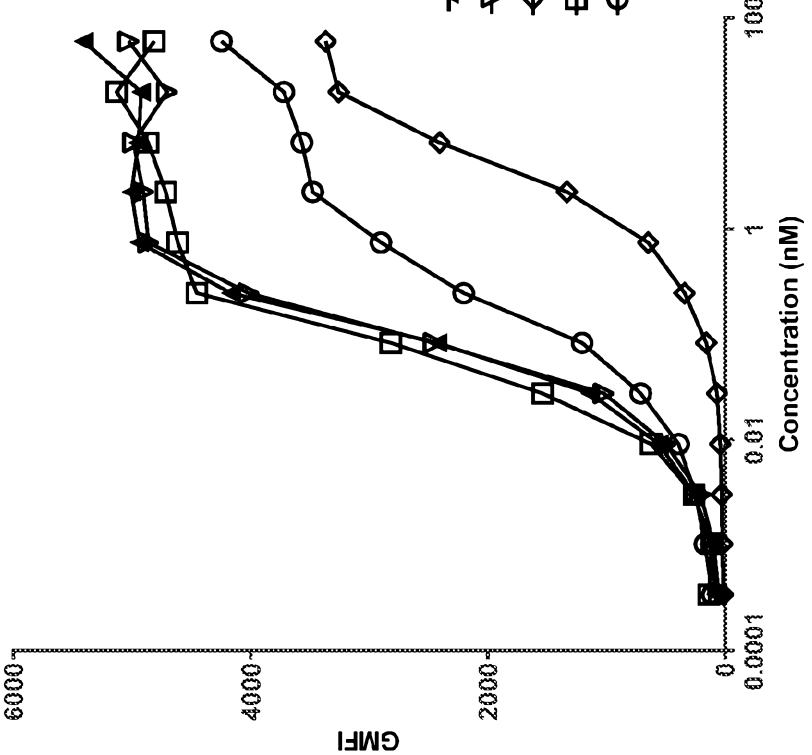
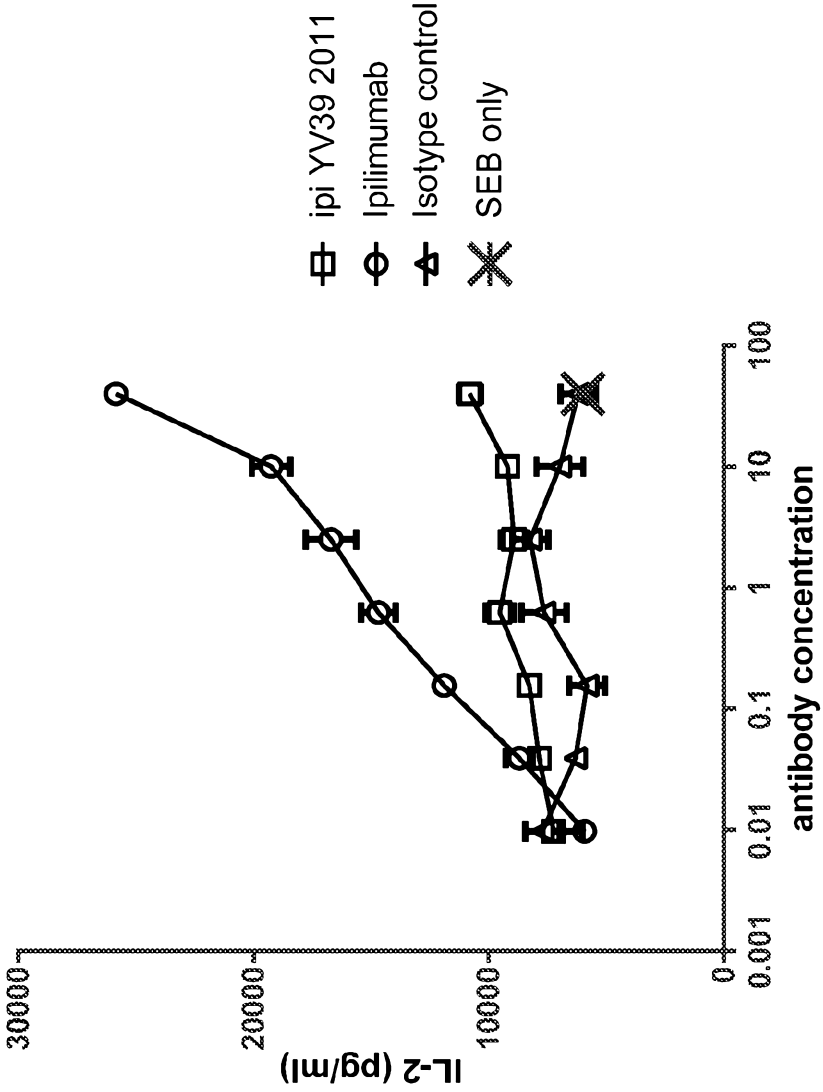


FIG. 7D

Sample	EC50 (nM)
Ipi YV39 2011	22
Ipilimumab	0.54
Ipi YV39 2011 MMP monoclipped	2.8
Ipi YV39 2011 MMP clipped	0.65
Ipi YV39 2011 μPA clipped	0.76

FIG. 8


ipi YV39 2011
Ipilimumab
Isotype control
SEB only
IL-2 (pg/ml)
30000
20000
10000
0
0.001
0.01
0.1
1
10
100
antibody concentration

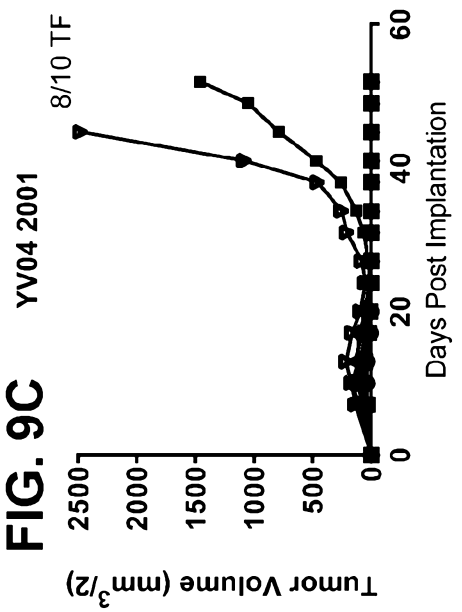


FIG. 9A
Control mg2a
0/10 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
2500
0
20
40
60

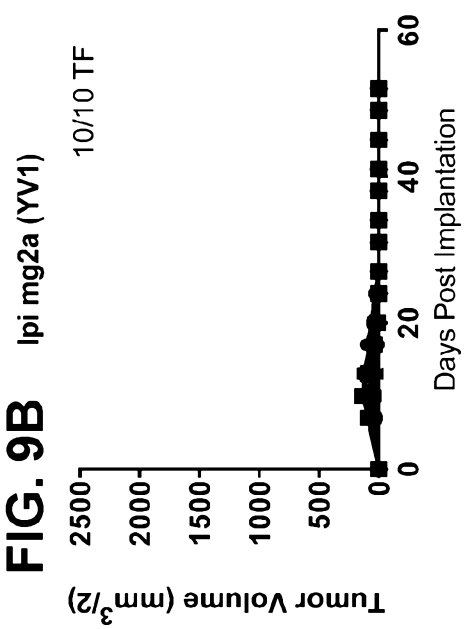


FIG. 9B
Ipi mg2a (YV1)
10/10 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
2500
0
20
40
60

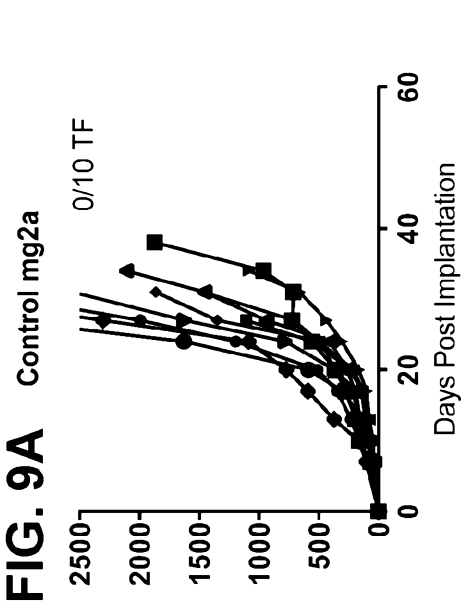


FIG. 9C
YV04 2001
8/10 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
2500
0
20
40
60

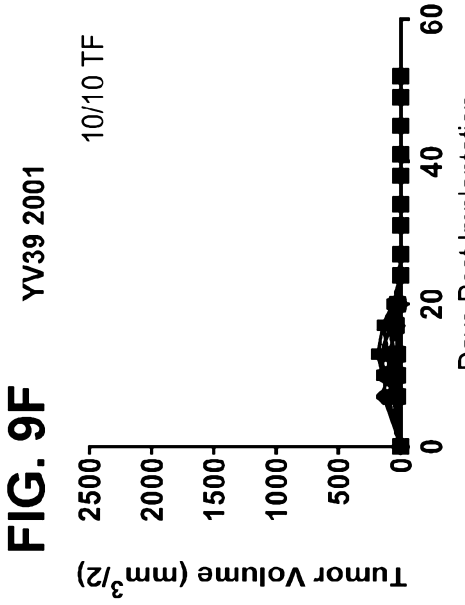


FIG. 9D
YV23 2001
9/10 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
2500
0
20
40
60

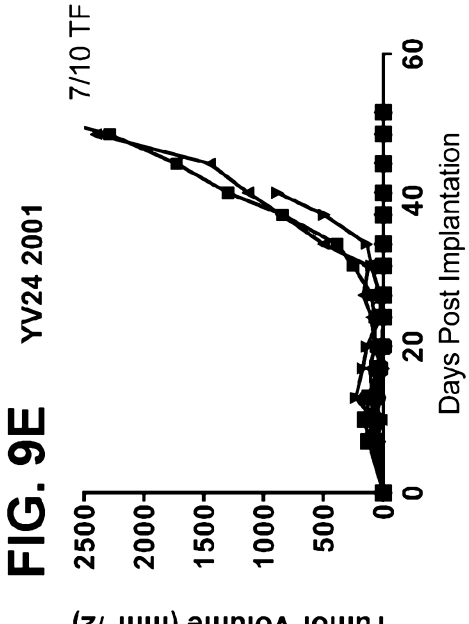


FIG. 9E
YV24 2001
7/10 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
2500
0
20
40
60

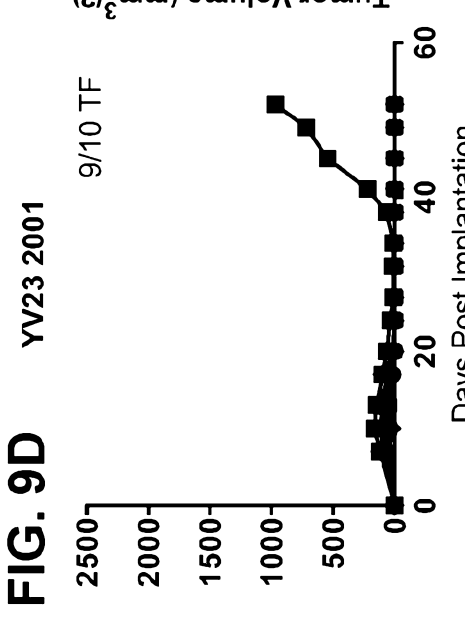


FIG. 9F
YV39 2001
10/10 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
2500
0
20
40
60

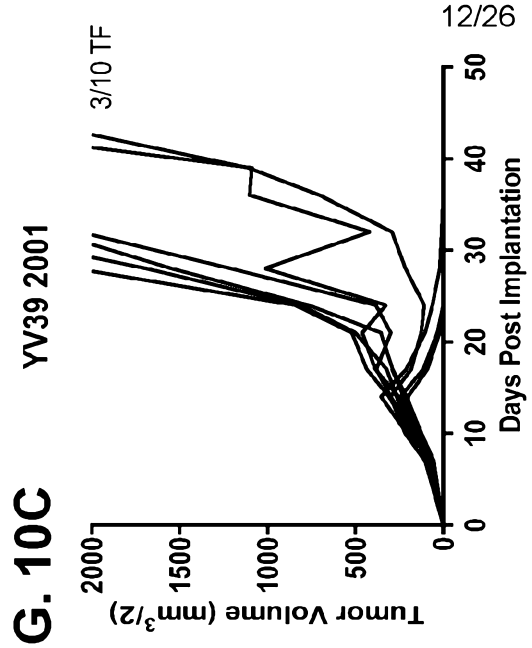


FIG. 10C
YV39 2001
3/10 TF
Tumor Volume (mm3/2)
Days Post Implantation

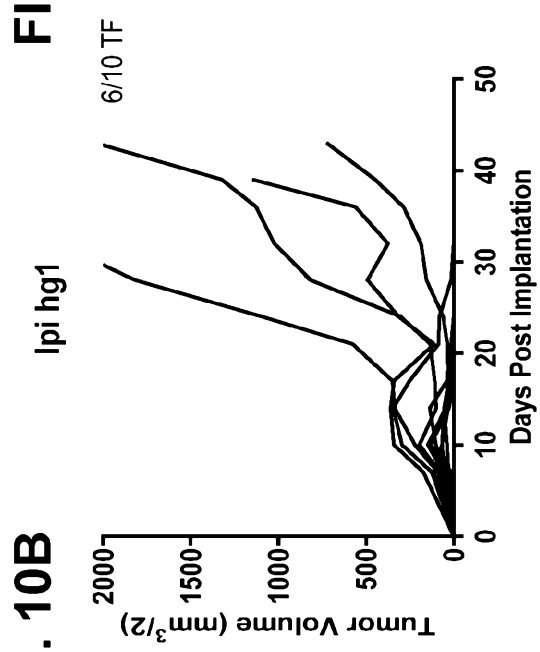


FIG. 10B
lpi hg1
6/10 TF
Tumor Volume (mm3/2)
Days Post Implantation

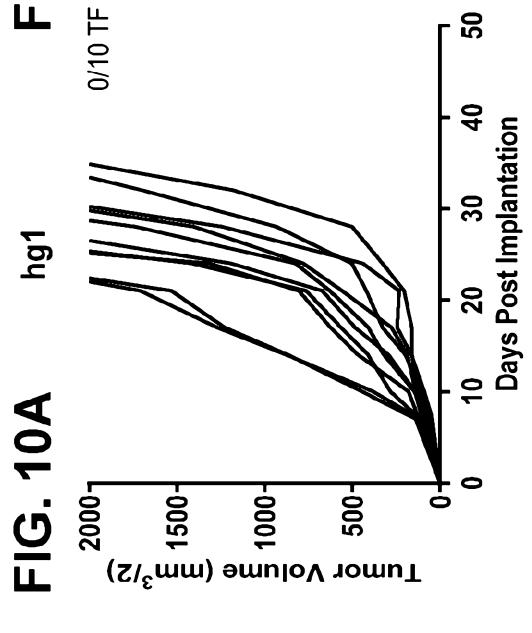


FIG. 10A
hg1
0/10 TF
Tumor Volume (mm3/2)
Days Post Implantation

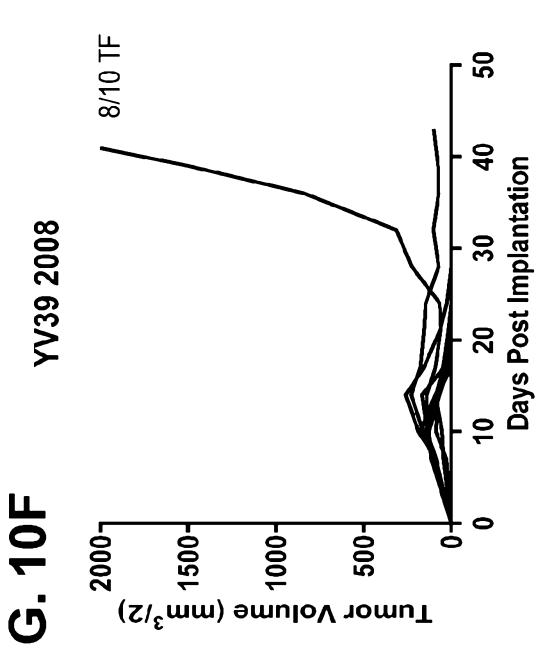


FIG. 10F
YV39 2008
8/10 TF
Tumor Volume (mm3/2)
Days Post Implantation

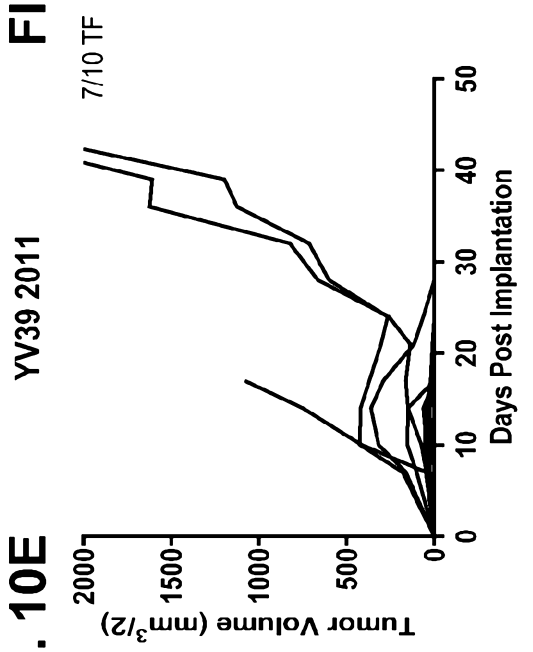


FIG. 10E
YV39 2011
7/10 TF
Tumor Volume (mm3/2)
Days Post Implantation

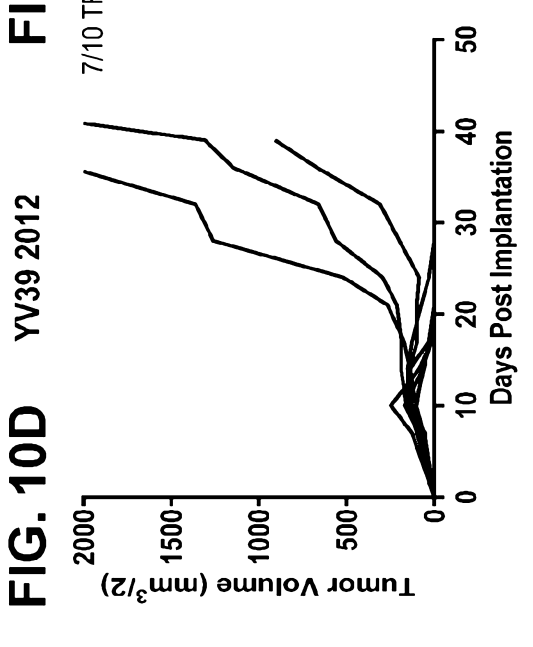


FIG. 10D
YV39 2012
7/10 TF
Tumor Volume (mm3/2)
Days Post Implantation

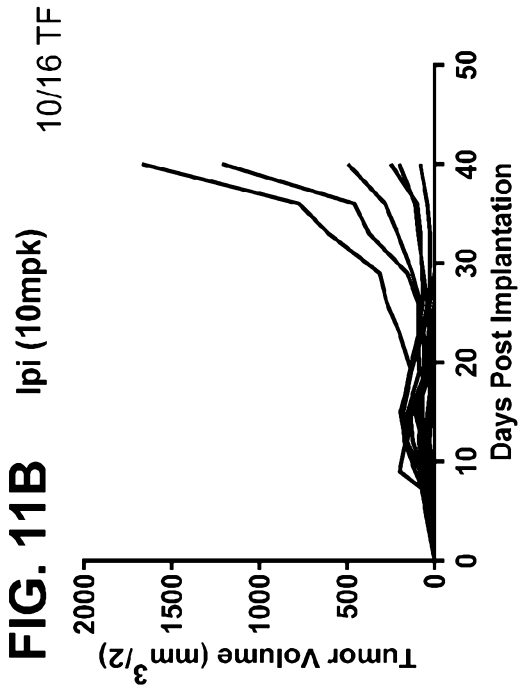


FIG. 11B
Ipi (10mpk)
10/16 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
0
10
20
30
40
50

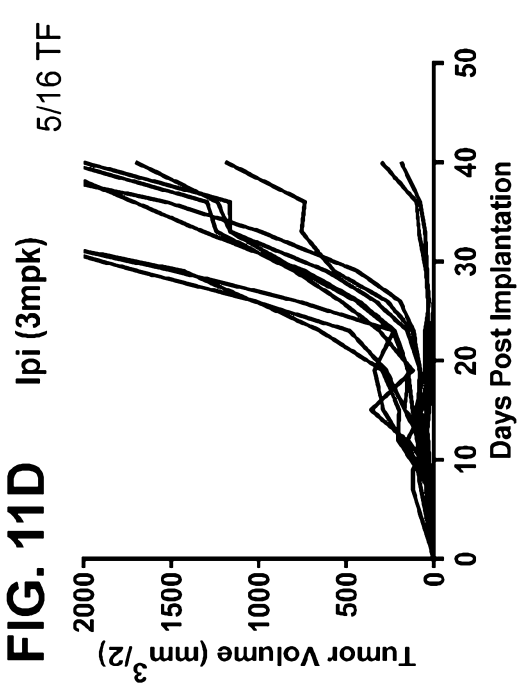


FIG. 11D
Ipi (3mpk)
5/16 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
0
10
20
30
40
50

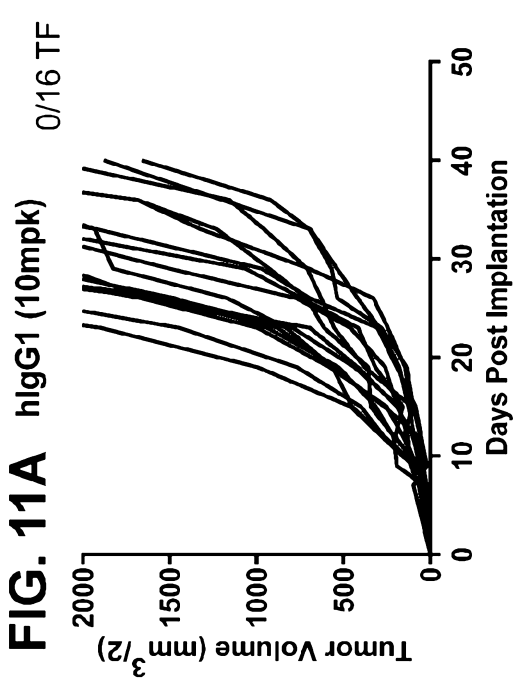


FIG. 11A
hIgG1 (10mpk)
0/16 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
0
10
20
30
40
50

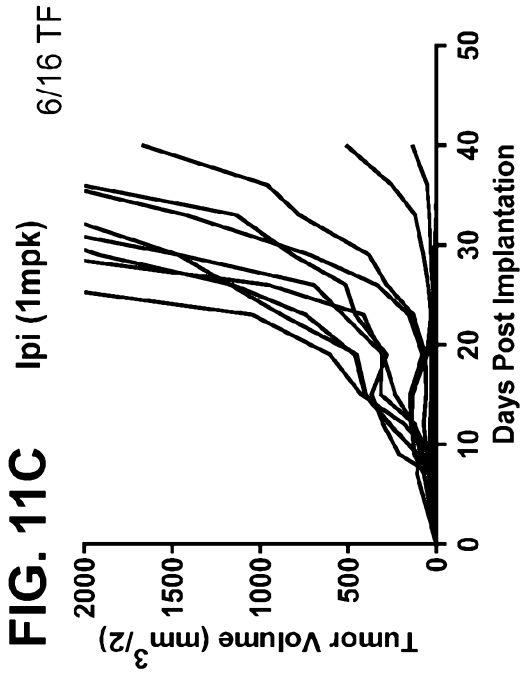


FIG. 11C
Ipi (1mpk)
6/16 TF
Tumor Volume (mm3/2)
Days Post Implantation
0
500
1000
1500
2000
0
10
20
30
40
50

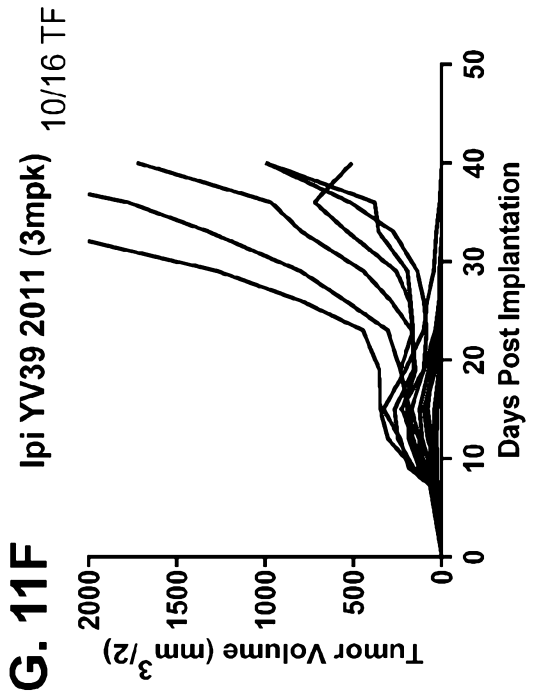


FIG. 11F

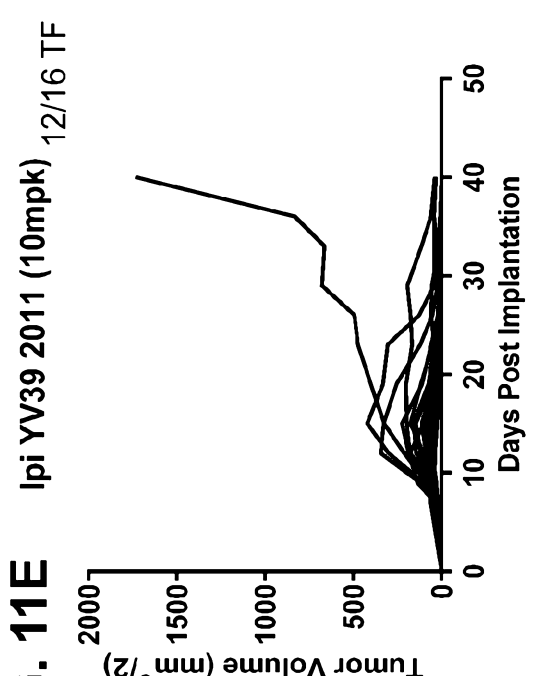


FIG. 11E

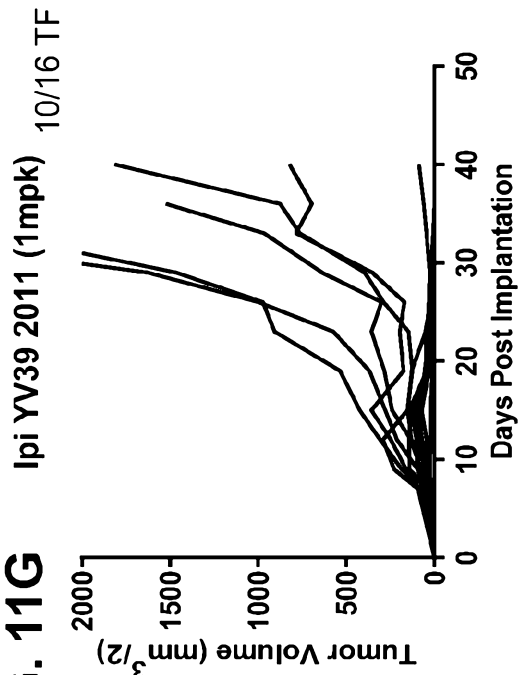


FIG. 11G

FIG. 12A

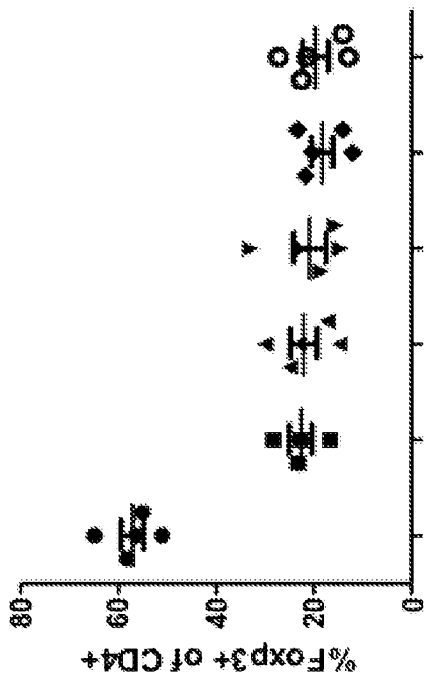


FIG. 12B

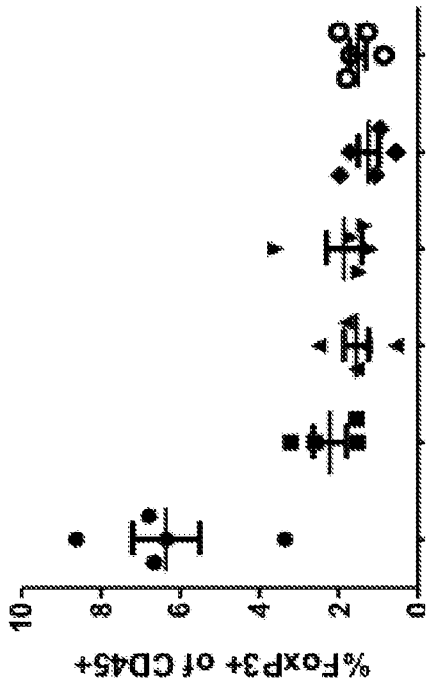


FIG. 12C

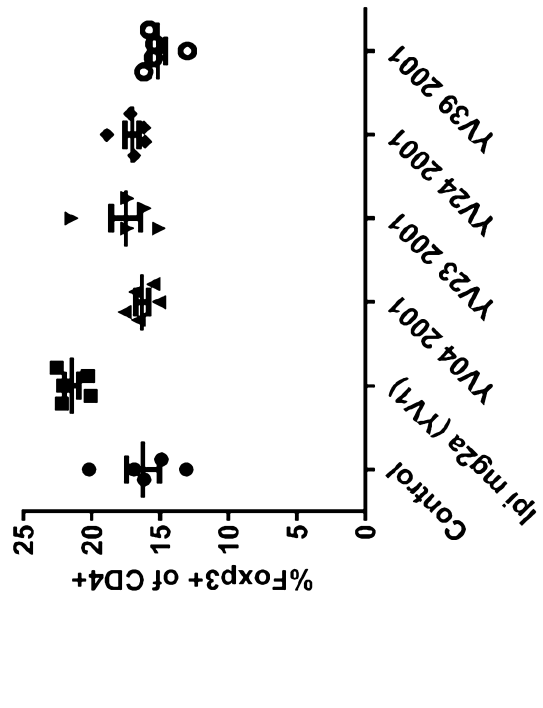


FIG. 12D

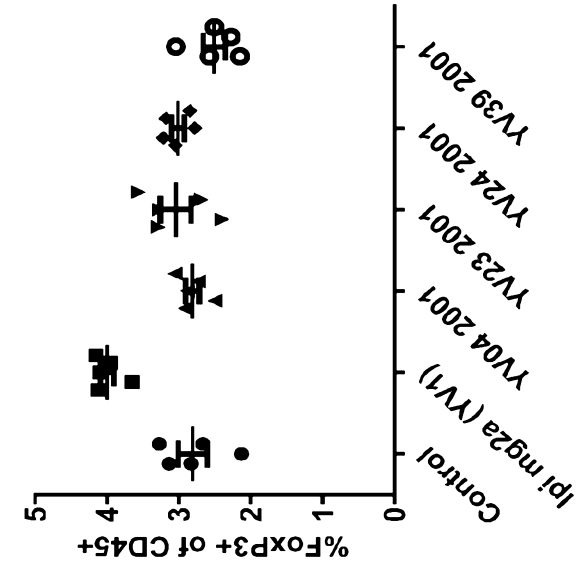


FIG. 12E

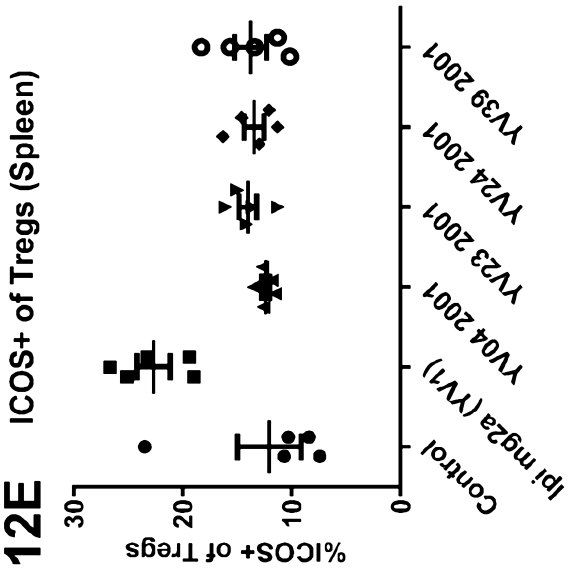
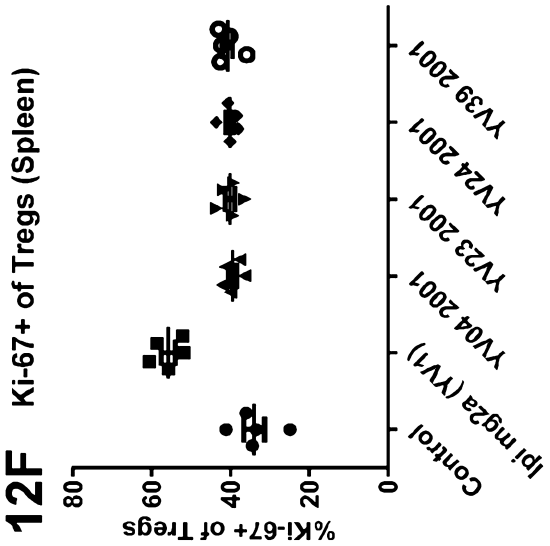


FIG. 12F



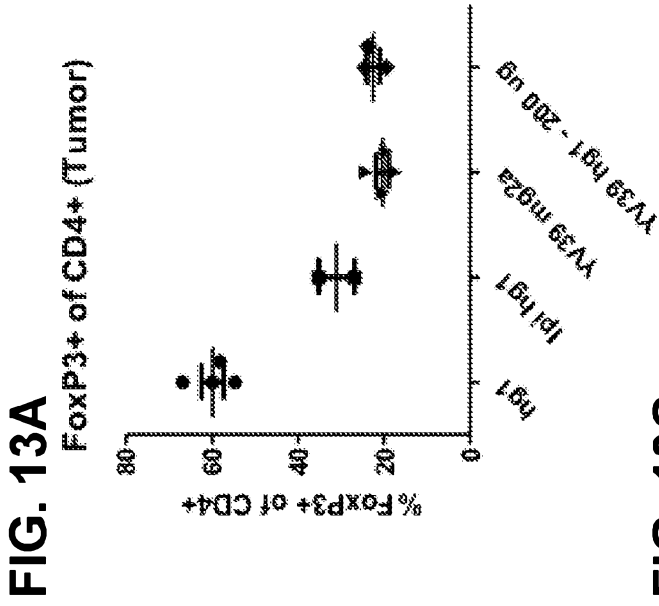


FIG. 13A
FoxP3+ of CD4+ (Tumor)
%FoxP3+ of CD4+
80
60
40
20
0
hIgG1
Ipi hIgG1
VV39 mIgG2a
VV39 hIgG1 - 200 ug

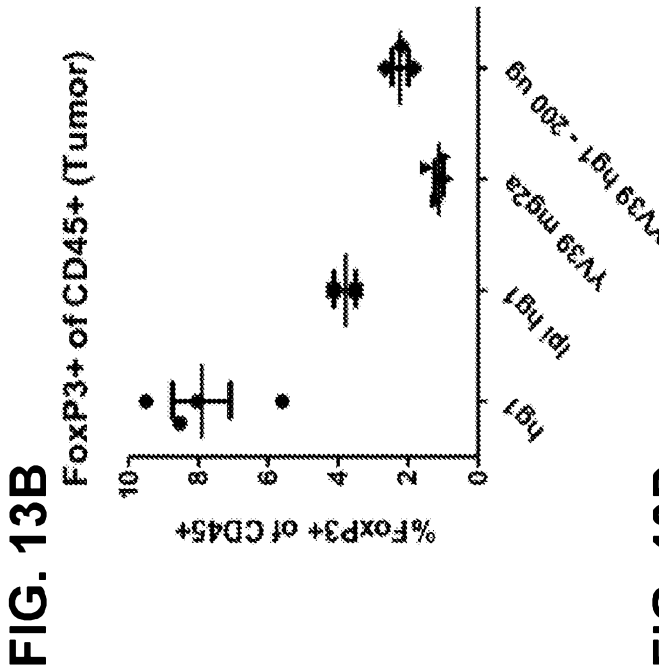


FIG. 13B
FoxP3+ of CD45+ (Tumor)
%FoxP3+ of CD45+
10
8
6
4
2
0
hIgG1
Ipi hIgG1
VV39 mIgG2a
VV39 hIgG1 - 200 ug

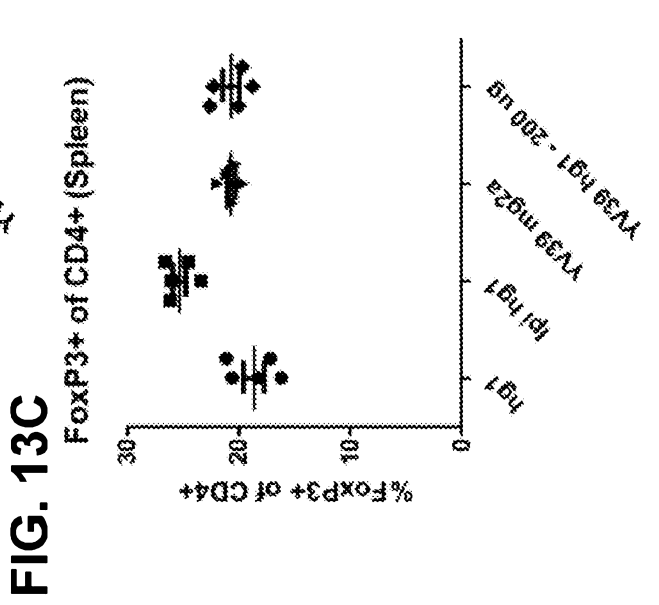


FIG. 13C
FoxP3+ of CD4+ (Spleen)
%FoxP3+ of CD4+
30
20
10
0
hIgG1
Ipi hIgG1
VV39 mIgG2a
VV39 hIgG1 - 200 ug

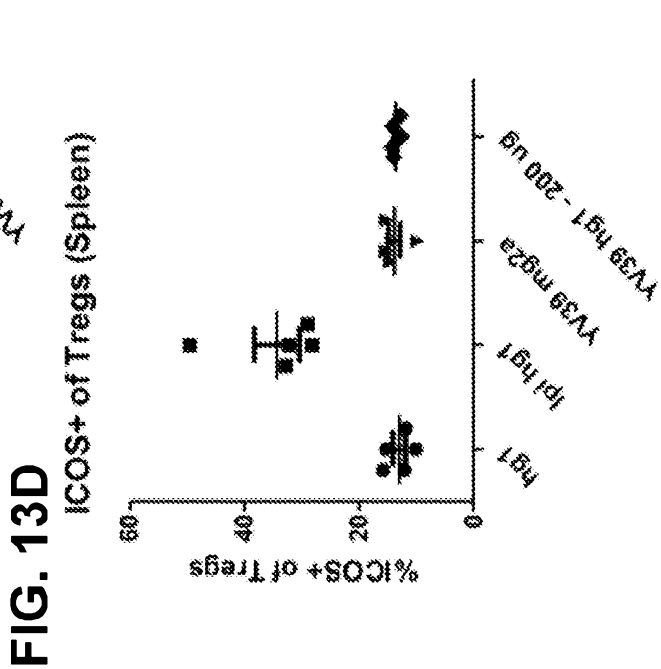


FIG. 13D
ICOS+ of Tregs (Spleen)
%ICOS+ of Tregs
60
40
20
0
hIgG1
Ipi hIgG1
VV39 mIgG2a
VV39 hIgG1 - 200 ug

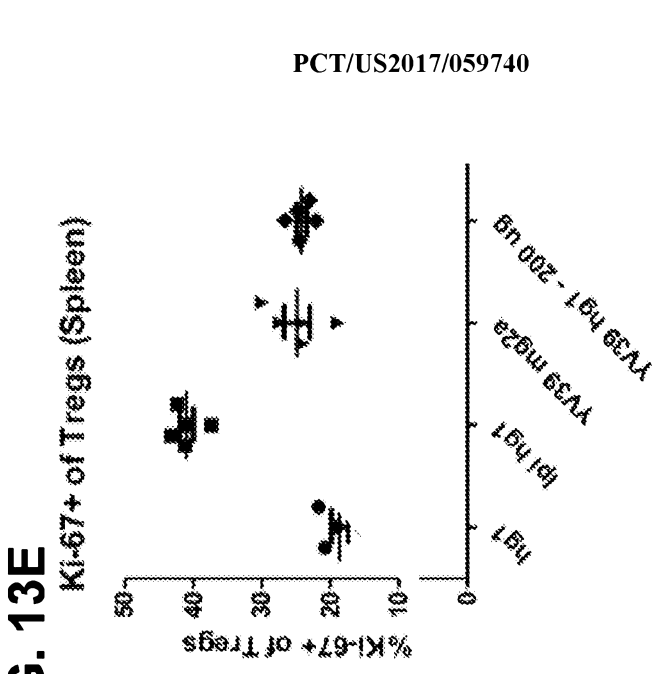


FIG. 13E
Ki-67+ of Tregs (Spleen)
%Ki-67+ of Tregs
50
40
30
20
10
0
hIgG1
Ipi hIgG1
VV39 mIgG2a
VV39 hIgG1 - 200 ug

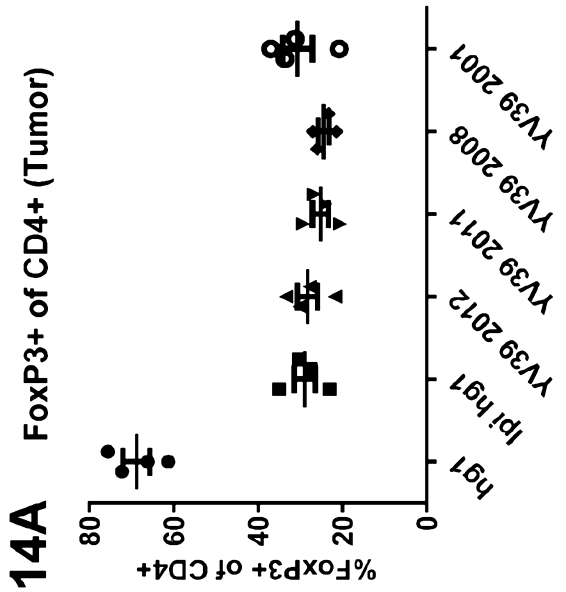


FIG. 14A
FoxP3+ of CD4+ (Tumor)
%FoxP3+ of CD4+
0
20
40
60
80
hg1
ipi hg1
VV39 2012
VV39 2011
VV39 2008
VV39 2001

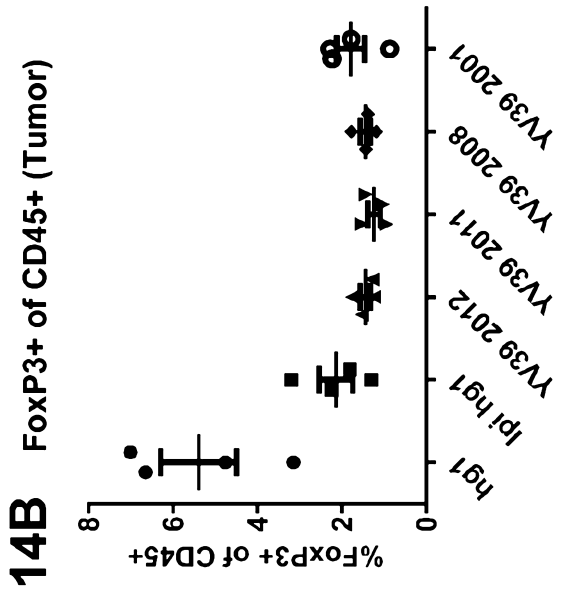


FIG. 14B
FoxP3+ of CD45+ (Tumor)
%FoxP3+ of CD45+
0
2
4
6
8
hg1
ipi hg1
VV39 2012
VV39 2011
VV39 2008
VV39 2001

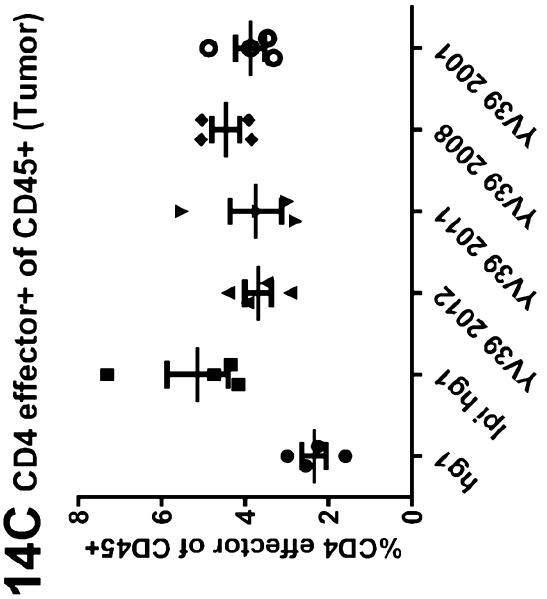


FIG. 14C
CD4 effector+ of CD45+ (Tumor)
%CD4 effector of CD45+
0
2
4
6
8
hg1
ipi hg1
VV39 2012
VV39 2011
VV39 2008
VV39 2001

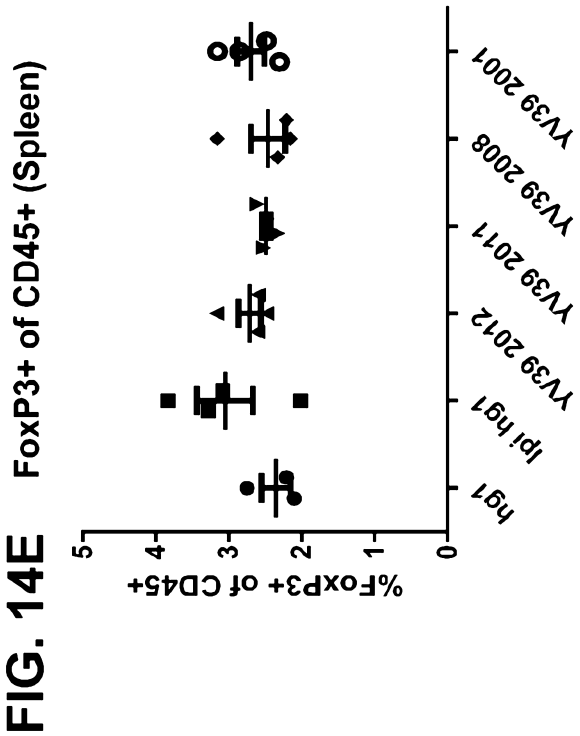


FIG. 14E

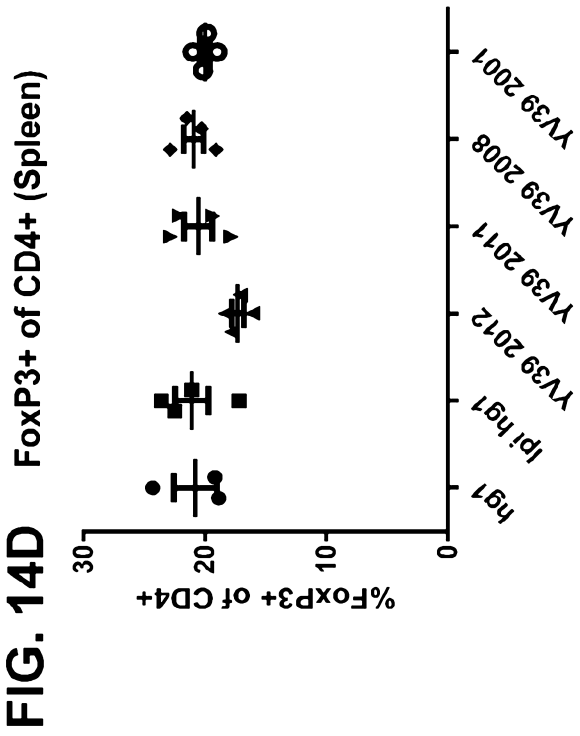


FIG. 14D

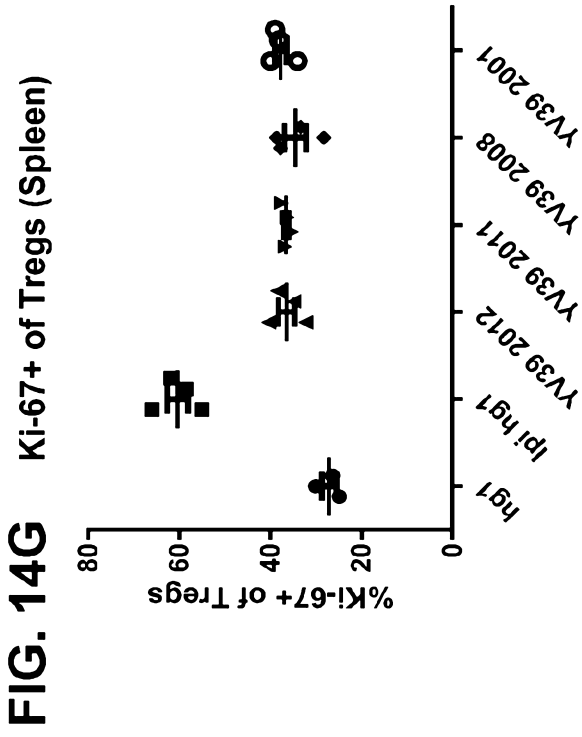


FIG. 14G

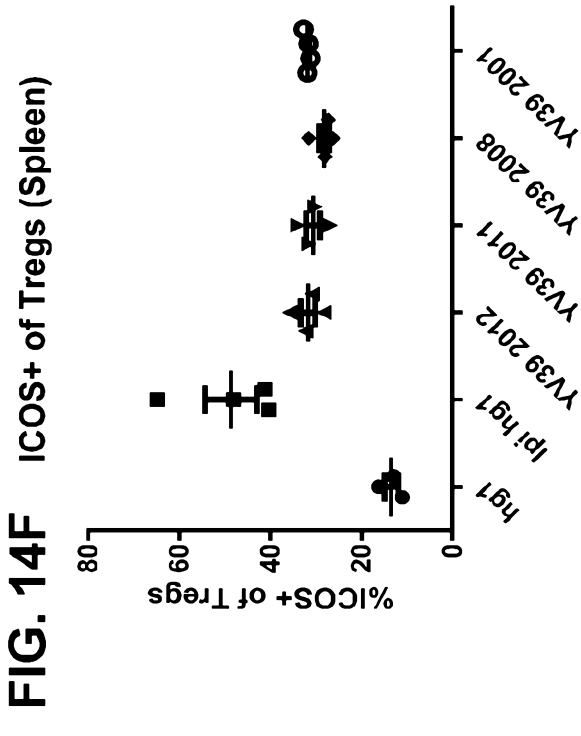


FIG. 14F

FIG. 15

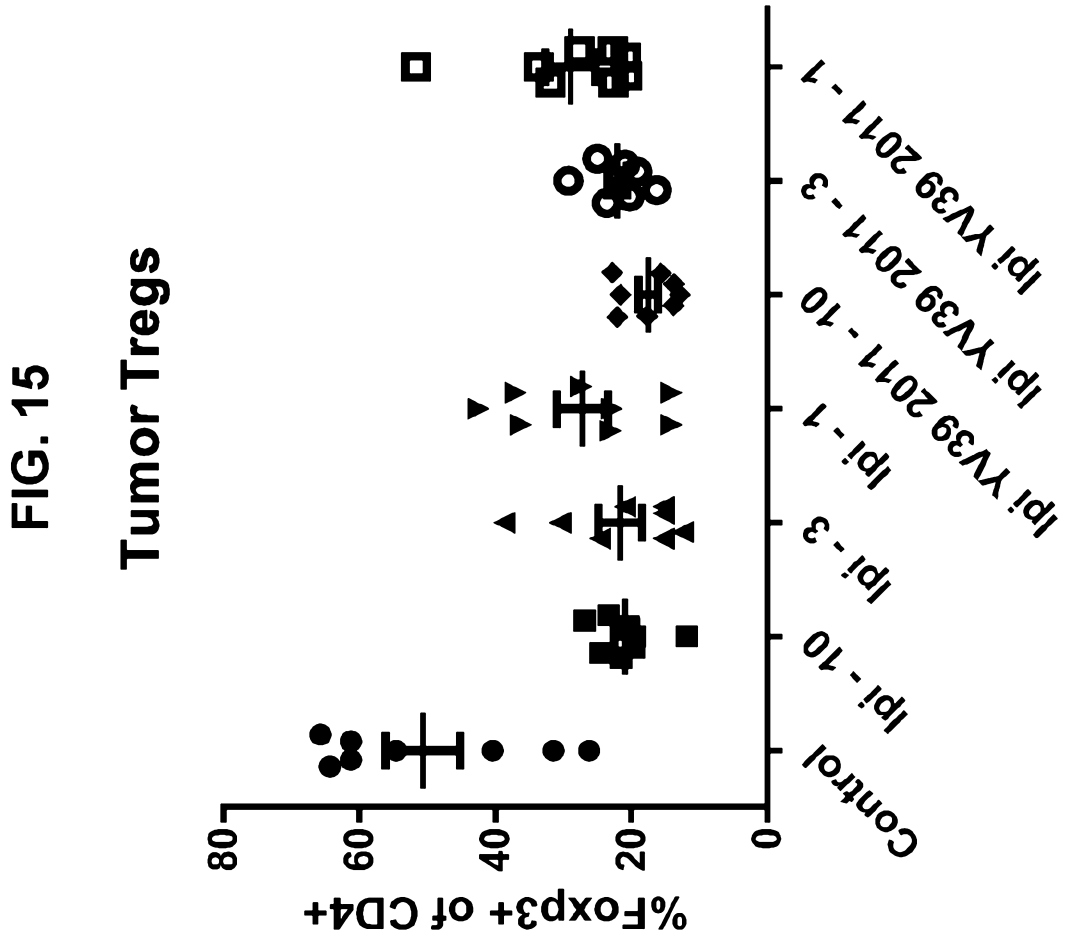

Tumor Tregs
%Foxp3+ of CD4+
0
20
40
60
80
Control
Ipi - 10
Ipi - 3
Ipi - 1
Ipi YV39 2011 - 10
Ipi YV39 2011 - 3
Ipi YV39 2011 - 1

FIG. 16A

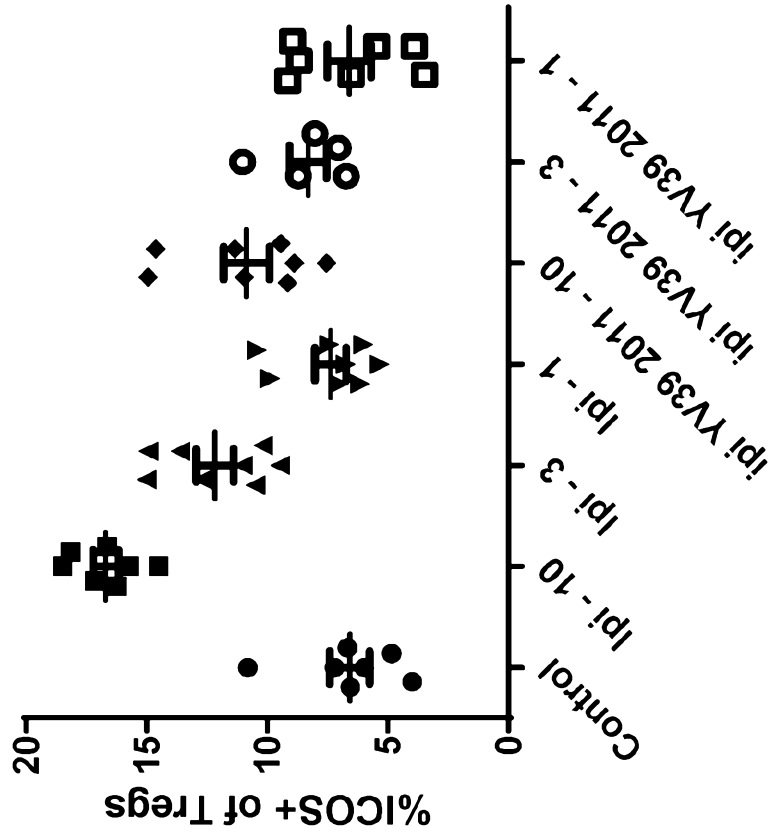


FIG. 16B

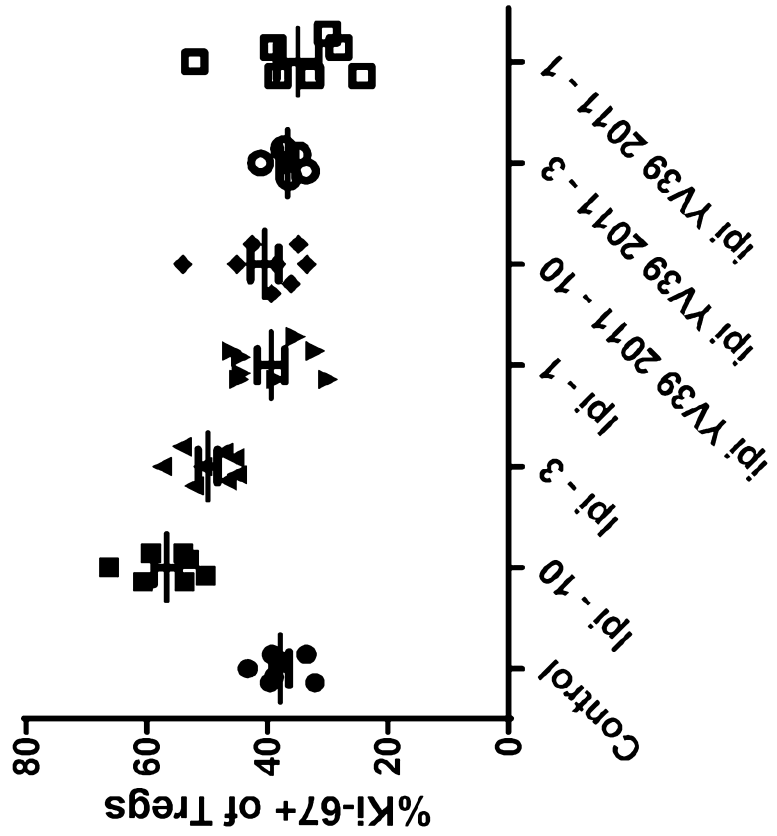


FIG. 17A

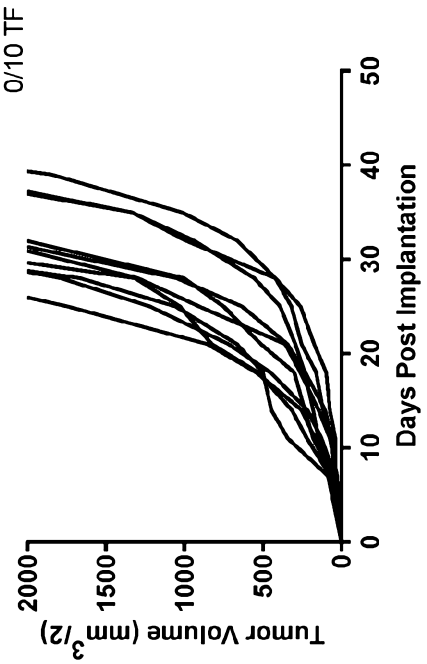


FIG. 17B

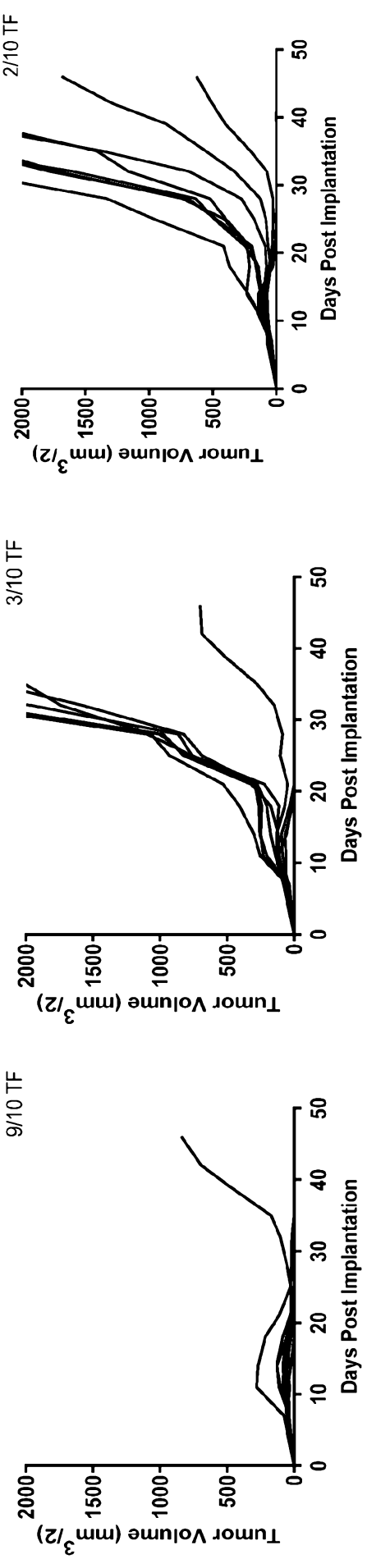
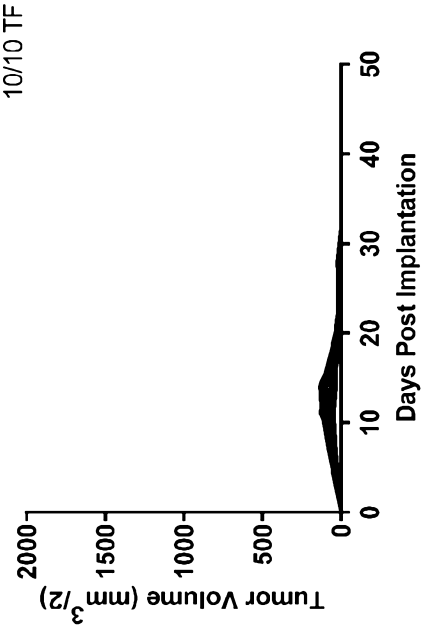
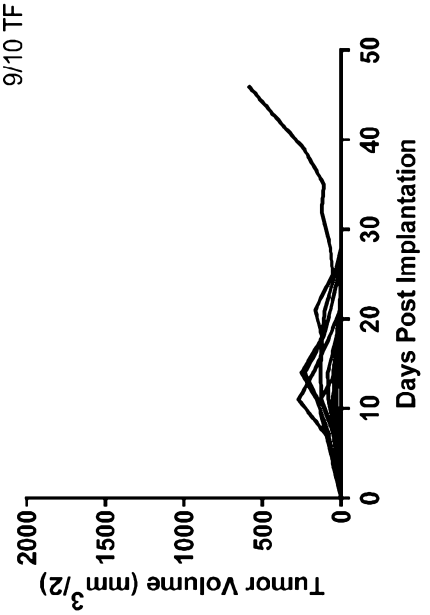


FIG. 17C





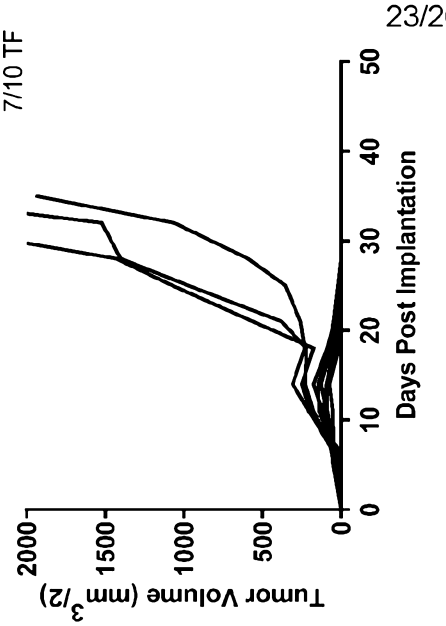
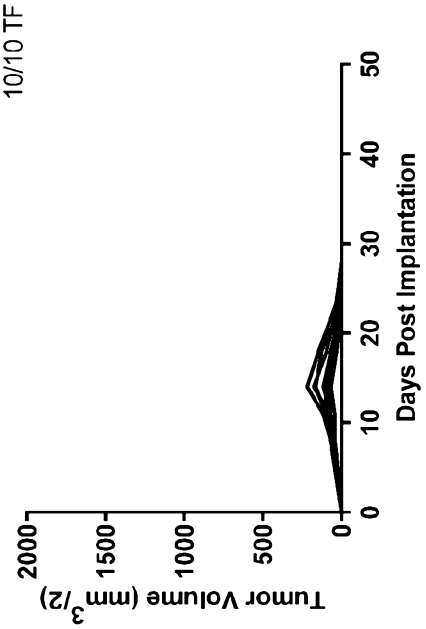
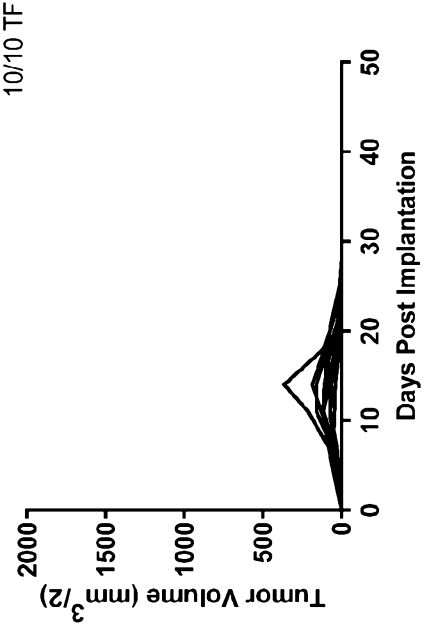
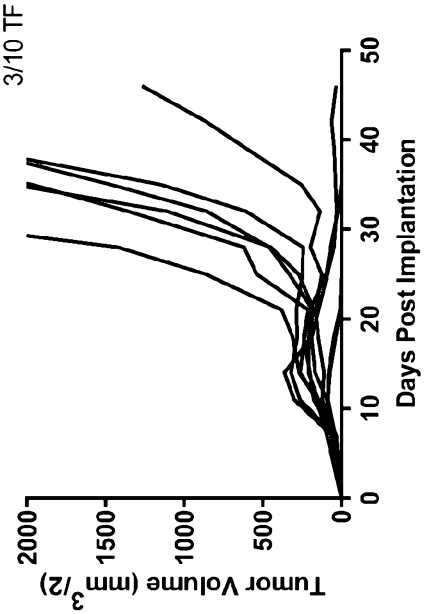


FIG. 17D







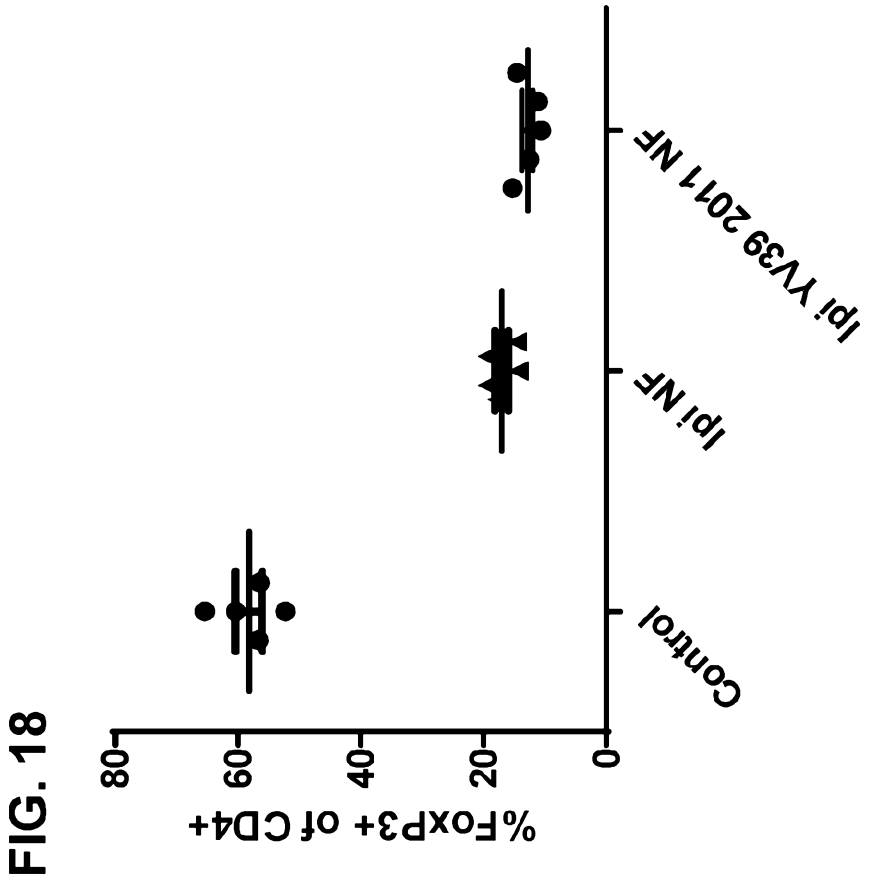
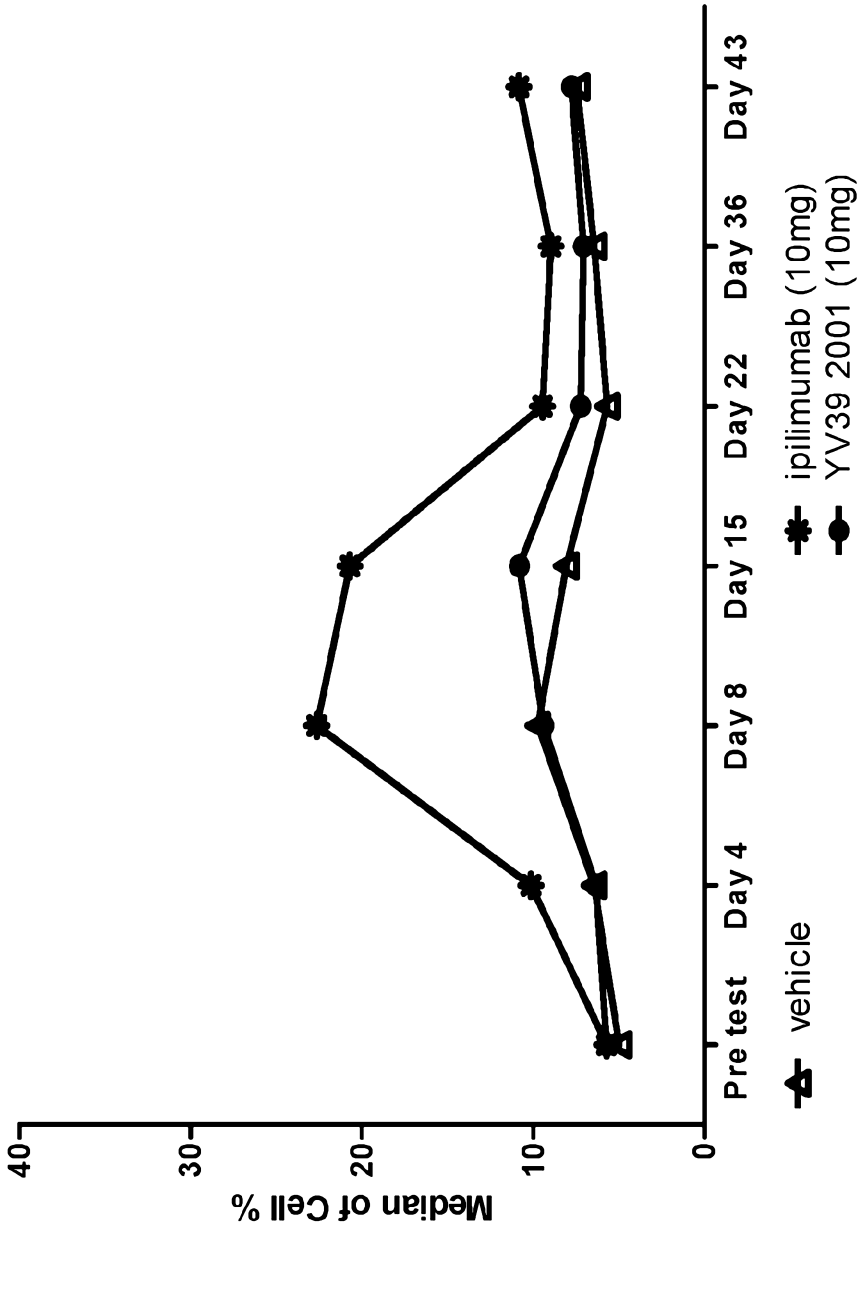


FIG. 18

FIG. 19

	FcR	IgG1 Ipi (nM)	NF Ipi NF (nM)
Human FcR	hCD64	0.2	0.18
	hCD32a-H131	920	900
	hCD32a-R131	1100	730
	hCD32b	>5000	4200
	hCD16a-V158	310	9.5
	hCD16a-F158	4600	190
	hCD16B-NA1	>5000	1800
	hCD16B-NA2	4200	110
Cyno FcR	cyCD64	11	5.6
	cyCD32a	2700	2300
	cyCD32b	1900	2000
	cyCD16	**370**	**7.5**
Mouse FcR	mCD64	62	69
	mCD32	1300	1100
	mCD16	3100	2700
	mFcγRIV	29	6.3

FIG. 20


Ki67 on CD4+ T cells
Median of Cell %
0
10
20
30
40
Pre test
Day 4
Day 8
Day 15
Day 22
Day 36
Day 43
vehicle
ipilimumab (10mg)
YV39 2001 (10mg)

SEQUENCE LISTING

<110> BRISTOL-MYERS SQUIBB COMPANY

<120> ACTIVATABLE ANTI-CTLA-4 ANTIBODIES AND USES THEREOF

<130> 3338.059PC02/ELE/PAC/DKC

<160> 570

<170> PatentIn version 3.5

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<213> Artificial Sequence

<220>
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1 5 10 15

<210> 2
<211> 15
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<213> Artificial Sequence

<220>
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<400> 2

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr
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1 5 10 15

<210> 4
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1 5 10 15

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Cys Thr Tyr Ser Phe Phe Asn Val Cys
1 5

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Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys
1 5 10

<210> 7
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<213> Artificial Sequence

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1 5

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Gly Thr Ala Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 9

Phe Gly Thr Ala Cys Pro Asn His Pro Met Cys His Asp Trp Gln
1 5 10 15

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<213> Artificial Sequence

<220>
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<400> 10

Ser Ala Cys Ala Tyr Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

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

<220>
<223> Masking Moiety - YV11

<400> 11

Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys
1   5   10

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 12

Cys Arg Thr Gln Ile Tyr Gly Tyr Asn Leu Cys
1   5   10

<210> 13
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<213> Artificial Sequence

<220>
<223> Masking Moiety - YV13

<400> 13

Leu His Cys Arg Thr Gln Ile Tyr Gly Tyr Asn Leu Cys Pro Tyr
1   5   10   15

<210> 14
<211> 11
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<220>
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<400> 14

Cys Pro Asn His Pro Met Cys His Asp Trp Gln
1   5   10

<210> 15
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<220>
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<400> 15

Gly Thr Ala Cys Pro Asn His Pro Met Cys His Asp Trp Gln
1 5 10

<210> 16
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Cys Ala Tyr Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 17

Gln Glu Cys His Leu Tyr Met Tyr Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 18
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1 5 10

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<220>
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<400> 19

Gly Gln Cys Gln Phe Tyr Met Phe Gly Tyr Asn Leu Cys Pro Tyr
1 5 10 15

<210> 20
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety - YV20

<400> 20

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1 5 10 15

<210> 21
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety - YV21

<400> 21

Cys Leu His Ser Met Tyr Asn Val Cys Leu Asp Pro
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<210> 22
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<223> Masking Moiety - YV22

<400> 22

Cys Leu His Ser Met Tyr Asn Val Cys
1   5

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<400> 23

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro
1   5   10

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<400> 24

Cys Leu His Ser Ala Tyr Asn Val Cys Leu Asp Pro
1   5   10

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<400> 25

Cys Met Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10

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<400> 26

Cys Met Tyr Ser Phe Phe Asn Val Cys
1 5

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<400> 27

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys
1 5 10

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<400> 28

Cys Ala Gln Leu Tyr Gly Tyr Ser Met Cys Pro His Thr
1 5 10

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<400> 29

Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Ala His Thr
1 5 10

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<400> 30

Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro Ala Thr
1 5 10

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<400> 31

Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr
1 5 10

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<400> 32

Cys Pro Asn His Pro Leu Cys His Asp Trp Gln
1 5 10

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<400> 33

Cys Pro Asn His Pro Met Cys Ala Asp Trp Gln
1 5 10

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<400> 34

Cys Pro Asn His Pro Met Cys His Ala Trp Gln
1 5 10

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<400> 35

Cys Pro Asn His Pro Met Cys His Asp Ala Gln
1 5 10

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<400> 36

Cys Pro Asn His Pro Met Cys His Asp Trp Ala
1 5 10

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<400> 37

Gly Thr Ala Cys Pro Asn His Pro Met Cys
1   5   10

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<400> 38

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys
1   5   10

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<400> 39

Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr
1   5   10

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<400> 40

Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Ala Tyr
1   5   10

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<400> 41

Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Ala
1 5 10

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<400> 42

Phe Gly Thr Ala Cys Pro Asn His Pro Leu Cys His Asp Trp Gln
1 5 10 15

<210> 43
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<212> PRT
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<400> 43

Cys Pro Asn His Pro Leu Cys His Asp Phe Gln
1 5 10

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<400> 44

Cys Pro Asn His Pro Leu Cys His Asp Tyr Gln
1   5   10

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<400> 45

Cys Pro Asn His Pro Leu Cys Pro Tyr
1   5

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<400> 46

Cys Pro Asn His Pro Leu Cys Pro Ala
1   5

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<400> 47

Cys Met Tyr Ser Phe Phe Asn Val Cys Tyr Pro
1   5   10

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<400> 48

Cys Met Tyr Ser Phe Phe Asn Val Cys Tyr Ala
1 5 10

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<400> 49

Cys Leu Tyr Ser Phe Phe Asn Val Cys Tyr Pro
1 5 10

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<400> 50

Cys Leu Tyr Ser Phe Phe Asn Val Cys Tyr Ala
1 5 10

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<400> 51

Phe Gly Ala Ala Cys Pro Asn His Pro Ile Cys His Asp Trp Gln
1 5 10 15

<210> 52
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<212> PRT
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<400> 52

Phe Gly Ala Ala Cys Pro Asn His Pro Leu Cys His Asp Trp Gln
1 5 10 15

<210> 53
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<400> 53

Phe Gly Ala Ala Cys Pro Asn His Pro Met Cys His Asp Ala Gln
1 5 10 15

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<220>
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<400> 54

Cys Leu His Ser Ala Tyr Asn Ala Cys Leu Asp Pro
1 5 10

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<400> 55

Cys Ala His Ser Ala Tyr Asn Val Cys Leu Asp Pro
1 5 10

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<400> 56

Cys Leu His Ser Ala Tyr Asn Val Cys Ala Asp Pro
1   5   10

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<400> 57

Cys Leu His Ser Ala Tyr Asn Val Cys Leu Ala Pro
1   5   10

<210> 58
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<400> 58

Cys Leu His Ser Ala Tyr Asn Val Cys Leu Asp Ala
1   5   10

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<400> 59

Lys Asn Thr Cys Thr Tyr Val Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 60
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<212> PRT
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<220>
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<400> 60

Tyr Ile Ser Asp Cys Pro Tyr His Pro Met Cys His Asp Tyr Gln
1 5 10 15

<210> 61
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<220>
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<400> 61

Phe Arg Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Arg
1 5 10 15

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<220>
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<400> 62

Arg Glu Cys His Met Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 63
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<220>
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<400> 63

Ala Val Cys His Met Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Phe
1   5   10   15

<210> 64
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<220>
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<400> 64

Arg Ser Cys Pro Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr
1   5   10   15

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<400> 65

Gln Pro Cys Ala Gln Met Phe Gly Tyr Ser Met Cys Pro His Thr
1   5   10   15

<210> 66
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<400> 66

Thr Ala Lys Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 67
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<400> 67

Asp Phe Ser Cys Leu Tyr Ser Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 68
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<400> 68

Asp Val Ser Cys Met Tyr Met Met Tyr Asn Phe Cys Leu Asp Pro
1 5 10 15

<210> 69
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<220>
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<400> 69

Cys Pro Asn His Pro Met Cys
1 5

<210> 70
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<400> 70

Cys Met Tyr Ser Phe Phe Asn Val Cys Pro Tyr
1 5 10

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<400> 71

Cys Met Tyr Ser Phe Phe Asn Val Cys Pro Ala
1 5 10

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<400> 72

Cys Thr Tyr Ser Phe Phe Asn Val Cys Pro Tyr
1 5 10

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<400> 73

Cys Thr Tyr Ser Phe Phe Asn Val Cys Pro Ala
1 5 10

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<400> 74

Gly Phe Pro Cys Met Tyr Ser Met Phe Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 75
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<400> 75

Gly Leu Ser Cys Met Tyr Ser Met Tyr Gly Tyr Cys Leu Asp Pro
1 5 10 15

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<400> 76

Ile Pro Cys Asp Tyr Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

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<400> 77

Gln Val Cys His Ala Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
1 5 10 15

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<400> 78

Arg Met Tyr Cys Thr Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 79

Ala Leu Ser Cys Met Tyr Ile Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 80

Asp Phe Ser Cys Met Tyr Val Met Phe Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 81

Asp Phe Ser Cys Val Tyr Ser Met Phe Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 82

Asp Met Asn Thr Cys Pro Asn His Pro Met Cys Tyr Asp Tyr Arg
1 5 10 15

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<400> 83

Asp Met Asn Thr Cys Pro Arg His Pro Met Cys His Asp Tyr His
1 5 10 15

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<400> 84

Asp Ser Arg Cys Met Tyr Val Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 85
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<220>
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<400> 85

Glu His Leu Cys Thr Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 86
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<220>
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<400> 86

Glu Leu Ser Cys Val Tyr Ser Met Phe Gly Phe Cys Leu Asp Pro
1 5 10 15

<210> 87
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<400> 87

Phe Thr Asn Asn Cys Pro Tyr His Pro Met Cys His Asp Tyr Leu
1 5 10 15

<210> 88
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<220>
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<400> 88

Gly Phe Ser Cys Thr Tyr Ile Met Tyr Asp Val Cys Leu Asp Pro
1 5 10 15

<210> 89
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<400> 89

Gly Ser Ser Cys Met Tyr Ser Met Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 90
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<400> 90

His Phe Ser Cys Met Tyr Ile Met Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 91
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<400> 91

Leu His Cys Gly Met Trp Met Phe Gly Val Asn Leu Cys Pro Lys
1   5   10   15

<210> 92
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<400> 92

Leu Pro Cys Gln Met Trp Met Phe Gly His Asn Leu Cys Pro His
1   5   10   15

<210> 93
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<400> 93

Leu Pro Cys Thr Met Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
1 5 10 15

<210> 94
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<400> 94

Leu Thr Cys His His Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 95
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<400> 95

Asn Phe Ser Cys Met Tyr Ser Met Phe Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 96

Asn Asn His Cys Met Tyr Ser Phe Phe Asn Ile Cys Leu Asp Pro
1 5 10 15

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<400> 97

Asn Arg Ser Cys Met Tyr Ile Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 98

Asn Ser Cys Thr Met Phe Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 99
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<220>
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<400> 99

Asn Thr Cys Glu Leu Tyr Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 100
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<220>

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<400> 100

Gln His Cys Asp Met Trp Met Phe Gly Tyr Asn Leu Cys Pro Tyr
1   5   10   15

<210> 101
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<400> 101

Gln His Cys Pro Met Tyr Met Phe Gly Tyr Asn Leu Cys Pro Phe
1   5   10   15

<210> 102
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<220>
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<400> 102

Gln Val Cys His Ile Gln Met Tyr Gly Phe Asp Leu Cys Pro His
1   5   10   15

<210> 103
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<400> 103

Arg Ala Cys Asp Tyr Trp Met Tyr Gly Val Asn Leu Cys Pro Tyr
1   5   10   15

<210> 104
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<220>
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<400> 104

Arg Gln Cys His Met Gln Met Phe Gly Tyr Asp Leu Cys Pro Phe
1 5 10 15

<210> 105
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<400> 105

Ser Gly Ser Cys Leu Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<220>
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<400> 106

Ser Asn Gly Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 107

Ser Thr Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His
1 5 10

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<400> 108

Ser Tyr Lys Cys Leu Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 109

Val Leu Tyr Cys Thr Tyr Val Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 110

Val Asn Cys Gly Met Trp Met Phe Gly Tyr Asn Leu Cys Pro Lys
1 5 10 15

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<400> 111

Tyr Gly Ser Cys Leu Tyr Ser Phe Tyr Asn Ile Cys Leu Asp Pro
1 5 10 15

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<400> 112

Tyr Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr
1 5 10 15

<210> 113
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<400> 113

Ala Ala Cys Asp Leu Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 114
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<400> 114

Ala Phe Cys Thr Leu Ala Pro Tyr Asn Gln Ala Cys Ile Ala Asn
1 5 10 15

<210> 115
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<400> 115

Ala Gly Ser Cys Leu Tyr Ser Met Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 116
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<400> 116

Ala Leu Cys Glu Asn Thr Met Tyr Gly Tyr His Leu Cys Pro Trp
1   5   10   15

<210> 117
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<400> 117

Ala Leu Ser Cys Met Tyr Ile Met Tyr Gly Val Cys Leu Asp Pro
1   5   10   15

<210> 118
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<400> 118

Ala Pro Val Cys Asp Val Leu Met Phe Gly Phe Cys Met Gln Pro
1   5   10   15

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<400> 119

Ala Gln Val Cys Ser Ile Met Met Tyr Gly Thr Cys Leu Met Pro
1 5 10 15

<210> 120
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<400> 120

Ala Ser Thr Cys Met Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 121
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<400> 121

Ala Val Cys Glu Phe Trp Met Phe Gly Phe Asn Leu Cys Pro Tyr
1 5 10 15

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<400> 122

Asp Ala Asn Thr Cys Pro Asn His Pro Met Cys Tyr Asp Tyr His
1 5 10 15

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<400> 123

Asp Phe Ser Cys Ile Tyr Ile Met Phe Asp Val Cys Leu Asp Pro
1 5 10 15

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<400> 124

Asp Phe Ser Cys Met Tyr Val Met Tyr Gly Phe Cys Leu Asp Pro
1 5 10 15

<210> 125
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<400> 125

Asp Phe Thr Cys Met Tyr Ser Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 126

Asp Phe Thr Cys Thr Tyr Ser Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

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<400> 127

Asp His Tyr Cys Thr Tyr Ile Met Tyr Ser Ile Cys Leu Asp Pro
1 5 10 15

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<400> 128

Asp Ile Cys Thr Asn Phe Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 129
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<400> 129

Asp Ile Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr His
1 5 10 15

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<400> 130

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Asp Met Ser Thr Cys Pro Asn His Pro Met Cys His Asp Tyr Met
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Asp Arg Asn Met Cys Pro Tyr His Pro Met Cys Tyr Asp Tyr Arg
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Asp Ser Cys Ala Phe Met Met Phe Gly Val Asn Leu Cys Pro Tyr
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Asp Ser Cys Arg Ser Val Phe Asp Met Val Trp Asn Cys Trp Asn
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Asp Thr Pro Asn Cys Pro His His Pro Met Cys His Asn His Met
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Asp Val Ser Cys Leu Tyr Val Met Tyr Ser Val Cys Leu Asp Pro
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Asp Trp Cys Ala Ser Met Met Phe Gly Tyr Asn Leu Cys Pro Tyr
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Glu Phe Ser Cys Met Tyr Ser Met Phe Asn Val Cys Leu Asp Pro
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Glu His Cys Asp Val Trp Met Phe Gly Phe Asn Leu Cys Pro Tyr
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Glu Pro Cys Asp Tyr Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
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Glu Gln Cys Thr Met Trp Met Tyr Gly Phe Asn Leu Cys Pro Tyr
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Glu Ser Ala Cys Ser Leu Arg Met Tyr Glu Val Cys Leu Gln Pro
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Glu Ser Cys Ser Tyr Trp Met Phe Gly Tyr Asn Leu Cys Pro Tyr
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Phe Ser Asn Thr Cys Pro His His Pro Met Cys Tyr Asp Tyr Arg
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Phe Trp Asn Thr Cys Pro His His Pro Met Cys His Asp Tyr Lys
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Phe Tyr Gln Asn Cys Tyr Pro Pro Thr Trp Cys Ser Met Phe Ser
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Gly Glu Cys Ser Tyr Trp Met Phe Gly Tyr Asn Leu Cys Pro Tyr
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Gly Gly Ser Cys Met Tyr Ser Phe Phe Asn Ile Cys Leu Asp Pro
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Gly Gly Ser Cys Val Tyr Val Met Tyr Asn Val Cys Leu Asp Pro
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Gly His Cys Leu Met His Met Tyr Gly Tyr Asn Leu Cys Pro Lys
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Gly His Cys Arg Met Ser Met Tyr Glu Met Thr Leu Cys Pro Arg
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Gly Ile Ser Cys Val His Ile Met Phe Asn Phe Cys Leu Asp Pro
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Gly Leu Cys Val Met Tyr Met Phe Gly Val Asn Leu Cys Pro Tyr
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Gly Ser Cys Asp Tyr Trp Met Phe Gly Tyr Asn Leu Cys Pro Tyr
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Gly Ser Tyr Cys Met Tyr Val Met Tyr Asn Val Cys Leu Asp Pro
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Gly Thr Lys Cys Ile Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
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<400> 166

Gly Thr Ser Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Arg
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<400> 167

Gly Thr Thr Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

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Gly Val Cys His Phe Phe Met Tyr Gly Val Ser Met Cys Pro Ala
1   5   10   15

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Gly Val Pro Cys Trp Tyr Ser Met Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

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Gly Val Ser Cys Met Tyr Ser Met Phe Asn Ile Cys Leu Asp Pro
1   5   10   15

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His Ala Lys Cys Val Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
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His Asp Ser Cys Met Tyr Ser Met Tyr Asn Phe Cys Leu Asp Pro
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His Gly Asn Thr Cys Pro Asn His Pro Met Cys His Asp Tyr Gln
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His Lys Gly Cys Leu Tyr Ser Phe Tyr Asn Ile Cys Leu Asp Pro
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His Thr Asn Met Cys Pro Tyr His Pro Met Cys Tyr Asp Tyr Lys
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Ile Met Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Gln
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Lys Lys Cys Asp Tyr Trp Phe Tyr Gly Val Asn Leu Cys Pro Tyr
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Lys Asn Thr Cys Val Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
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Lys Arg Pro Cys Met Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
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Lys Thr Thr Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
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Leu Asp Cys Gln Met Tyr Trp Trp Phe Gly Ala Cys Gly Asp Met
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Leu His Cys Ala Ile Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Phe
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Leu His Cys Pro Phe Gln Met Tyr Gly Tyr Asn Leu Cys Pro His
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Leu His Cys Ser Met Tyr Met Tyr Gly Phe Asn Leu Cys Pro Asn
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<400> 193

Arg Glu Cys Met Ala Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
1   5   10   15

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

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Leu Tyr Arg Cys Ile Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

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

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Asn Ala Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr
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Asn Asp Cys Asp Ile Ser Met Phe Asp Gln Ser Leu Cys Pro Tyr
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Asn Phe Ser Cys Val Tyr Val Met Phe Asn Val Cys Leu Asp Pro
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Asn Phe Thr Cys Ala Leu Thr Met Tyr Glu Val Cys Leu Asp Pro
1   5   10   15

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Asn Leu Cys His Ala Phe Met Phe Gly Phe Asn Leu Cys Pro Tyr
1   5   10   15

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Asn Leu Asn Asn Cys Pro His His Pro Met Cys His Asp Tyr Gln
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Asn Pro Pro Cys Met Tyr Ser Phe Phe Asn Ile Cys Leu Asp Pro
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Asn Ser Ala Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
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Asn Val Cys Thr Val Ser Met Phe Gly Val Met Leu Cys Pro Ser
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<400> 226

Pro Ala Cys Ala Thr Leu Met Tyr Ser Val Pro Leu Cys Pro Ala
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<400> 227

Pro Ala Pro Cys Met Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
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Pro Leu Cys Ala Glu Met Tyr Gly Tyr Ser Met Cys Pro His Asn
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Pro Gln Cys His Leu Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
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Pro Arg Pro Cys Met Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

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Gln His Cys Pro Phe Gln Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
1   5   10   15

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Gln His Cys Gln Met His Met Phe Gly Tyr Asn Leu Cys Pro Tyr
1   5   10   15

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Gln His Ser Cys Met Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

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Gln Lys Cys His Ser Tyr Leu Tyr Gly Val Asn Leu Cys Pro Tyr
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<400> 235

Gln Lys Cys Asn Met Phe Met Phe Gly Tyr Asn Leu Cys Pro Tyr
1 5 10 15

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<400> 236

Gln Met Asn Asp Cys Pro Asn His Pro Met Cys His Asp Tyr His
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<400> 237

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro Ala Thr
1 5 10 15

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<400> 238

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro Arg Thr
1 5 10 15

<210> 239
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<220>
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<400> 239

Arg Glu Cys His Phe Phe Phe Tyr Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 240
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 240

Leu Asn Cys Gly Met Phe Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
1 5 10 15

<210> 241
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<220>
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<400> 241

Arg Leu Cys Thr Ser Tyr Met Phe Gly Tyr Asn Leu Cys Pro Gln
1 5 10 15

<210> 242
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<220>
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<400> 242

Arg Leu Ser Cys Met Tyr Ser Met Phe Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 243
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<220>
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<400> 243

Arg Asn Cys Pro Phe Val Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 244
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<212> PRT
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<220>
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<400> 244

Arg Asn Gly Cys Met Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 245
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<212> PRT
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<220>
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<400> 245

Arg Asn Gly Cys Val Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 246
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<213> Artificial Sequence

<220>
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<400> 246

Arg Pro Cys His Leu Tyr Met Phe Gly Tyr Asn Leu Cys Pro Asp
1   5   10   15

<210> 247
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<220>
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<400> 247

Arg Pro Cys His Ser Tyr Met Tyr Gly Ile Asn Leu Cys Pro Tyr
1   5   10   15

<210> 248
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<220>
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<400> 248

Arg Ser Cys Asp Met Ile Met Phe Gly Phe Asn Leu Cys Pro Tyr
1   5   10   15

<210> 249
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<220>
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<400> 249

Arg Ser Cys Pro Met Trp Phe Tyr Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 250
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<220>
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<400> 250

Arg Ser Thr Val Cys Phe Tyr Asp Phe Cys Gly Pro Trp Glu Arg
1 5 10 15

<210> 251
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<220>
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<400> 251

Arg Thr Cys His Phe Tyr Met Tyr Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 252
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<212> PRT
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<220>
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<400> 252

Arg Thr Cys Ser Met Val Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 253
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 253

Ser Gly Lys Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 254
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<220>
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<400> 254

Ser Ile Val Cys Asp Leu Tyr Trp Glu Ala Thr Cys Leu Arg Pro
1 5 10 15

<210> 255
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<220>
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<400> 255

Ser Leu Ser Cys Thr Tyr Ser Phe Phe Asn Ile Cys Leu Asp Pro
1 5 10 15

<210> 256
<211> 15
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<213> Artificial Sequence

<220>

<223> Masking Moiety

<400> 256

Ser Met Asn Thr Cys Pro Tyr His Pro Met Cys Phe Asp Tyr Lys
1   5   10   15

<210> 257
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<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 257

Ser Gln Cys Trp Met Trp Met Tyr Gly Tyr Asn Leu Cys Pro Lys
1   5   10   15

<210> 258
<211> 15
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<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 258

Ser Ser Ser Cys Met Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 259
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 259

Ser Thr Ala Cys Thr Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 260
<211> 15

<212> PRT
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<220>
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<400> 260

Ser Thr Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr
1 5 10 15

<210> 261
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<220>
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<400> 261

Ser Thr Arg Cys Val Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 262
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 262

Thr Ala Cys Gly Ala Trp Met Phe Gly Val Asn Leu Cys Pro Tyr
1 5 10 15

<210> 263
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 263

Thr Gly Ala Cys Met Tyr Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 264
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<212> PRT
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<220>
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<400> 264

Thr Leu Ser Cys Met Tyr Ser Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 265
<211> 15
<212> PRT
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<220>
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<400> 265

Thr Ser Cys Thr Val Thr Met Tyr Gln Ile Ser Met Cys Pro Tyr
1 5 10 15

<210> 266
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<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 266

Val Gly Gly Cys Arg His Ser Phe Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 267
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 267

Val His Cys Gln Met Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
1 5 10 15

<210> 268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 268

Val His Asn Cys Met Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 269
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 269

Val Met Cys Lys Leu His Met Tyr Gly Ile Pro Val Cys Pro Lys
1 5 10 15

<210> 270
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<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 270

Val Asn Phe Cys Asn Tyr Ser Met Tyr Gly Ile Cys Leu Leu Pro
1 5 10 15

<210> 271
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<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 271

Val Asn Phe Cys Tyr Ala Cys Tyr Cys Met Ser Cys Val Phe Ser
1   5   10   15

<210> 272
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 272

Val Asn Gln Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 273
<211> 15
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<220>
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<400> 273

Val Pro Cys Pro Phe His Met Phe Gly Tyr Asn Leu Cys Pro Tyr
1   5   10   15

<210> 274
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 274

Val Arg Cys Gln Met Trp Met Tyr Gly Phe Asn Leu Cys Pro His
1   5   10   15

<210> 275
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 275

Val Arg Pro Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 276
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<212> PRT
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<220>
<223> Masking Moiety

<400> 276

Val Ser Gly Cys Thr Tyr Ser Phe Phe Asn Ile Cys Leu Asp Pro
1 5 10 15

<210> 277
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 277

Tyr Cys Ser Ser Trp Asp Thr Met Thr Ile Pro Ala Cys Asn Asn
1 5 10 15

<210> 278
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 278

Tyr Asp Cys Asp Leu Ser Met Phe Gly Ile Glu Met Cys Pro Gln
1   5   10   15

<210> 279
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 279

Tyr Gly Asn Thr Cys Pro Phe His Pro Met Cys His Asp Tyr Lys
1   5   10   15

<210> 280
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<212> PRT
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<220>
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<400> 280

Tyr Gly Tyr Cys Met Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 281
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 281

Tyr His Cys Thr Met His Met Phe Gly Tyr Asn Leu Cys Pro Phe
1   5   10   15

<210> 282
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Masking Moiety

<400> 282

Tyr Met Asn Thr Cys Pro Asn His Pro Met Cys Phe Asp Tyr Gln
1   5   10   15

<210> 283
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<220>
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<400> 283

Tyr Met Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Leu
1   5   10   15

<210> 284
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<212> PRT
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<220>
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<400> 284

Tyr Met Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Arg
1   5   10   15

<210> 285
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<212> PRT
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<220>
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<400> 285

Tyr Asn Asn Cys Thr Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 286
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<212> PRT
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<220>
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<400> 286

Tyr Pro Gly Cys Gln Tyr Ser Phe Phe Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 287
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<212> PRT
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<220>
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<400> 287

Tyr Arg Ser Cys Thr His Ile Met Tyr Asn Val Cys Leu Asp Pro
1 5 10 15

<210> 288
<211> 15
<212> PRT
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<220>
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<400> 288

Tyr Ser Phe Cys Asp Met Leu Met Tyr Asp Val Cys Leu Val Pro
1 5 10 15

<210> 289
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 289

Tyr Ser Ile Asp Cys Gly Leu Ser Trp Trp Cys Gly Gly Met Thr
1 5 10 15

<210> 290
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 290

Tyr Ser Thr Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr His
1 5 10 15

<210> 291
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 291

Tyr Val Asn Thr Cys Pro His His Pro Met Cys His Asp Tyr His
1 5 10 15

<210> 292
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety

<400> 292

Tyr Val Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Asn
1 5 10 15

<210> 293
<211> 15
<212> PRT
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<220>
<223> Masking Moiety - MY03

<400> 293

Met Cys Leu Pro Pro Leu Phe Glu Leu Ala Ser Thr Cys Pro Tyr
1 5 10 15

<210> 294
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety - MY11

<400> 294

Leu Pro Asp Cys Gly Met Trp Gly Ile Ser Cys Gly Gly Thr Val
1 5 10 15

<210> 295
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety - MY16

<400> 295

Arg Asp His Thr Cys Asn Pro Arg Asn Cys His Pro Asn Met Phe
1 5 10 15

<210> 296
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Masking Moiety - MY04

<400> 296

Trp Arg Cys Met Pro Pro Thr Trp Glu Thr Thr Gln Cys His Thr
1 5 10 15

<210> 297
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2001

<400> 297

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
1   5   10

<210> 298
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2003

<400> 298

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Arg Gly
1   5   10   15

<210> 299
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2005

<400> 299

Ala Val Gly Leu Leu Ala Pro Pro Ser Gly Arg Ser Ala Asn Pro Arg
1   5   10   15

Gly

<210> 300
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2006

<400> 300

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asp His
1   5   10

<210> 301
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2007

<400> 301

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Ile His
1   5   10

<210> 302
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2008

<400> 302

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln His
1   5   10

<210> 303
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2009

<400> 303

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Thr His
1   5   10

<210> 304
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Cleavable Moiety - 2011

<400> 304

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro
1   5   10

<210> 305
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 2012

<400> 305

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro
1   5   10

<210> 306
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 3001

<400> 306

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1   5   10   15

Asn His

<210> 307
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 3006

<400> 307

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1   5   10   15

Asp His

<210> 308
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 3007

<400> 308

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1 5 10 15

Ile His

<210> 309
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 3008

<400> 309

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1 5 10 15

Gln His

<210> 310
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 3009

<400> 310

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1 5 10 15

Thr His

<210> 311
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 3011

<400> 311

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1 5 10 15

Asn Pro

<210> 312
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety - 3012

<400> 312

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

Asn Pro

<210> 313
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 313

Leu Ser Gly Arg Ser Asp Asn His
1 5

<210> 314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 314

Leu Ser Gly Arg Ser Ala Asn Pro Arg Gly
1 5 10

<210> 315
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 315

Thr Gly Arg Gly Pro Ser Trp Val
1 5

<210> 316
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 316

Pro Leu Thr Gly Arg Ser Gly Gly
1 5

<210> 317
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 317

Thr Ala Arg Gly Pro Ser Phe Lys
1   5

<210> 318
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 318

Asn Thr Leu Ser Gly Arg Ser Glu Asn His Ser Gly
1   5   10

<210> 319
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 319

Asn Thr Leu Ser Gly Arg Ser Gly Asn His Gly Ser
1   5   10

<210> 320
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 320

Thr Ser Thr Ser Gly Arg Ser Ala Asn Pro Arg Gly
1   5   10

<210> 321
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 321

Thr Ser Gly Arg Ser Ala Asn Pro
1 5

<210> 322
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 322

Val His Met Pro Leu Gly Phe Leu Gly Pro
1 5 10

<210> 323
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 323

Ala Val Gly Leu Leu Ala Pro Pro
1 5

<210> 324
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 324

Ala Gln Asn Leu Leu Gly Met Val
1   5

<210> 325
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 325

Gln Asn Gln Ala Leu Arg Met Ala
1   5

<210> 326
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 326

Leu Ala Ala Pro Leu Gly Leu Leu
1   5

<210> 327
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 327

Ser Thr Phe Pro Phe Gly Met Phe
1   5

<210> 328
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Cleavable Moiety

<400> 328

Ile Ser Ser Gly Leu Leu Ser Ser
1   5

<210> 329
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 329

Pro Ala Gly Leu Trp Leu Asp Pro
1   5

<210> 330
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 330

Val Ala Gly Arg Ser Met Arg Pro
1   5

<210> 331
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 331

Val Val Pro Glu Gly Arg Arg Ser
1   5

<210> 332
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 332

Ile Leu Pro Arg Ser Pro Ala Phe
1 5

<210> 333
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 333

Met Val Leu Gly Arg Ser Leu Leu
1 5

<210> 334
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 334

Val Ala Gly Arg Ser Met Arg Pro
1 5

<210> 335
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 335

Gln Gly Arg Ala Ile Thr Phe Ile
1 5

<210> 336
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 336

Ser Pro Arg Ser Ile Met Leu Ala
1   5

<210> 337
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 337

Ser Met Leu Arg Ser Met Pro Leu
1   5

<210> 338
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 338

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1   5   10   15

Tyr His

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

<220>
<223> Cleavable Moiety

<400> 339

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

Asn Ile

<210> 340
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 340

Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp
1   5   10   15

Asn Ile

<210> 341
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 341

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Tyr His
1   5   10

<210> 342
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<223> Cleavable Moiety

<400> 342

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Ile
1   5   10

<210> 343
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Cleavable Moiety

<400> 343

Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Ile
1   5   10

<210> 344
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab-VL

<400> 344

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1   5   10   15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
            20   25   30

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

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 345
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab-VH

<400> 345

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

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

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

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 346
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<223> Human Kappa constant LC

<400> 346

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

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

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 347
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse Kappa constant LC

<400> 347

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
1 5 10 15

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
20 25 30

```
Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
        35                  40                  45


Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
    50                  55                  60


Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
65                  70                  75                  80


Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
                85                  90                  95


Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
            100                 105


<210>  348
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ipilimumab-Human Kappa LC

<400>  348

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
            20                  25                  30


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


Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
```

```
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


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


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


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


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


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


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


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


Ser Phe Asn Arg Gly Glu Cys
    210                 215


<210>  349
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ipilimumab-Mouse Kappa LC

<400>  349

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
            20                  25                  30
```

```
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

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

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
        115                 120                 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
    130                 135                 140

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

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
                165                 170                 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
            180                 185                 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
        195                 200                 205

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

<210> 350
<211> 329

<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG1 constant HC

<400> 350

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


Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30


Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45


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


Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80


Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95


Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110


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


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


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


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

```
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190


His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205


Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220


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


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


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


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


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


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


Gln Lys Ser Leu Ser Leu Ser Pro Gly
                325


<210>  351
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse IgG1 constant HC

<400>  351

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

```
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

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

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

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

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

Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

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

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


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


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


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


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


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


Gln Lys Ser Leu Ser Leu Ser Pro Gly
                325


<210>  352
<211>  330
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Mouse IgG2a constant HC

<400>  352

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly
1               5                   10                  15


Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
            20                  25                  30


Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser
        35                  40                  45
```

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

Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
65                  70                  75                  80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
                85                  90                  95

Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
            100                 105                 110

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

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

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

Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
                165                 170                 175

Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
            180                 185                 190

His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
        195                 200                 205

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

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

Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
                245                 250                 255
```

```
Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
            260                 265                 270


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


Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
    290                 295                 300


Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
305                 310                 315                 320


Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
                325                 330


<210>  353
<211>  447
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ipilimumab-VH-Human IgG1 constant HC

<400>  353

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


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


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


Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


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


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

```
Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

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

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

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

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

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

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

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

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

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
    290                 295                 300
```

```
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320


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


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


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


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


Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400


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


Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430


Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445


<210>  354
<211>  447
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Ipilimumab-VH-Mouse IgG1 constant HC

<400>  354

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

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

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

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

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

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

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

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

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

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

```
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225                 230                 235                 240


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


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


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


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


Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320


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


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


Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365


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


Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385                 390                 395                 400


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


Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
```

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 355
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Ipilimumab-VH-Mouse IgG2a constant HC

<400> 355

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

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

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

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro
115 120 125

Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly
130 135 140

Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn
145 150 155 160

```
Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr
            180                 185                 190

Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser
        195                 200                 205

Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro
    210                 215                 220

Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser
225                 230                 235                 240

Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu
                245                 250                 255

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

Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala
        275                 280                 285

Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val
    290                 295                 300

Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe
305                 310                 315                 320

Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr
                325                 330                 335

Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu
            340                 345                 350

Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys
        355                 360                 365
```

```
Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn
    370                 375                 380


Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp
385                 390                 395                 400


Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys
                405                 410                 415


Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly
            420                 425                 430


Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
        435                 440                 445


<210>  356
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV01-2001  LC

<400>  356

Gln Gly Gln Ser Gly Gln Gly Asp Phe Ser Cys Leu His Ser Met Tyr
1               5                   10                  15


Asn Val Cys Leu Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80
```

```
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220

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

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

Phe Asn Arg Gly Glu Cys
            260
```

<210> 357
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV01-2001 LC

<400> 357

```
Asp Phe Ser Cys Leu His Ser Met Tyr Asn Val Cys Leu Asp Pro Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80


Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95


Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110


Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125


Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140


Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190
```

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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  358
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV02-2001 LC

<400>  358

Gln Gly Gln Ser Gly Gln Gly Gln Pro Cys Ala Gln Met Tyr Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95
```

```
Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  359
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV02-2001 LC
```

<400> 359

```
Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                  10                  15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30

Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

```
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  360
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV03-2001 LC

<400>  360

Gln Gly Gln Ser Gly Gln Gly Leu His Cys Arg Thr Gln Met Tyr Gly
1               5                   10                  15


Tyr Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  361
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV03-2001 LC

<400>  361

Leu His Cys Arg Thr Gln Met Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15
```

```
Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30

Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220
```

```
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  362
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV04-2001 LC

<400>  362

Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1               5                   10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125
```

```
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  363
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV04-2001 LC

<400>  363

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30
```

```
Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240
```

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
245 250 255

<210> 364
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV06-2001 LC

<400> 364

Gln Gly Gln Ser Gly Ser Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys
1 5 10 15

Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly
20 25 30

Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
35 40 45

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
50 55 60

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65 70 75 80

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
85 90 95

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
100 105 110

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
115 120 125

Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
130 135 140

```
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160


Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175


Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190


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


Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220


Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240


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


<210>  365
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV06-2001 LC

<400>  365

Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Gly Gly Gly Ser Ser Gly
1               5                   10                  15


Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly
            20                  25                  30


Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
        35                  40                  45


Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
    50                  55                  60
```

```
Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
65                  70                  75                  80

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

Arg Phe Ser Gly Ser Gly Tyr Val Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125

Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190

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

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

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250
```

<210> 366
<211> 263

<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV09-2001 LC

<400> 366

Gln Gly Gln Ser Gly Ser Phe Gly Tyr Val Thr Ala Cys Pro Asn His
1 5 10 15

Pro Met Cys His Asp Trp Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile
20 25 30

Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser
35 40 45

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
50 55 60

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
85 90 95

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
100 105 110

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
115 120 125

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
130 135 140

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
145 150 155 160

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
165 170 175

```
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
            180                 185                 190


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
        195                 200                 205


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
    210                 215                 220


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


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


Ser Phe Asn Arg Gly Glu Cys
            260


<210>  367
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV09-2001 LC

<400>  367

Phe Gly Thr Ala Cys Pro Asn His Pro Met Cys His Asp Trp Gln Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80
```

```
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 368
<211> 258
<212> PRT
<213> Artificial Sequence

<220>

<223> Spacer - YV23-2001 LC

<400> 368

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                  10                  15


Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30


Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45


Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60


Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80


Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95


Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110


Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125


Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140


Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160


Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175


Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190
```

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


Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220


Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240


Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255


Glu Cys



<210>  369
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV23-2001 LC

<400>  369

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
            20                  25                  30


His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
        35                  40                  45


Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
    50                  55                  60


Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65                  70                  75                  80


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

```
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125

Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190

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

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

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250
```

<210> 370
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV24-2001 LC

<400> 370

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Val Cys Leu
1               5                  10                  15

Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30

Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190

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

```
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220


Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240


Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255


Glu Cys



<210>  371
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV24-2001 LC

<400>  371

Cys Leu His Ser Ala Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
            20                  25                  30


His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
        35                  40                  45


Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
    50                  55                  60


Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65                  70                  75                  80


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


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110
```

```
Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125


Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140


Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  372
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV27-2001 LC

<400>  372

Gln Gly Gln Ser Gly Ser Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser
1               5                   10                  15
```

```
Met Cys Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30

Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220
```

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225 230 235 240

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
245 250 255

Glu Cys

<210> 373
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> YV27-2001 LC

<400> 373

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
20 25 30

His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
35 40 45

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
50 55 60

Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65 70 75 80

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
100 105 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
115 120 125

```
Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190

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

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

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  374
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV29-2001 LC

<400>  374

Gln Gly Gln Ser Gly Ser Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys
1               5                   10                  15

Ala His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30
```

```
Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60

Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
225                 230                 235                 240
```

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
245 250 255

Gly Glu Cys

<210> 375
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> YV29-2001 LC

<400> 375

Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Ala His Thr Gly Gly Gly
1 5 10 15

Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
20 25 30

Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
35 40 45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
50 55 60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65 70 75 80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
100 105 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
115 120 125

Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
130 135 140

```
Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160


Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175


Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190


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


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


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  376
<211>  257
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV32-2001 LC

<400>  376

Gln Gly Gln Ser Gly Ser Cys Pro Asn His Pro Leu Cys His Asp Trp
1               5                   10                  15


Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser
            20                  25                  30


Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
        35                  40                  45
```

```
Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
    50                  55                  60

Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln
65                  70                  75                  80

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser
                85                  90                  95

Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
            100                 105                 110

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

Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly
    130                 135                 140

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
145                 150                 155                 160

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                165                 170                 175

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
            180                 185                 190

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

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

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
225                 230                 235                 240

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                245                 250                 255
```

Cys

<210> 377
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> YV32-2001 LC

<400> 377

Cys Pro Asn His Pro Leu Cys His Asp Trp Gln Gly Gly Gly Ser Ser
1 5 10 15

Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
20 25 30

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
35 40 45

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
50 55 60

Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
65 70 75 80

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
100 105 110

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
115 120 125

Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
130 135 140

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
145 150 155 160

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


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
            180                 185                 190


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


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
    210                 215                 220


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
225                 230                 235                 240


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  378
<211>  257
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV33-2001 LC

<400>  378

Gln Gly Gln Ser Gly Ser Cys Pro Asn His Pro Met Cys Ala Asp Trp
1               5                   10                  15


Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser
            20                  25                  30


Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
        35                  40                  45


Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
    50                  55                  60
```

```
Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln
65                  70                  75                  80

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser
                85                  90                  95

Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
            100                 105                 110

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

Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly
    130                 135                 140

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
145                 150                 155                 160

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                165                 170                 175

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
            180                 185                 190

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

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

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
225                 230                 235                 240

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                245                 250                 255

Cys
```

<210> 379
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> YV33-2001 LC

<400> 379

Cys Pro Asn His Pro Met Cys Ala Asp Trp Gln Gly Gly Gly Ser Ser
1 5 10 15

Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
20 25 30

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
35 40 45

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
50 55 60

Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
65 70 75 80

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
100 105 110

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
115 120 125

Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
130 135 140

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
145 150 155 160

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

```
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
            180                 185                 190


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


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
    210                 215                 220


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
225                 230                 235                 240


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  380
<211>  257
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV35-2001 LC

<400>  380

Gln Gly Gln Ser Gly Ser Cys Pro Asn His Pro Met Cys His Asp Ala
1               5                   10                  15


Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser
            20                  25                  30


Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
        35                  40                  45


Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
    50                  55                  60


Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln
65                  70                  75                  80
```

```
Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser
                85                  90                  95

Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
            100                 105                 110

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

Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly
    130                 135                 140

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
145                 150                 155                 160

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                165                 170                 175

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
            180                 185                 190

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

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

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
225                 230                 235                 240

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                245                 250                 255

Cys
```

<210> 381
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> YV35-2001 LC

<400> 381

```
Cys Pro Asn His Pro Met Cys His Asp Ala Gln Gly Gly Gly Ser Ser
1               5                  10                  15


Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
            20                  25                  30


Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
        35                  40                  45


Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
    50                  55                  60


Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
65                  70                  75                  80


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


Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
            100                 105                 110


Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
        115                 120                 125


Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
    130                 135                 140


Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
145                 150                 155                 160


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


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
            180                 185                 190
```

```
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
        195                 200                 205


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
    210                 215                 220


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
225                 230                 235                 240


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  382
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-2001 LC

<400>  382

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                   10                  15


Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30


Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95
```

```
Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110


Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125


Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140


Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175


Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190


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


Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220


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


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys



<210>  383
<211>  253
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV39-2001 LC
```

<400> 383

```
Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly Gly Gly
1               5                   10                  15

Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
            20                  25                  30

Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125

Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190

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

```
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
    210                 215                 220


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  384
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV41-2001 LC

<400>  384

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                   10                  15


Cys Pro Ala Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30


Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95


Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110
```

```
Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125


Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140


Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175


Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190


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


Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220


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


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys



<210>  385
<211>  253
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV41-2001 LC

<400>  385

Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Ala Gly Gly Gly
1               5                   10                  15
```

```
Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
            20                  25                  30

Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125

Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190

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

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
    210                 215                 220
```

```
Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  386
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV51-2001 LC

<400>  386

Gln Gly Gln Ser Gly Ser Phe Gly Ala Ala Cys Pro Asn His Pro Ile
1               5                   10                  15


Cys His Asp Trp Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125
```

```
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  387
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV51-2001 LC

<400>  387

Phe Gly Ala Ala Cys Pro Asn His Pro Ile Cys His Asp Trp Gln Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30
```

```
Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240
```

```
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  388
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV52-2001 LC

<400>  388

Gln Gly Gln Ser Gly Ser Phe Gly Ala Ala Cys Pro Asn His Pro Leu
1               5                   10                  15


Cys His Asp Trp Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140
```

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


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  389
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV52-2001 LC

<400>  389

Phe Gly Ala Ala Cys Pro Asn His Pro Leu Cys His Asp Trp Gln Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45
```

```
Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 390
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV53-2001 LC

<400> 390

```
Gln Gly Gln Ser Gly Ser Phe Gly Ala Ala Cys Pro Asn His Pro Met
1               5                   10                  15


Cys His Asp Ala Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


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

```
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
                165                 170                 175


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  391
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV53-2001 LC

<400>  391

Phe Gly Ala Ala Cys Pro Asn His Pro Met Cys His Asp Ala Gln Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60
```

```
Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255

<210>  392
<211>  258
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV54-2001 LC

<400> 392

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Ala Cys Leu
1 5 10 15

Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
20 25 30

Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
35 40 45

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
50 55 60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65 70 75 80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
85 90 95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
100 105 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
115 120 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
130 135 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145 150 155 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
165 170 175

```
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190


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


Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220


Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240


Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255


Glu Cys



<210>  393
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV54-2001 LC

<400>  393

Cys Leu His Ser Ala Tyr Asn Ala Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
            20                  25                  30


His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
        35                  40                  45


Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
    50                  55                  60


Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65                  70                  75                  80
```

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125

Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190

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

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

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250
```

<210> 394
<211> 258
<212> PRT
<213> Artificial Sequence

<220>

<223> Spacer - YV55-2001 LC

<400> 394

```
Gln Gly Gln Ser Gly Ser Cys Ala His Ser Ala Tyr Asn Val Cys Leu
1               5                  10                  15


Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30


Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45


Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60


Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80


Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95


Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110


Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125


Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140


Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160


Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175


Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190
```

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


Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220


Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240


Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255


Glu Cys



<210>  395
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV55-2001 LC

<400>  395

Cys Ala His Ser Ala Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
            20                  25                  30


His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
        35                  40                  45


Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
    50                  55                  60


Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65                  70                  75                  80


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

```
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110


Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125


Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140


Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  396
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV56-2001 LC

<400>  396
```

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Val Cys Ala
1               5                   10                  15


Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30


Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45


Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60


Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80


Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95


Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110


Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125


Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140


Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160


Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175


Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190


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

```
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220


Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240


Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255


Glu Cys



<210>  397
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV56-2001 LC

<400>  397

Cys Leu His Ser Ala Tyr Asn Val Cys Ala Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
            20                  25                  30


His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
        35                  40                  45


Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
    50                  55                  60


Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65                  70                  75                  80


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


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110
```

```
Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125


Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140


Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  398
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV57-2001 LC

<400>  398

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Val Cys Leu
1               5                   10                  15
```

```
Ala Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30

Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220
```

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225 230 235 240

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
245 250 255

Glu Cys

<210> 399
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> YV57-2001 LC

<400> 399

Cys Leu His Ser Ala Tyr Asn Val Cys Leu Ala Pro Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
20 25 30

His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
35 40 45

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
50 55 60

Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65 70 75 80

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
100 105 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
115 120 125

```
Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190

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

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

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  400
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV58-2001 LC

<400>  400

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Val Cys Leu
1               5                   10                  15

Asp Ala Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30
```

```
Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240
```

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
245 250 255

Glu Cys

<210> 401
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> YV58-2001 LC

<400> 401

Cys Leu His Ser Ala Tyr Asn Val Cys Leu Asp Ala Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
20 25 30

His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
35 40 45

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
50 55 60

Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65 70 75 80

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
100 105 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
115 120 125

Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
130 135 140

```
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  402
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV61-2001 LC

<400>  402

Gln Gly Gln Ser Gly Ser Tyr Ile Ser Asp Cys Pro Tyr His Pro Met
1               5                   10                  15


Cys His Asp Tyr Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45
```

```
Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
                245                 250                 255
```

Asn Arg Gly Glu Cys
260

<210> 403
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV61-2001 LC

<400> 403

Tyr Ile Ser Asp Cys Pro Tyr His Pro Met Cys His Asp Tyr Gln Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
115 120 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
130 135 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145 150 155 160

```
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  404
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV62-2001 LC

<400>  404

Gln Gly Gln Ser Gly Ser Phe Arg Asn Thr Cys Pro Tyr His Pro Met
1               5                   10                  15


Cys His Asp Tyr Arg Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60
```

```
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

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

Asn Arg Gly Glu Cys
            260
```

<210> 405
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV62-2001 LC

<400> 405

Phe Arg Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Arg Gly
1   5   10   15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20   25   30

Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35   40   45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50   55   60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65   70   75   80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85   90   95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100   105   110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115   120   125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130   135   140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145   150   155   160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165   170   175

```
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  406
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV63-2001 LC

<400>  406

Gln Gly Gln Ser Gly Ser Arg Glu Cys His Met Trp Met Phe Gly Val
1               5                   10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80
```

```
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

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

Asn Arg Gly Glu Cys
            260
```

<210> 407
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV63-2001 LC

<400> 407

```
Arg Glu Cys His Met Trp Met Phe Gly Val Asn Leu Cys Pro Tyr Gly
1               5                  10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80


Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95


Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110


Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125


Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140


Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190
```

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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  408
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV64-2001 LC

<400>  408

Gln Gly Gln Ser Gly Ser Ala Val Cys His Met Tyr Met Tyr Gly Tyr
1               5                   10                  15


Asn Leu Cys Pro Phe Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95
```

```
Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  409
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV64-2001 LC
```

<400> 409

```
Ala Val Cys His Met Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Phe Gly
1               5                  10                  15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30

Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

```
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  410
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV65-2001 LC

<400>  410

Gln Gly Gln Ser Gly Gln Gly Arg Ser Cys Pro Gln Met Tyr Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  411
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV65-2001 LC

<400>  411

Arg Ser Cys Pro Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                   10                  15
```

```
Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30

Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220
```

```
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  412
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV66-2001 LC

<400>  412

Gln Gly Gln Ser Gly Gln Gly Gln Pro Cys Ala Gln Met Phe Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125
```

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  413
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV66-2001 LC

<400>  413

Gln Pro Cys Ala Gln Met Phe Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30
```

```
Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240
```

```
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  414
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV04-2006 LC

<400>  414

Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1               5                   10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140
```

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


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys Cys
            260


<210>  415
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV04-2006 LC

<400>  415

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asp His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45
```

```
Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 416
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV23-2006 LC

<400> 416

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                  10                  15


Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30


Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45


Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60


Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80


Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95


Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110


Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125


Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140


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

```
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175


Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190


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


Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220


Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240


Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255


Glu Cys



<210>  417
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV23-2006 LC

<400>  417

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asp
            20                  25                  30


His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
        35                  40                  45


Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
    50                  55                  60
```

```
Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65                  70                  75                  80

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125

Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190

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

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

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250
```

<210> 418
<211> 259

<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV39-2006 LC

<400> 418

```
Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                  10                  15


Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30


Leu Ser Gly Arg Ser Asp Asp His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95


Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110


Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125


Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140


Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175
```

```
Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190


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


Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220


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


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys



<210>  419
<211>  253
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV39-2006 LC

<400>  419

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


Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
            20                  25                  30


Asp His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45


Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60


Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80
```

```
Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly
                85                  90                  95

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125

Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190

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

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

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250
```

<210> 420
<211> 261
<212> PRT
<213> Artificial Sequence

<220>

<223> Spacer - YV04-2007 LC

<400> 420

```
Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1               5                  10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Ile His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190
```

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
210 215 220

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

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

Asn Arg Gly Glu Cys
260

<210> 421
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV04-2007 LC

<400> 421

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Asp Ile His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

```
Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  422
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV23-2007 LC

<400>  422
```

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                  10                  15

Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30

Ser Gly Arg Ser Asp Ile His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190

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

```
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220


Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240


Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255


Glu Cys



<210>  423
<211>  252
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV23-2007 LC

<400>  423

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Ile
            20                  25                  30


His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
        35                  40                  45


Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
    50                  55                  60


Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65                  70                  75                  80


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


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110
```

```
Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125


Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140


Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  424
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-2007 LC

<400>  424

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                   10                  15
```

```
Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30

Leu Ser Gly Arg Ser Asp Ile His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60

Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220
```

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

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
245 250 255

Gly Glu Cys

<210> 425
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> YV39-2007 LC

<400> 425

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

Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
20 25 30

Ile His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
35 40 45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
50 55 60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65 70 75 80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
100 105 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
115 120 125

```
Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140


Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160


Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175


Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190


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


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


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  426
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV04-2008 LC

<400>  426

Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1               5                   10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30
```

```
Gly Leu Leu Ser Gly Arg Ser Asp Gln His Gly Gly Gly Ser Glu Ile
        35                  40                  45

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
225                 230                 235                 240
```

```
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
                245                 250                 255


Asn Arg Gly Glu Cys
            260


<210>  427
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV04-2008 LC

<400>  427

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Gln His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80


Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95


Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110


Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125


Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140
```

```
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  428
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV23-2008 LC

<400>  428

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                   10                  15


Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30


Ser Gly Arg Ser Asp Gln His Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45
```

```
Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
    210                 215                 220

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225                 230                 235                 240

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                245                 250                 255
```

Glu Cys

<210> 429
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> YV23-2008 LC

<400> 429

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Gln
20 25 30

His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
35 40 45

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
50 55 60

Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65 70 75 80

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
100 105 110

Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
115 120 125

Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
130 135 140

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145 150 155 160

```
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  430
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-2008 LC

<400>  430

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                   10                  15


Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30


Leu Ser Gly Arg Ser Asp Gln His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60
```

```
Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220

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

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255

Gly Glu Cys
```

<210> 431
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> YV39-2008 LC

<400> 431

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

Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
20 25 30

Gln His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
35 40 45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
50 55 60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65 70 75 80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
100 105 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
115 120 125

Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
130 135 140

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145 150 155 160

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
165 170 175

```
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190


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


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


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  432
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV04-2009 LC

<400>  432

Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1               5                   10                  15


Asn Leu Cys Pro Tyr Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30


Leu Ser Gly Arg Ser Asp Thr His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80
```

```
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220

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

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255

Gly Glu Cys
```

<210> 433
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> YV04-2009 LC

<400> 433

```
Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                  10                  15


Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
            20                  25                  30


Thr His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45


Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60


Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80


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


Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110


Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125


Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140


Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160


Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175


Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190
```

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


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


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  434
<211>  256
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV23-2009 LC

<400>  434

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                   10                  15


Asp Pro Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly
            20                  25                  30


Arg Ser Asp Thr His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
        35                  40                  45


Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
    50                  55                  60


Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65                  70                  75                  80


Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
                85                  90                  95
```

```
Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            100                 105                 110

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
        115                 120                 125

Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
    130                 135                 140

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190

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

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 435
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> YV23-2009 LC

<400> 435

```
Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Ser Ser Gly
1               5                   10                  15
```

```
Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Thr His Gly
            20                  25                  30

Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
        35                  40                  45

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
    50                  55                  60

Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
65                  70                  75                  80

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
            100                 105                 110

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
        115                 120                 125

Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
    130                 135                 140

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
145                 150                 155                 160

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
                165                 170                 175

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
            180                 185                 190

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

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
    210                 215                 220
```

```
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
225                 230                 235                 240


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  436
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-2009 LC

<400>  436

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                   10                  15


Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30


Leu Ser Gly Arg Ser Asp Thr His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95


Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110


Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125
```

```
Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140


Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175


Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190


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


Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220


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


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys



<210>  437
<211>  253
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV39-2009 LC

<400>  437

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


Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
            20                  25                  30
```

```
Thr His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125

Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190

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

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

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240
```

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
245 250

<210> 438
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV01-2011 LC

<400> 438

Gln Gly Gln Ser Gly Gln Gly Asp Phe Ser Cys Leu His Ser Met Tyr
1 5 10 15

Asn Val Cys Leu Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
20 25 30

Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu
35 40 45

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
50 55 60

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65 70 75 80

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
85 90 95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
100 105 110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
115 120 125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
130 135 140

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys Cys
            260


<210>  439
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV01-2011 LC

<400>  439

Asp Phe Ser Cys Leu His Ser Met Tyr Asn Val Cys Leu Asp Pro Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45
```

```
Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 440
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV02-2011 LC

<400> 440

Gln Gly Gln Ser Gly Gln Gly Gln Pro Cys Ala Gln Met Tyr Gly Tyr
1   5   10   15

Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20   25   30

Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu
        35   40   45

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50   55   60

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65   70   75   80

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85   90   95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100   105   110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115   120   125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130   135   140

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145   150   155   160

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  441
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV02-2011 LC

<400>  441

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60
```

```
Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 442
<211> 262

<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV03-2011 LC

<400> 442

```
Gln Gly Gln Ser Gly Gln Gly Leu His Cys Arg Thr Gln Met Tyr Gly
1               5                  10                  15


Tyr Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175
```

```
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  443
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV03-2011 LC

<400>  443

Leu His Cys Arg Thr Gln Met Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80
```

```
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 444
<211> 261
<212> PRT
<213> Artificial Sequence

<220>

<223> Spacer - YV04-2011 LC

<400> 444

```
Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1               5                  10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190
```

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
210 215 220

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

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

Asn Arg Gly Glu Cys
260

<210> 445
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV04-2011 LC

<400> 445

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

```
Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  446
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV23-2011 LC

<400>  446
```

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                  10                  15

Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30

Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60

Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95

Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125

Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
210 215 220

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225 230 235 240

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
245 250 255

Glu Cys

<210> 447
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> YV23-2011 LC

<400> 447

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn
20 25 30

Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
35 40 45

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
50 55 60

Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65 70 75 80

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

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
100 105 110

```
Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125


Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140


Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  448
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-2011 LC

<400>  448

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                   10                  15
```

```
Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30

Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60

Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220
```

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

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
245 250 255

Gly Glu Cys

<210> 449
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> YV39-2011 LC

<400> 449

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

Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
20 25 30

Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
35 40 45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
50 55 60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65 70 75 80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
100 105 110

Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
115 120 125

```
Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190

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

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

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  450
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV61-2011 LC

<400>  450

Gln Gly Gln Ser Gly Ser Tyr Ile Ser Asp Cys Pro Tyr His Pro Met
1               5                   10                  15

Cys His Asp Tyr Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30
```

```
Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
225                 230                 235                 240
```

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

Asn Arg Gly Glu Cys
260

<210> 451
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV61-2011 LC

<400> 451

Tyr Ile Ser Asp Cys Pro Tyr His Pro Met Cys His Asp Tyr Gln Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
115 120 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
130 135 140

```
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  452
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV62-2011 LC

<400>  452

Gln Gly Gln Ser Gly Ser Phe Arg Asn Thr Cys Pro Tyr His Pro Met
1               5                   10                  15


Cys His Asp Tyr Arg Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45
```

```
Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
                245                 250                 255
```

Asn Arg Gly Glu Cys
260

<210> 453
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV62-2011 LC

<400> 453

Phe Arg Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Arg Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
115 120 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
130 135 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145 150 155 160

```
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  454
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV63-2011 LC

<400>  454

Gln Gly Gln Ser Gly Ser Arg Glu Cys His Met Trp Met Phe Gly Val
1               5                   10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60
```

```
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

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

Asn Arg Gly Glu Cys
            260
```

<210> 455
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV63-2011 LC

<400> 455

Arg Glu Cys His Met Trp Met Phe Gly Val Asn Leu Cys Pro Tyr Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
115 120 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
130 135 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145 150 155 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
165 170 175

```
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  456
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV64-2011 LC

<400>  456

Gln Gly Gln Ser Gly Ser Ala Val Cys His Met Tyr Met Tyr Gly Tyr
1               5                   10                  15


Asn Leu Cys Pro Phe Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80
```

```
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

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

Asn Arg Gly Glu Cys Cys
            260
```

<210> 457
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV64-2011 LC

<400> 457

```
Ala Val Cys His Met Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Phe Gly
1               5                  10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80


Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95


Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110


Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125


Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140


Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190
```

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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  458
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV65-2011 LC

<400>  458

Gln Gly Gln Ser Gly Gln Gly Arg Ser Cys Pro Gln Met Tyr Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95
```

```
Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  459
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV65-2011 LC
```

<400> 459

```
Arg Ser Cys Pro Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                  10                  15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30

Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

```
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  460
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV66-2011 LC

<400>  460

Gln Gly Gln Ser Gly Gln Gly Gln Pro Cys Ala Gln Met Phe Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110
```

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  461
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV66-2011 LC

<400>  461

Gln Pro Cys Ala Gln Met Phe Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                   10                  15
```

```
Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30

Ser Asp Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220
```

```
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  462
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV01-2012 LC

<400>  462

Gln Gly Gln Ser Gly Gln Gly Asp Phe Ser Cys Leu His Ser Met Tyr
1               5                   10                  15


Asn Val Cys Leu Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125
```

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  463
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV01-2012 LC

<400>  463

Asp Phe Ser Cys Leu His Ser Met Tyr Asn Val Cys Leu Asp Pro Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30
```

```
Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240
```

```
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  464
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV02-2012 LC

<400>  464

Gln Gly Gln Ser Gly Gln Gly Gln Pro Cys Ala Gln Met Tyr Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140
```

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  465
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV02-2012 LC

<400>  465

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45
```

```
Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 466
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV03-2012 LC

<400> 466

```
Gln Gly Gln Ser Gly Gln Gly Leu His Cys Arg Thr Gln Met Tyr Gly
1               5                   10                  15


Tyr Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160
```

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  467
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV03-2012 LC

<400>  467

Leu His Cys Arg Thr Gln Met Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60
```

```
Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 468
<211> 261

<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV04-2012 LC

<400> 468

Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1 5 10 15

Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
20 25 30

Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile
35 40 45

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
50 55 60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65 70 75 80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
85 90 95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
100 105 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
115 120 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
130 135 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145 150 155 160

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

```
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  469
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV04-2012 LC

<400>  469

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80
```

```
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  470
<211>  258
<212>  PRT
<213>  Artificial Sequence

<220>
```

<223> Spacer - YV23-2012 LC

<400> 470

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                  10                  15


Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu
            20                  25                  30


Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr
        35                  40                  45


Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
    50                  55                  60


Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr
65                  70                  75                  80


Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe
                85                  90                  95


Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
            100                 105                 110


Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
        115                 120                 125


Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln
    130                 135                 140


Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
145                 150                 155                 160


Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
                165                 170                 175


Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
            180                 185                 190
```

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

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
210 215 220

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
225 230 235 240

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
245 250 255

Glu Cys

<210> 471
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> YV23-2012 LC

<400> 471

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn
20 25 30

Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu
35 40 45

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
50 55 60

Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
65 70 75 80

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

```
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
            100                 105                 110


Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
        115                 120                 125


Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
    130                 135                 140


Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
145                 150                 155                 160


Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
                165                 170                 175


Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
            180                 185                 190


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


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


Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
225                 230                 235                 240


Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  472
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-2012 LC

<400>  472
```

```
Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                  10                  15

Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu
            20                  25                  30

Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60

Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
        195                 200                 205
```

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
210 215 220

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

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
245 250 255

Gly Glu Cys

<210> 473
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> YV39-2012 LC

<400> 473

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

Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala
20 25 30

Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
35 40 45

Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
50 55 60

Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65 70 75 80

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

Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
100 105 110

```
Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125


Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140


Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160


Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175


Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190


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


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


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  474
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV61-2012 LC

<400>  474

Gln Gly Gln Ser Gly Ser Tyr Ile Ser Asp Cys Pro Tyr His Pro Met
1               5                   10                  15
```

```
Cys His Asp Tyr Gln Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30

Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220
```

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

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

Asn Arg Gly Glu Cys
260

<210> 475
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV61-2012 LC

<400> 475

Tyr Ile Ser Asp Cys Pro Tyr His Pro Met Cys His Asp Tyr Gln Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
115 120 125

```
Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140


Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  476
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV62-2012 LC

<400>  476

Gln Gly Gln Ser Gly Ser Phe Arg Asn Thr Cys Pro Tyr His Pro Met
1               5                   10                  15


Cys His Asp Tyr Arg Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30
```

```
Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
225                 230                 235                 240
```

```
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
                245                 250                 255


Asn Arg Gly Glu Cys
            260


<210>  477
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV62-2012 LC

<400>  477

Phe Arg Asn Thr Cys Pro Tyr His Pro Met Cys His Asp Tyr Arg Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80


Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95


Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110


Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125


Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140
```

```
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  478
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV63-2012 LC

<400>  478

Gln Gly Gln Ser Gly Ser Arg Glu Cys His Met Trp Met Phe Gly Val
1               5                   10                  15


Asn Leu Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45
```

```
Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
                245                 250                 255
```

Asn Arg Gly Glu Cys
260

<210> 479
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV63-2012 LC

<400> 479

Arg Glu Cys His Met Trp Met Phe Gly Val Asn Leu Cys Pro Tyr Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
20 25 30

Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
100 105 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
115 120 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
130 135 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145 150 155 160

```
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  480
<211>  261
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV64-2012 LC

<400>  480

Gln Gly Gln Ser Gly Ser Ala Val Cys His Met Tyr Met Tyr Gly Tyr
1               5                   10                  15


Asn Leu Cys Pro Phe Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser
            20                  25                  30


Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60
```

```
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220

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

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

Asn Arg Gly Glu Cys
            260
```

<210> 481
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV64-2012 LC

<400> 481

Ala Val Cys His Met Tyr Met Tyr Gly Tyr Asn Leu Cys Pro Phe Gly
1   5   10   15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20   25   30

Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35   40   45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50   55   60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65   70   75   80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85   90   95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100   105   110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115   120   125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130   135   140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145   150   155   160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165   170   175

```
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  482
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV65-2012 LC

<400>  482

Gln Gly Gln Ser Gly Gln Gly Arg Ser Cys Pro Gln Met Tyr Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80
```

```
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220

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

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

Phe Asn Arg Gly Glu Cys
            260
```

<210> 483
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV65-2012 LC

<400> 483

```
Arg Ser Cys Pro Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                  10                  15


Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30


Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80


Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95


Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110


Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125


Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140


Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190
```

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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  484
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV66-2012 LC

<400>  484

Gln Gly Gln Ser Gly Gln Gly Gln Pro Cys Ala Gln Met Phe Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ile Ser
            20                  25                  30


Ser Gly Leu Leu Ser Gly Arg Ser Ala Asn Pro Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95
```

```
Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  485
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV66-2012 LC
```

<400> 485

```
Gln Pro Cys Ala Gln Met Phe Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                   10                  15

Gly Gly Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg
            20                  25                  30

Ser Ala Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

```
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  486
<211>  267
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV01-3001 LC

<400>  486

Gln Gly Gln Ser Gly Gln Gly Asp Phe Ser Cys Leu His Ser Met Tyr
1               5                   10                  15


Asn Val Cys Leu Asp Pro Gly Gly Gly Ser Ser Gly Gly Ser Ala Val
            20                  25                  30


Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His
        35                  40                  45


Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
    50                  55                  60


Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
65                  70                  75                  80


Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
                85                  90                  95


Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro
            100                 105                 110
```

```
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        115                 120                 125


Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
    130                 135                 140


Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
145                 150                 155                 160


Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                165                 170                 175


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


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        195                 200                 205


Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    210                 215                 220


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
225                 230                 235                 240


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


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210>  487
<211>  260
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV01-3001 LC

<400>  487

Asp Phe Ser Cys Leu His Ser Met Tyr Asn Val Cys Leu Asp Pro Gly
1               5                   10                  15
```

```
Gly Gly Ser Ser Gly Gly Ser Ala Val Gly Leu Leu Ala Pro Pro Gly
            20                  25                  30

Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val
        35                  40                  45

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
    50                  55                  60

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala
65                  70                  75                  80

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
                85                  90                  95

Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
            100                 105                 110

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
        115                 120                 125

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe
    130                 135                 140

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
145                 150                 155                 160

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
                165                 170                 175

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
            180                 185                 190

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

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
    210                 215                 220
```

```
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
225                 230                 235                 240


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


Arg Gly Glu Cys
            260


<210>  488
<211>  267
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV02-3001 LC

<400>  488

Gln Gly Gln Ser Gly Gln Gly Gln Pro Cys Ala Gln Met Tyr Gly Tyr
1               5                   10                  15


Ser Met Cys Pro His Thr Gly Gly Gly Ser Ser Gly Gly Ser Ala Val
            20                  25                  30


Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His
        35                  40                  45


Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
    50                  55                  60


Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
65                  70                  75                  80


Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
                85                  90                  95


Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro
            100                 105                 110
```

```
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        115                 120                 125


Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
    130                 135                 140


Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
145                 150                 155                 160


Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                165                 170                 175


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


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        195                 200                 205


Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    210                 215                 220


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
225                 230                 235                 240


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


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210>  489
<211>  260
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV02-3001 LC

<400>  489

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Pro His Thr Gly
1               5                   10                  15
```

```
Gly Gly Ser Ser Gly Gly Ser Ala Val Gly Leu Leu Ala Pro Pro Gly
            20                  25                  30

Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val
        35                  40                  45

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
    50                  55                  60

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala
65                  70                  75                  80

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
                85                  90                  95

Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
            100                 105                 110

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
        115                 120                 125

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe
    130                 135                 140

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
145                 150                 155                 160

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
                165                 170                 175

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
            180                 185                 190

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

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
    210                 215                 220
```

```
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
225                 230                 235                 240


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


Arg Gly Glu Cys
            260


<210>  490
<211>  267
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV03-3001 LC

<400>  490

Gln Gly Gln Ser Gly Gln Gly Leu His Cys Arg Thr Gln Met Tyr Gly
1               5                   10                  15


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


Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His
        35                  40                  45


Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
    50                  55                  60


Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
65                  70                  75                  80


Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
                85                  90                  95


Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro
            100                 105                 110
```

```
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        115                 120                 125


Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
    130                 135                 140


Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
145                 150                 155                 160


Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
                165                 170                 175


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


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        195                 200                 205


Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    210                 215                 220


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
225                 230                 235                 240


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


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210>  491
<211>  260
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV03-3001 LC

<400>  491

Leu His Cys Arg Thr Gln Met Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15
```

```
Gly Gly Ser Ser Gly Gly Ser Ala Val Gly Leu Leu Ala Pro Pro Gly
            20                  25                  30

Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val
        35                  40                  45

Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
    50                  55                  60

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala
65                  70                  75                  80

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
                85                  90                  95

Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
            100                 105                 110

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
        115                 120                 125

Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe
    130                 135                 140

Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
145                 150                 155                 160

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
                165                 170                 175

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
            180                 185                 190

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

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
    210                 215                 220
```

```
Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
225                 230                 235                 240


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


Arg Gly Glu Cys
            260


<210>  492
<211>  265
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV04-3001 LC

<400>  492

Gln Gly Gln Ser Gly Ser Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr
1               5                   10                  15


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


Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly
        35                  40                  45


Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
    50                  55                  60


Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly
65                  70                  75                  80


Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
                85                  90                  95


Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg
            100                 105                 110
```

```
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
        115                 120                 125


Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser
    130                 135                 140


Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
145                 150                 155                 160


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                165                 170                 175


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            180                 185                 190


Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        195                 200                 205


Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
    210                 215                 220


Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
225                 230                 235                 240


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


Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210>  493
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV04-3001 LC

<400>  493

Leu His Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly
1               5                   10                  15
```

```
Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly
            20                  25                  30

Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60

Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220
```

```
Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
225                 230                 235                 240


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys



<210>  494
<211>  260
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV06-3001 LC

<400>  494

Gln Gly Gln Ser Gly Ser Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys
1               5                   10                  15


Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly
            20                  25                  30


Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val
        35                  40                  45


Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
    50                  55                  60


Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala
65                  70                  75                  80


Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
                85                  90                  95


Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly
            100                 105                 110
```

```
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
        115                 120                 125


Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe
    130                 135                 140


Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
145                 150                 155                 160


Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
                165                 170                 175


Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
            180                 185                 190


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


Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
    210                 215                 220


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


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


Arg Gly Glu Cys
            260


<210>  495
<211>  254
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV06-3001 LC

<400>  495

Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Gly Gly Gly Ser Ser Gly
1               5                   10                  15
```

```
Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser
            20                  25                  30

Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
        35                  40                  45

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
    50                  55                  60

Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
65                  70                  75                  80

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            100                 105                 110

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
        115                 120                 125

Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
    130                 135                 140

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
145                 150                 155                 160

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
                165                 170                 175

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
            180                 185                 190

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

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
    210                 215                 220
```

```
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
225                 230                 235                 240


Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  496
<211>  265
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV09-3001 LC

<400>  496

Gln Gly Gln Ser Gly Ser Phe Gly Thr Ala Cys Pro Asn His Pro Met
1               5                   10                  15


Cys His Asp Trp Gln Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu
            20                  25                  30


Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly
        35                  40                  45


Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
    50                  55                  60


Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly
65                  70                  75                  80


Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
                85                  90                  95


Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg
            100                 105                 110


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
        115                 120                 125
```

```
Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser
    130                 135                 140


Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
145                 150                 155                 160


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                165                 170                 175


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            180                 185                 190


Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        195                 200                 205


Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
    210                 215                 220


Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
225                 230                 235                 240


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


Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210>  497
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV09-3001 LC

<400>  497

Phe Gly Thr Ala Cys Pro Asn His Pro Met Cys His Asp Trp Gln Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly
            20                  25                  30
```

```
Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60

Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
225                 230                 235                 240
```

```
Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys



<210>  498
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV23-3001 LC

<400>  498

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Leu Tyr Asn Val Cys Leu
1               5                   10                  15


Asp Pro Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro
            20                  25                  30


Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125
```

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  499
<211>  256
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV23-3001 LC

<400>  499

Cys Leu His Ser Leu Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly
            20                  25                  30
```

```
Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
        35                  40                  45

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
    50                  55                  60

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65                  70                  75                  80

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
                85                  90                  95

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            100                 105                 110

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
        115                 120                 125

Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
    130                 135                 140

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190

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

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240
```

```
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  500
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV27-3001 LC

<400>  500

Gln Gly Gln Ser Gly Ser Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser
1               5                   10                  15


Met Cys Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro
            20                  25                  30


Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60


Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140
```

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260


<210>  501
<211>  256
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV27-3001 LC

<400>  501

Gln Pro Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly
            20                  25                  30


Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
        35                  40                  45
```

```
Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
    50                  55                  60

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65                  70                  75                  80

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
                85                  90                  95

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            100                 105                 110

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
        115                 120                 125

Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
    130                 135                 140

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190

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

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 502
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV29-3001 LC

<400> 502

```
Gln Gly Gln Ser Gly Ser Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys
1               5                   10                  15


Ala His Thr Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala
            20                  25                  30


Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser
        35                  40                  45


Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
    50                  55                  60


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


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
                85                  90                  95


Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
            100                 105                 110


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
        115                 120                 125


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
    130                 135                 140


Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
145                 150                 155                 160
```

```
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
                165                 170                 175


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
            180                 185                 190


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
        195                 200                 205


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
    210                 215                 220


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


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


Ser Phe Asn Arg Gly Glu Cys
            260


<210>  503
<211>  257
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV29-3001 LC

<400>  503

Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Ala His Thr Gly Gly Gly
1               5                   10                  15


Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser
            20                  25                  30


Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
        35                  40                  45


Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
    50                  55                  60
```

```
Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln
65                  70                  75                  80

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser
                85                  90                  95

Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
            100                 105                 110

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

Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly
    130                 135                 140

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
145                 150                 155                 160

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                165                 170                 175

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
            180                 185                 190

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

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

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
225                 230                 235                 240

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                245                 250                 255

Cys
```

<210> 504
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV32-3001 LC

<400> 504

```
Gln Gly Gln Ser Gly Ser Cys Pro Asn His Pro Leu Cys His Asp Trp
1               5                   10                  15


Gln Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro
            20                  25                  30


Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


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

```
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
                165                 170                 175


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  505
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV32-3001 LC

<400>  505

Cys Pro Asn His Pro Leu Cys His Asp Trp Gln Gly Gly Gly Ser Ser
1               5                   10                  15


Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60
```

```
Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 506
<211> 261

<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV33-3001 LC

<400> 506

Gln Gly Gln Ser Gly Ser Cys Pro Asn His Pro Met Cys Ala Asp Trp
1 5 10 15

Gln Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro
20 25 30

Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
35 40 45

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
50 55 60

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65 70 75 80

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
85 90 95

Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
100 105 110

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
115 120 125

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
130 135 140

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145 150 155 160

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

```
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190


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


Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
    210                 215                 220


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


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


Asn Arg Gly Glu Cys
            260


<210>  507
<211>  255
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV33-3001 LC

<400>  507

Cys Pro Asn His Pro Met Cys Ala Asp Trp Gln Gly Gly Gly Ser Ser
1               5                   10                  15


Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg
            20                  25                  30


Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
        35                  40                  45


Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
    50                  55                  60


Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65                  70                  75                  80
```

```
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
                85                  90                  95

Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110

Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125

Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190

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

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255
```

<210> 508
<211> 261
<212> PRT
<213> Artificial Sequence

<220>

<223> Spacer - YV35-3001 LC

<400> 508

```
Gln Gly Gln Ser Gly Ser Cys Pro Asn His Pro Met Cys His Asp Ala
1               5                  10                  15


Gln Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro
            20                  25                  30


Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile
        35                  40                  45


Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
    50                  55                  60


Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
65                  70                  75                  80


Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
                85                  90                  95


Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
            100                 105                 110


Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
        115                 120                 125


Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
    130                 135                 140


Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
145                 150                 155                 160


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


Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
            180                 185                 190
```

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

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
210 215 220

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

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

Asn Arg Gly Glu Cys
260

<210> 509
<211> 255
<212> PRT
<213> Artificial Sequence

<220>
<223> YV35-3001 LC

<400> 509

Cys Pro Asn His Pro Met Cys His Asp Ala Gln Gly Gly Gly Ser Ser
1 5 10 15

Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg
20 25 30

Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro
35 40 45

Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
50 55 60

Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
65 70 75 80

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala
85 90 95

```
Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
            100                 105                 110


Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
        115                 120                 125


Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys
    130                 135                 140


Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
145                 150                 155                 160


Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                165                 170                 175


Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            180                 185                 190


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


Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
    210                 215                 220


Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
225                 230                 235                 240


Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250                 255


<210>  510
<211>  263
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-3001 LC

<400>  510
```

```
Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                  10                  15

Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala
            20                  25                  30

Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser
        35                  40                  45

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
    50                  55                  60

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
                85                  90                  95

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
            100                 105                 110

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
        115                 120                 125

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
    130                 135                 140

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
145                 150                 155                 160

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
                165                 170                 175

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
            180                 185                 190

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
        195                 200                 205
```

```
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
    210                 215                 220


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


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


Ser Phe Asn Arg Gly Glu Cys
            260


<210>  511
<211>  257
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV39-3001 LC

<400>  511

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


Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser
            20                  25                  30


Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
        35                  40                  45


Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
    50                  55                  60


Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln
65                  70                  75                  80


Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser
                85                  90                  95


Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
            100                 105                 110
```

```
Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val
        115                 120                 125


Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly
    130                 135                 140


Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
145                 150                 155                 160


Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                165                 170                 175


Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
            180                 185                 190


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


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


Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
225                 230                 235                 240


His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                245                 250                 255


Cys
```

<210> 512
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV41-3001 LC

<400> 512

```
Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                  10                  15

Cys Pro Ala Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala
            20                  25                  30

Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser
        35                  40                  45

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
    50                  55                  60

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
                85                  90                  95

Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
            100                 105                 110

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
        115                 120                 125

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
    130                 135                 140

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
145                 150                 155                 160

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
                165                 170                 175

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
            180                 185                 190

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
        195                 200                 205
```

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
210 215 220

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

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

Ser Phe Asn Arg Gly Glu Cys
260

<210> 513
<211> 257
<212> PRT
<213> Artificial Sequence

<220>
<223> YV41-3001 LC

<400> 513

Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Ala Gly Gly Gly
1 5 10 15

Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser
20 25 30

Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln
35 40 45

Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
50 55 60

Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln
65 70 75 80

Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser
85 90 95

Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
100 105 110

```
Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val
        115                 120                 125


Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly
    130                 135                 140


Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
145                 150                 155                 160


Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                165                 170                 175


Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
            180                 185                 190


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


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


Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
225                 230                 235                 240


His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                245                 250                 255


Cys
```

<210> 514
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV51-3001 LC

<400> 514

```
Gln Gly Gln Ser Gly Ser Phe Gly Ala Ala Cys Pro Asn His Pro Ile
1               5                   10                  15


Cys His Asp Trp Gln Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu
            20                  25                  30


Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly
        35                  40                  45


Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
    50                  55                  60


Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly
65                  70                  75                  80


Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
                85                  90                  95


Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg
            100                 105                 110


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
        115                 120                 125


Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser
    130                 135                 140


Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
145                 150                 155                 160


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                165                 170                 175


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            180                 185                 190


Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        195                 200                 205
```

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
210 215 220

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
225 230 235 240

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

Thr Lys Ser Phe Asn Arg Gly Glu Cys
260 265

<210> 515
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> YV51-3001 LC

<400> 515

Phe Gly Ala Ala Cys Pro Asn His Pro Ile Cys His Asp Trp Gln Gly
1 5 10 15

Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly
20 25 30

Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
35 40 45

Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
50 55 60

Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65 70 75 80

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
85 90 95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
100 105 110

```
Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125


Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140


Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175


Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190


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


Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220


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


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys



<210>  516
<211>  265
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV52-3001 LC

<400>  516
```

```
Gln Gly Gln Ser Gly Ser Phe Gly Ala Ala Cys Pro Asn His Pro Leu
1               5                   10                  15


Cys His Asp Trp Gln Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu
            20                  25                  30


Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly
        35                  40                  45


Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
    50                  55                  60


Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly
65                  70                  75                  80


Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
                85                  90                  95


Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg
            100                 105                 110


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
        115                 120                 125


Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser
    130                 135                 140


Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
145                 150                 155                 160


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                165                 170                 175


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            180                 185                 190


Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        195                 200                 205
```

```
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
    210                 215                 220


Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
225                 230                 235                 240


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


Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210>  517
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV52-3001 LC

<400>  517

Phe Gly Ala Ala Cys Pro Asn His Pro Leu Cys His Asp Trp Gln Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly
            20                  25                  30


Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95


Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110
```

```
Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125


Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140


Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175


Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190


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


Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220


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


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys
```

<210> 518
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV53-3001 LC

<400> 518

```
Gln Gly Gln Ser Gly Ser Phe Gly Ala Ala Cys Pro Asn His Pro Met
1               5                   10                  15


Cys His Asp Ala Gln Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu
            20                  25                  30


Leu Ala Pro Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly
        35                  40                  45


Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
    50                  55                  60


Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly
65                  70                  75                  80


Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
                85                  90                  95


Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg
            100                 105                 110


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
        115                 120                 125


Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser
    130                 135                 140


Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
145                 150                 155                 160


Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
                165                 170                 175


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
            180                 185                 190


Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
        195                 200                 205
```

```
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
    210                 215                 220


Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
225                 230                 235                 240


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


Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210>  519
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV53-3001 LC

<400>  519

Phe Gly Ala Ala Cys Pro Asn His Pro Met Cys His Asp Ala Gln Gly
1               5                   10                  15


Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly
            20                  25                  30


Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80


Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95


Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110
```

```
Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125


Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140


Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175


Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190


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


Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220


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


Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255


Gly Glu Cys
```

<210> 520
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer - YV54-3001 LC

<400> 520

```
Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Ala Cys Leu
1               5                  10                  15

Asp Pro Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro
            20                  25                  30

Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205
```

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
210 215 220

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

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

Phe Asn Arg Gly Glu Cys
260

<210> 521
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> YV54-3001 LC

<400> 521

Cys Leu His Ser Ala Tyr Asn Ala Cys Leu Asp Pro Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly
20 25 30

Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
35 40 45

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
50 55 60

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65 70 75 80

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
85 90 95

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
100 105 110

```
Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
        115                 120                 125


Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
    130                 135                 140


Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160


Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175


Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190


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


Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220


Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240


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


<210>  522
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV55-3001 LC

<400>  522

Gln Gly Gln Ser Gly Ser Cys Ala His Ser Ala Tyr Asn Val Cys Leu
1               5                   10                  15
```

```
Asp Pro Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro
            20                  25                  30

Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220
```

```
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
225                 230                 235                 240


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


Phe Asn Arg Gly Glu Cys
            260


<210>  523
<211>  256
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV55-3001 LC

<400>  523

Cys Ala His Ser Ala Tyr Asn Val Cys Leu Asp Pro Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly
            20                  25                  30


Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
        35                  40                  45


Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
    50                  55                  60


Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65                  70                  75                  80


Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
                85                  90                  95


Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            100                 105                 110


Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
        115                 120                 125
```

```
Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
    130                 135                 140

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190

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

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240

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


<210>  524
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV56-3001 LC

<400>  524

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Val Cys Ala
1               5                   10                  15

Asp Pro Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro
            20                  25                  30
```

```
Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
225                 230                 235                 240
```

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

Phe Asn Arg Gly Glu Cys
260

<210> 525
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> YV56-3001 LC

<400> 525

Cys Leu His Ser Ala Tyr Asn Val Cys Ala Asp Pro Gly Gly Gly Ser
1 5 10 15

Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly
20 25 30

Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
35 40 45

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
50 55 60

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65 70 75 80

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
85 90 95

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
100 105 110

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
115 120 125

Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
130 135 140

```
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160


Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175


Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190


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


Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220


Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240


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


<210>  526
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV57-3001 LC

<400>  526

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Val Cys Leu
1               5                   10                  15


Ala Pro Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro
            20                  25                  30


Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45
```

```
Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95

Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220

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

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

Phe Asn Arg Gly Glu Cys
            260

<210> 527
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> YV57-3001 LC

<400> 527

Cys Leu His Ser Ala Tyr Asn Val Cys Leu Ala Pro Gly Gly Gly Ser
1   5   10   15

Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly
            20   25   30

Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
        35   40   45

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
    50   55   60

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65   70   75   80

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
                85   90   95

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            100   105   110

Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
        115   120   125

Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
    130   135   140

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145   150   155   160

```
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175


Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190


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


Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220


Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240


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


<210>  528
<211>  262
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV58-3001 LC

<400>  528

Gln Gly Gln Ser Gly Ser Cys Leu His Ser Ala Tyr Asn Val Cys Leu
1               5                   10                  15


Asp Ala Gly Gly Gly Ser Ser Gly Gly Ala Val Gly Leu Leu Ala Pro
            20                  25                  30


Pro Gly Gly Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser Glu
        35                  40                  45


Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
    50                  55                  60
```

```
Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr
65                  70                  75                  80


Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                85                  90                  95


Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
            100                 105                 110


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
        115                 120                 125


Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp
    130                 135                 140


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
145                 150                 155                 160


Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                165                 170                 175


Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            180                 185                 190


Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        195                 200                 205


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    210                 215                 220


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


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


Phe Asn Arg Gly Glu Cys
            260
```

<210> 529
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> YV58-3001 LC

<400> 529

```
Cys Leu His Ser Ala Tyr Asn Val Cys Leu Asp Ala Gly Gly Gly Ser
1               5                   10                  15


Ser Gly Gly Ala Val Gly Leu Leu Ala Pro Pro Gly Gly Leu Ser Gly
            20                  25                  30


Arg Ser Asp Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser
        35                  40                  45


Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
    50                  55                  60


Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
65                  70                  75                  80


Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg
                85                  90                  95


Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            100                 105                 110


Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr
        115                 120                 125


Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr
    130                 135                 140


Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
145                 150                 155                 160


Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
                165                 170                 175
```

```
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
            180                 185                 190


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


Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
    210                 215                 220


Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
225                 230                 235                 240


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


<210>  530
<211>  259
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Spacer - YV39-NSUB LC

<400>  530

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1               5                   10                  15


Cys Pro Tyr Gly Gly Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
            20                  25                  30


Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Glu Ile Val Leu
        35                  40                  45


Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr
    50                  55                  60


Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp
65                  70                  75                  80
```

```
Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
                85                  90                  95

Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser
            100                 105                 110

Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe
        115                 120                 125

Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly
    130                 135                 140

Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
145                 150                 155                 160

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                165                 170                 175

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            180                 185                 190

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

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    210                 215                 220

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

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                245                 250                 255

Gly Glu Cys
```

<210> 531
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> YV39-NSUB LC

<400> 531

```
Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu Cys Pro Tyr Gly Gly Gly
1               5                   10                  15


Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly
            20                  25                  30


Gly Gly Ser Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45


Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60


Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80


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


Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110


Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125


Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140


Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
145                 150                 155                 160


Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                165                 170                 175


Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            180                 185                 190
```

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


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


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
225                 230                 235                 240


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                245                 250


<210>  532
<211>  2
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Linkers


<220>
<221>  MISC_FEATURE
<222>  (1)..(2)
<223>  sequence may be repeated any number of times

<400>  532

Gly Ser
1


<210>  533
<211>  3
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Linkers


<220>
<221>  MISC_FEATURE
<222>  (1)..(3)
<223>  sequence may be repeated any number of times
```

<400> 533

Gly Gly Ser
1

<210> 534
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> sequence may be repeated any number of times

<400> 534

Gly Ser Gly Gly Ser
1   5

<210> 535
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<220>
<221> MISC_FEATURE
<222> (1)..(4)
<223> sequence may be repeated any number of times

<400> 535

Gly Gly Gly Ser
1

<210> 536
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> Linkers

<400> 536

Gly Gly Ser Gly
1

<210> 537
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<400> 537

Gly Gly Ser Gly Gly
1   5

<210> 538
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<400> 538

Gly Ser Gly Ser Gly
1   5

<210> 539
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<400> 539

Gly Ser Gly Gly Gly
1   5

<210> 540
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<400> 540

Gly Gly Gly Ser Gly
1   5

<210> 541
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<400> 541

Gly Ser Ser Ser Gly
1   5

<210> 542
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<400> 542

Gly Gly Gly Ser Ser Gly Gly Ser
1   5

<210> 543
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Linkers

<400> 543

Gly Gly Gly Ser
1

<210> 544
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 544

Gln Gly Gln Ser Gly Gln Gly
1   5

<210> 545
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 545

Gly Gln Ser Gly Gln Gly
1   5

<210> 546
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 546

Gln Gly Gln Ser Gly Ser
1   5

<210> 547
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 547

Gln Gly Gln Ser Gly Gln
1   5

<210> 548
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 548

Gln Ser Gly Gln Gly
1   5

<210> 549
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 549

Gly Gln Ser Gly Ser
1   5

<210> 550
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 550

Gln Gly Gln Ser Gly
1   5

<210> 551
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 551

Ser Gly Gln Gly
1

<210> 552
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 552

Gln Ser Gly Ser
1

<210> 553
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer

<400> 553

Gln Gly Gln Ser
1

<210> 554
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<220>
<221> MISC_FEATURE
<222> (1)..(2)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (4)..(6)
<223> Xaa can be any amino acid

<400> 554

Xaa Xaa Cys Xaa Xaa Xaa Met Tyr Gly Tyr Asn Leu Cys Pro Tyr
1   5   10   15

<210> 555
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence

<220>
<221> MISC_FEATURE
<222> (1)..(3)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be any amino acid

<400> 555

Xaa Xaa Xaa Cys Xaa His Ser Met Tyr Asn Val Cys Leu Asp Pro
1   5   10   15

<210> 556
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Spacer-YV39

<400> 556

Gln Gly Gln Ser Gly Ser Cys Arg Thr Gln Leu Tyr Gly Tyr Asn Leu
1   5   10   15

Cys Pro Tyr

<210> 557
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 HC for Ipilimumab

<400> 557

Ser Tyr Thr Met His
1   5

<210> 558
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 HC for Ipilimumab

<400> 558

Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1   5   10   15

Gly

<210> 559
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 HC for Ipilimumab

<400> 559

Thr Gly Trp Leu Gly Pro Phe Asp Tyr
1   5

<210> 560
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1 LC for Ipilimumab

<400> 560

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala
1   5   10

<210> 561
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2 LC for Ipilimumab

<400> 561

Gly Ala Phe Ser Arg Ala Thr
1   5

<210> 562
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3 LC for Ipilimumab

<400> 562

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1   5

<210> 563
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> YV39-2001 VL

<400> 563

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

```
Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
            20                  25                  30


Asn His Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45


Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60


Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80


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


Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110


Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125


Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140


Ile Lys
145


<210>  564
<211>  146
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV39-2011 VL

<400>  564

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


Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp
            20                  25                  30
```

```
Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45


Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60


Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80


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


Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110


Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125


Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140


Ile Lys
145


<210>  565
<211>  146
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  YV39-2012 VL

<400>  565

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


Ser Ser Gly Gly Ser Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Ala
            20                  25                  30
```

```
Asn Pro Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr
        35                  40                  45


Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
    50                  55                  60


Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
65                  70                  75                  80


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


Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            100                 105                 110


Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln
        115                 120                 125


Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    130                 135                 140


Ile Lys
145


<210>  566
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  MM Consensus Sequence 1


<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  Xaa can be L, M, V or T

<220>
<221>  MISC_FEATURE
<222>  (4)..(4)
<223>  Xaa can be S, V or I

<220>
```

<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be F, L, M or A

<220>
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Cys Xaa Tyr Xaa Xaa Xaa Asn Xaa Cys Leu Asp Pro
1 5 10

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Cys Ala Gln Met Tyr Gly Tyr Ser Met Cys Xaa Xaa Thr
1 5 10

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Cys Xaa Xaa Xaa Xaa Tyr Gly Xaa Xaa Leu Cys Pro Xaa
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<400> 569

Xaa Xaa Cys Pro Xaa His Pro Xaa Cys Xaa Asp Xaa
1   5   10

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Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1   5   10